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Mathematical modeling of the effect of seasonal weather variations on the dynamics of plague disease

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MATHEMATICAL MODELING OF THE EFFECT OF SEASONAL WEATHER VARIATIONS ON THE DYNAMICS OF PLAGUE DISEASE

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ABSTRACT

A mathematical model to study the effect of seasonal weather variation on the dynamics of plague disease is developed and analyzed. Apart from being historical, plague disease caused by a gram negative bacteria called *Yersinia pestis* is still considered as a major threat around the world. In this work we investigate three main forms of plague disease which are bubonic, septicemic and pneumonic plague. It gives answers to various questions that relate to the complex dynamics of plague disease and the effect of seasonal weather variation in its transmission and spread. In particular we give answers to mainly four questions pertaining to the formulation and analyses of the mathematical models of bubonic Plague, formulation and analysis of the mathematical models of pneumonic plague, formulation and analysis of the combined mathematical model for the dynamics of plague disease that includes all three forms of plague disease and all major ways/modes of plague disease transmission. Lastly we formulate and analyze the plague disease model incorporating parameters that are affected by seasonal weather variation and study its effects on the dynamics of plague disease.

Using ordinary differential equations, we formulate a model for the dynamics of plague disease in four settings namely: Human beings, Rodents, Fleas and Pathogens in the environment. We compute the basic reproduction numbers and apply them to establish the conditions for local and global stability of both disease free and endemic equilibrium points. We further assess the effect of seasonal weather variation, in which we modify the transmission rates and take them as sinusoidal functions. Using fundamental existence-uniqueness theorem, we were able to prove the existence of positive periodic solutions. We then establish the conditions for local and global stability of both Positive Periodic Solution (PPS) and Disease Free Solution (DFS).

The results show that the transmission and dynamics of bubonic plague are dictated by: the rate at which fleas get infected; the infectious periods of fleas, rodents and human beings; the probability that rodents and human beings survive the infected class; and the adequacy of contact rates and the rate at which human beings and rodents become exposed to bubonic plague disease. We also found that the environment condition, the abundance of pathogens in the environment and the increase of the number of individuals with pneumonic plague greatly influence the increase of pneumonic plague disease infectives. In the combined model, we found that the variation in number of plague disease cases mainly depend on: the transmission rate of infection from one individual to another; the incubation period of an individual and the time that an individual remains infectious. The analysis further reveals that the effects posed by seasonal weather variation depends on the extent to which the weather variation favours the transmission of plague disease (amplitude of seasonality) and the duration that it remains in favour of the increase or decrease of the rate of disease transmission and spread. Therefore the control strategies should target these factors and parameters (the transmission rate of infection

from one individual to another, the incubation period of an individual and the time that an individual remains infectious) that according to our results stated above have shown to have a significant effect on the dynamics of plague disease.

We thus recommend to the government, national security system and other health stake holders that in order to have an effective way of controlling the disease we must ensure that there is provision of education on plague disease infection, transmission and spread to raise peoples awareness, continuous monitoring of factors that may lead to plague outbreak, easy access of plague disease treatment for all and the strong collaboration with neighboring countries on health related issues.

DECLARATION

I, Rigobert Charles Ngeleja do hereby declare to the Senate of Nelson Mandela African Institution of Science and Technology that this dissertation is my own original work and that it has neither been submitted nor being concurrently submitted for degree award in any other institution.

Rigobert Charles Ngeleja, PhD candidate — **Date** 8/3/2019

The above declaration is confirmed

Prof. Livingstone S. Luboobi, Principal Supervisor — **Date** 8th March 2019

Prof. Verdiana Masanja, Internal Supervisor — **Date** 11th March 2019

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CERTIFICATION

The undersigned certify that they have read and found the dissertation acceptable by the Nelson Mandela African Institution of Science and Technology.

Prof. Livingstone S. Luboobi, Principal Supervisor

8th March 2019

Date

Prof. Verdiana Masanja, Internal Supervisor

11th March 2019

Date

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DEDICATION

I dedicate this work to my entire family, especially to my beloved son Kelvin, my late parents Mr. & Mrs. Charles Ngeleja, my lovely sister Bernadetha and my brothers for their unconditional love, moral, psychological, spiritual and material support.

I also dedicate this work to all my colleagues and friends who stood by me in times of difficulty especially when things seemed impossible. I appreciate all their love and effort.

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LIST OF ABBREVIATIONS

DFE	Disease Free Equilibrium
EE	Endemic Equilibrium
DFS	Disease Free Solution
Y. Pestis	Yersinia pestis
WHO	World Health Organization
NM-AIST	Nelson Mandela African Institution of Science and Technology
PPS	Positive Periodic Solution

CHAPTER ONE
Introduction

1.1 Background

In recent years, the issue of emerging and re-emerging infectious diseases has progressively become of great concern in public health (Watch, 2014, accessed March 14, 2016). These days Infectious diseases threaten us with the fear of death which as a result dictate social behaviors and policy decisions at individual, national and international levels (Aginam, 2005). Most of the infectious diseases like plague, HIV, Ebola haemorrhagic fever, Marburg fever and others are evolving at an extraordinary rate, often with the ability to cross geographical borders rapidly and spread (Liu *et al.*, 2014). This makes infectious diseases a global concern as they pose universal vulnerability, which call for a global solidarity to plan for the way forward to a better future.

The exceedingly itinerant, mutually dependent and interconnectedness that characterize the world today, pave a way to numerous opportunities for the rapid spread of infectious diseases. The spread of infectious diseases nowadays is much faster compared to other times in history (Tatem *et al.*, 2006). Due to human mobility today, it is said that if there is an outbreak or epidemic in any one part of the world, it is only a few hours away from becoming a pending threat somewhere else (Newman, 2002). In addition, the zoonotic nature of most of the pathogens and ability of viruses, bacteria and parasites to change over time makes the infectious diseases very difficult to combat. That is why, despite the magnificent growth of antibiotics and vaccines, infectious diseases are still reported as the second leading cause of death worldwide next to cardiovascular diseases (Fauci *et al.*, 2005; Bennett *et al.*, 2014).

Plague is a zoonotic infection and serious bacterial disease that can be deadly. The disease is caused by bacteria called *Yersinia pestis* a pleomorphic, gram-negative non-spore-forming coccobacillus that is more accurately classified as a subspecies of Y pseudotuberculosis, named after the French-Swiss bacteriologist Alexandre Yersin. These bacteria are found in animals throughout the world. They mainly infect rats and other rodents which are the prime reservoirs for the bacteria. Due to the unrivaled scale of death and devastation it brought, plague disease remains to be notorious and a threat to human societies throughout history (Jackson, 1916; Devaux, 2013).

1.1.1 Historical background of Plague disease

Plague disease has an extraordinary place in history. It led to mammoth effects on the development of modern civilization. Due to the fact that the causes of plague disease were unknown it presented a disaster for people in different parts of the world which contributed to enormous fear in areas where it appeared (Benedictow, 2004; CDC, accessed January 10, 2016). There have been three great world pandemics of plague disease that caused devastating mortality of people and animals across the globe.

The first undeniable great pandemic of plague disease is the Great Plague of Justinian that occurred around AD 532 in Egypt and spread through the Middle East and the Mediterranean basin and then spread farther to Turkey, Constantinople, Greece, Italy, and the territories of France and Germany (Zietz and Dunkelberg, 2004). It is estimated that between 50% and 60% of the total population in North Africa, Europe, and central and southern Asia was lost (Perry and Fetherston, 1997)

After the first great pandemic, many other smaller outbreaks followed for the following two centuries; thus linking the first and second great pandemics of plague (Prasad, 2009). The second plague disease pandemic, also known as the Black Death or Great Pestilence, occurred in 1334 in different cities of China and India (Ziegler, 2013). The disease was spread to different places by the infected rodents and human, and from country to country by ships. It killed nearly 20 to 30 million people in Europe which was equivalent to more than one third of the European population at that time (Slack, 1989).

The third and last great plague pandemic occurred in Canton and Hong Kong in 1894. Just after the occurrence of the third pandemic, different countries started to investigate the origin of the disease and how to get rid of it. Among them was Japan and France that dispatched a commission including the bacteriologist Shibasaburo Kitasato and Alexandre Yersin respectively (Riedel, 2005). They ultimately identified a new bacterium from tissues found from dead rodents and human beings. Although it is possible that Kitasato was the first to describe the new organism, Yersin's description and explanations seemed to be more accurate, with all striking characteristics of the disease emphasized (Treille and Yersin, 1894). This is the reason why in 1970, the bacteria causing plague disease was named Yersinia pestis as a recognition of his significant contribution (Perry and Fetherston, 1997).

Since its discovery in the 16 century AD in Egypt and then other parts of the world e.g. Syria, North Africa, and much of Europe, Plague still exists in different parts of the world. It is widely distributed in the tropics and subtropics and in warmer areas of temperate countries. However,

most of the plague cases today occur in Africa as most of her people do not have access to antibiotics. The reported plague cases in sub-Saharan Africa and Madagascar, account for over 95% of all reported cases (Stenseth *et al.*, 2008). For instance in 2003 there were about 2,100 human cases and 180 deaths mostly in Africa. Also in 2006 at least 50 people died due to plague disease in the Democratic Republic of the Congo in Central Africa (Meerburg *et al.*, 2009). Until June 2007, plague was one of the three epidemic diseases specifically reportable to the World Health Organization (the other two being cholera and yellow fever) (Dennis and Staples, 2009; Society, accessed May 02, 2016).

In East Africa, the first outbreak is said to have occurred in Mombasa, Kenya in 1697 from Oman (Neerinckx *et al.*, 2010; Ziwa *et al.*, 2013). However, the earliest plague infection in East Africa was recorded in Uganda in 1877. The outbreak was reported by missionaries who also noted that the disease was already locally known by the Buganda people as "kawumpuli" (Orochi Orach, 2002; Eisen *et al.*, 2010). In Tanzania, Plague disease is informally believed to have been introduced from Middle East or India by various traders and slaves from Egypt and Saudi Arabia (Laudisoit *et al.*, 2007). However, historical data shows that there is a possibility that plague already existed in the Kagera area long before the 1887 outbreak. The local people were already aware of the disease and referred to it as a sporadic disease, locally known as "rubunga" (Kilonzo *et al.*, 2005). Figure 1 depicts the plague introduction and spread in Tanzania:

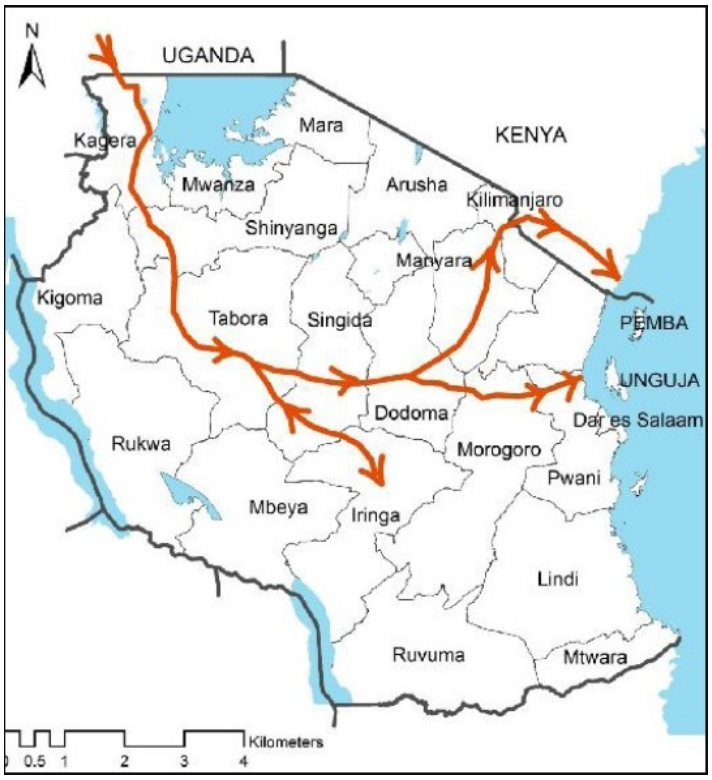


Figure 1: Plague introduction and spread in Tanzania (Ziwa *et al.*, 2014)

1.2 Epidemiology of plague disease

Plague bacteria in most cases are transmitted through the bite of an infected flea. When plague affect non-human animals (epizootics), specifically rodents in a particular area, causes massive loss of rodents. This cause hungry fleas to find other sources of blood. When human beings and other animals visit places where rodents have recently died from plague are at risk of being plague infectives as a result of flea bites (Benedictow, 2004). Mice, rats, rabbits, squirrels, chipmunks, prairie dogs and other domestic animals may also bring plague-infected fleas into the home. The study by Scott and Duncan (2001) postulates that transmission of the plague to people can also occur from eating infected animals such as squirrels and other infected domestic animals. Once an individual has the plague bacteria in his/her lungs, depending on the sanitary conditions, the bacteria can be spread via aerosol droplets. Other ways are by direct contact and contacting the contaminated undercooked food or materials. Below is the summary of the different modes of transmission of plague diseases:

(i) **Direct physical contact:** Touching an infected person, including sexual contact;

(ii) **Vector borne transmission:** Carried by insects; the Flea in particular;

(iii) **Airborne transmission:** droplet contact via coughing or sneezing on another person, – if the microorganism can remain in the air for long periods;

(iv) **Indirect contact:** by eating infected animals, touching contaminated soil or a contaminated surface, fecal-oral transmission – usually from contaminated food or water sources.

1.2.1 Forms of Plague disease

Plague disease may occur in different forms; however there are three main forms of plague disease. These forms differ in their symptoms, way they are transmitted, parts of the body that they affect and severity of the infection (Crook and Tempest, 1992; Burkle *et al.*, 1973). These forms are as given below:

(i) **Bubonic Plague**

The most common form of plague is bubonic plague. It is usually contracted when an infected flea bites a susceptible individual (human beings, rodents or other domestic animals). In rare cases, one can get the bacteria causing bubonic plague disease from material that has come into contact with an infected individual. Bubonic plague infect lymphatic system (immune system), causing inflammation of lymphoid organs such as the spleen

and the thymus. If not treated bubonic plague, can move into the bloodstream and cause septicemic plague, or to the lungs, causing pneumonic plague.

Bubonic Plague Symptoms: Symptoms of bubonic plague generally appear within two to seven days and include: Fever and chills, headache, muscle pain, general weakness and seizures. One may also experience painful swollen lymph glands called buboes, which appear in the groin, armpits, neck, or site of the insect bite or scratch. The buboes are what give bubonic plague its name.

(ii) **Pneumonic Plague**

It is the serious form of the plague disease which occur when the bacteria multiply in the lungs. It can be transmitted through airborne transmission in which, a susceptible individuals with lungs breath in the air containing bacteria. When a person with pneumonic plague coughs, the bacteria from their lungs are expelled into the air. Depending on the weather condition these released bacteria may stay infectious in the air for a very long time.

Pneumonic Plague Symptoms: Pneumonic plague symptoms may appear as quickly as one day after exposure to the bacteria and include: difficulty with breathing, chest pain, cough, fever, headache, overall weakness and bloody sputum (saliva and mucus or pus from the lungs).

(iii) **Septicemic Plague**

This form of the plague disease occurs when the bacteria multiply in the bloodstream. It can be transmitted through physical contact that involves touching the infected individual including sexual contact, bite by the infected flea, eating the infected animals, touching contaminated soil or a contaminated surface and fecal-oral transmission. Untreated septicemic plague may graduate to pneumonic plague.

Septicemic Plague Symptoms: Symptoms usually start within two to seven days after exposure. Septicemic plague can lead to death before symptoms even appear. Symptoms includes: abdominal pain, diarrhea, nausea and vomiting, fever and chills, weakness, bleeding (blood may not be able to clot) and shock.

Without medical intervention, about 50 percent of people who have bubonic and septicemic plague and almost 100 percent of people with pneumonic plague die. Treatment reduces the death rate to 50 percent for both varieties (Antolin *et al.*, 2002). Plague can lead to gangrene if blood vessels in an individual's fingers and toes disrupt blood flow and cause death to tissue. In rare cases, plague can cause an inflammation of membranes that surround an individual's spinal cord and brain known as meningitis.

Plague outbreaks are most common in rural areas and in areas characterized by overcrowding, poor sanitation and a large rat population. In human beings the risk of developing plague depends on one's lifestyle and the surrounding environment (Inglesby *et al.*, 2000). For example, the nature of occupation one has may increase the risk of getting plague disease. Veterinarians and their assistants have a higher risk, as most of their time they work close to animals which may have been infected with plague bacteria. Hobbies like camping, hunting or hiking in areas where there are animals that are infected can increase one's risk of being bitten by an infected flea or contacting with the contaminated materials or environment (Poland and Dennis, 1998). Other factors that may also increase risk of plague disease infection transmission are pet ownership, direct contact with animal-reservoir especially during the hunting season and living in one house with an infected individual (Cleri *et al.*, 1997).

Despite being a historical disease, plague disease continues to be a threat and is endemic in many natural foci around the world. Using the data from WHO there are approximately 1000 - 3000 cases per year of the plague disease, distributed mostly between Africa, South America and Asia. Recent outbreaks have justified that plague disease may reoccur in areas that have long remained silent (Andrianaivoarimanana *et al.*, 2013). This behavior makes plague a global and all time threat that should be prioritized and given a special attention by all health stake holders around the world.

1.3 Plague disease as bio-weapon

Throughout history, plague disease has been one of the most shocking epidemic diseases to mankind (Morens *et al.*, 2008). The vast transmission capability, the capacity for mass production, aerosol dissemination, high fatality rate and the potential for rapid secondary spread, makes plague disease as very devastating infectious disease and gives it a great potential of being used as a bio-weapon (Meyer *et al.*, 2014; Balali-Mood *et al.*, 2013). In 20th century, countries including the United States, Japan and Rusia (the former Soviet Union,) industrialized ways for using plague bacteria as a weapon (Borio, 2005). This has raised concern and it is now considered as a very important national security threat as it can be used by terrorists (Nikoleli *et al.*, 2016). As a bio-weapon, plague disease may be applied through different warfare strategies that includes catapulting corpses over walls, dropping infected fleas from airplanes and aerosolizing the bacteria (Riedel, 2004).

The threat posed by plague disease as bio-weapon depends on the number of biological agent released for an attack and the environmental conditions. Yersinia pestis has an extraordinary ability to overcome the defense mechanisms of mammalian hosts and to devastate them with

enormous growth (Cornelis, 2000). When plague disease is used as a weapon, the infection would differ significantly from the one that occurs naturally. For example when the bacteria are to be released as an aerosol will result to pneumonic plague and the symptoms may be serious as those of the severe respiratory infections (Pechous *et al.*, 2016).

1.4 Plague disease and Weather Variation

The combined effects of rapid demographic change, environmental, social, technological and others that we experience today, dictates our ways-of-living. This also consequently affect the dynamics, occurrence and the re-occurrence of infectious diseases which challenge the traditional plans and strategies to control infectious diseases (Patz *et al.*, 2000). Weather variation affect most of the important determinants of plague disease transmission (Xu *et al.*, 2011; Parham *et al.*, 2011; Altizer *et al.*, 2013). These include rodent's, pathogen's and flea's survival, reproduction and death rates, the flea's biting rate, the pathogen's incubation rate within flea and human being, rodent and flea immigration rates (Gubler *et al.*, 2001). Others are: Flea, pathogens and hosts (human beings, rodents and other domestic animals) each survive and reproduce within a range of optimal weather conditions. We consider temperature, humidity, rainfall and precipitation as the most important weather elements that affects the transmission of plague disease. The effect posed by these elements of weather affect to a great extent the plague disease cycle and as a result affect the transmission and spread of plague disease (Relman *et al.*, 2008).

1.5 Motivation of the Study

Different studies have been carried out with the aim of understanding the plague disease in terms of the factors that led to the occurrence of the disease and its dynamics. The aim is to develop proper ways of controlling and overcoming the epidemic when it occurs. However, most of these studies considered vector borne transmission as the only way of transmission of plague and did not consider other major modes of transmission through direct physical contact, airborne transmission and indirect contact.

There are few studies that considered other agents apart from the vector flea in plague transmission but most of them did not consider the enzootic cycles in non-human hosts, and for those that did they assumed non-human hosts as being incapable of transmitting plague disease. Most studies consider non-human hosts as a reservoir of the Yersinia pestis that will be taken to human beings through a vector flea. Moreover, although most of the parameters that dictate the

transmission and spread of plague disease are affected by seasonal weather variation, available studies have not exhaustively analyzed mathematically the effect of seasonal weather variation in the dynamics of plague disease. It is then extremely important to study dynamics of plague disease that includes the parameters that are affected by of seasonal weather variation.

Even though the number of human infected by plague disease is not high, it would be a blunder to ignore the menace posed to humanity, because of the disease inherent communicability, rapid spread, rapid clinical course, and high mortality if left untreated (Mack *et al.*, 2008). It is then wise to have a comprehensive study in terms of occurrence, transmission and spread for the design of proper control strategies, effective plans to reduce its impact and ultimately eradicate the disease. Regardless of the available studies and findings on plague disease the disease still exist and kills millions of people and animal around the world. This justifies that there is a strong need of a study that will address the disease by covering some of the missing aspects.

1.6 Statement of the problem

Available studies lack one or more of the following: most of them considered vector borne transmission as the only way of transmission of plague, did not consider non-human hosts as potential agents of plague transmission, the role of environment in the transmission and spread of plague disease. In this study, we explore the mathematical modeling of the dynamics of the plague infections. We consider human host, non-human host and environment as plague disease transmission agents. We consider possible ways/modes of transmission of plague disease which are mainly direct physical contact, vector borne transmission, airborne transmission and indirect contact with respect to the features of the form of plague disease one has. We also extend our study to cover the effect of the parameters that may be affected by seasonal weather variation on the dynamics of the plague disease. We then develop a generic plague model (the model that combine all three forms of plague disease) that considers all factors that enable plague disease transmission including that of seasonal weather variation in order to extensively understand the dynamic of plague disease. We analyze the model to explain the conditions for existence, persistent and extinction of the disease, the stability and existence of positive periodic solution, disease-free equilibrium and the system's behavior through numerical simulation.

1.7 Research Objective

In order to answer the stated problem we set the general objective, specific objectives and research questions as given below:

1.7.1 General Objective

The main objective of this study was to develop a fully bodied mathematical models to study the dynamics of plague disease, and asses the effect of seasonal weather variations on its transmission.

1.7.2 Specific Objectives

The specific objectives of this study were:

(i) To formulate and analyze basic mathematical models for bubonic plague dynamics and explore its behavior using numerical simulations

(ii) To formulate and analyze basic mathematical models for pneumonic plague dynamics and explore its behavior using numerical simulations.

(iii) To formulate and analyze the basic combined deterministic mathematical model for the dynamics of plague disease that will include all three forms of plague disease and all major ways/modes of plague disease transmission

(iv) To formulate and analyze the plague disease model incorporating with parameters that are affected by seasonal weather variation.

1.7.3 Research Questions

The study was guided by the following research questions:

(i) What are the modes of interspecies transmission of bubonic, pneumonic and Septicemic plague disease?

(ii) How can the mathematical model for dynamic of bubonic plague disease be formulated?

(iii) How can the mathematical model for dynamic of bubonic plague and pneumonic plague disease be formulated?

(iv) How can the combined deterministic mathematical model for the dynamics of plague disease that will include all three forms of plague disease and all major ways/modes of plague disease transmission be formulated?

(v) What seasonal factors affect the dynamics and transmission and of plague disease?

(vi) How can the mathematical model that includes the effect of seasonal variation in the dynamics of plague disease be formulated?

(vii) Are the equilibrium points of the formulated models locally and globally asymptotically stable?

(viii) Under what conditions does the endemic equilibrium (EE) exist?

(ix) Under what conditions does the positive periodic solution exist?

1.8 Structure of the Dissertation

The dissertation involves several phases of analysis which are organized in chapters as follows:

Chapter 2: In this chapter, we study the features and characteristics of bubonic plague in order to determine its major ways of transmission and spread. We then use the results to formulate the bubonic plague disease model that exhaust possible ways of transmission. We then analyze the dynamics of the model and determine its behavior through numerical simulation.

Chapter 3: This chapter presents the stability analysis of the model formulated in Chapter Two. We determine the conditions under which the disease free and endemic equilibrium points are locally and globally asymptotically stable.

Chapter 4: We study the features and characteristics of pneumonic plague to understand all possible ways in which it can be transmitted. Then, based on the characteristics of pneumonic plague and the link it has with bubonic plague, we formulate the pneumonic plague disease model that also includes currently known factors that link it with bubonic plague. We then analyze the model, determine its behavior using numerical simulations and study the conditions for stability of its equilibrium points.

Chapter 5: In this chapter, we first explore the features and characteristics of septicemic plague specifically its ways of transmission and spread. We then include these feature in the model formulated in Chapter Four to get a plague disease model. This model includes all three forms of plague disease namely Bubonic plague, septicemic plague and pneumonic plague. We then analyze the model and determine the conditions for its stability, the main factors that control its dynamics and behavior .

Chapter 6: In this chapter, we formulate the plague disease model that incorporates the param-

eters that are affected by seasonal weather variation. We analyze the model to determine feasible region, we then define and compute the time-average basic reproduction number. Through numerical simulations we show that the average number of secondary cases of plague disease depend on progression rates from one primary form to a secondary form of plague infection, flea's infection rate and the vector flea abundance. Based on the illustration, we suggest different ways to control transmission and spread of plague disease.

Chapter 7: In this chapter, we analyze the global dynamics of plague disease model with seasonal transmission rate. We use the basic reproduction number to establish the conditions for global stability of disease free equilibrium solution. We then use fundamental existence-uniqueness theorem to prove the existence of positive periodic solutions. We further establish the conditions for global stability of periodic solutions of the model and finally using numerical simulations we validate the analytical solutions.

Chapter 8: This chapter gives the general summary, conclusion and recommendations of the whole study. Using the parameters that define the basic reproduction number, we also point out control strategies that may be used to control plague disease and suggest the possible ways in which this study can be extended.

CHAPTER TWO

Modeling the Dynamics of Bubonic Plague with Yersinia Pestis in the Environment [1]

Abstract: Bubonic plague is an infectious disease that is caused by the bacteria *Yersinia pestis* when it affects a part of circulatory system namely lymphatic system. It is mainly transferred between populations through flea bites. In this chapter, we develop a deterministic model that includes four compartments namely Human beings, Rodents, Fleas and pathogens in the environment to study the dynamics and spread of bubonic plague. The model is analyzed to determine the role and magnitude of the influence of each the four sub-populations in the transmission and spread of the disease. We use the next generation method to find the disease threshold R_0. A sensitivity analysis is carried out to determine the most, medium and least sensitive model parameters that negatively or positively affect the basic reproduction number. The result reveals that the probability at which flea become infected (β) has the biggest influence on the basic reproduction number R_0. Other significant parameters are adequate contact rates (Γ_{fh}), (Γ_{hf}), (Γ_{fr}), (Γ_{fr}) and (Γ_{rf}); probability that human and rodent become exposed to the disease (α_1) and (γ_1) respectively; progression rates (α_2) and (γ_2); and the pathogens in the environment under condition that the their survival is favored by the environment. The numerical simulations results are in agreement with the analytical solutions. Based on our results, we recommend that control strategies should target parameters that have shown to have a significant contribution to the increase of the basic reproduction number R_0.

Keywords: Bubonic Plague; Pathogens in the environment; Stability and Sensitivity analysis.

2.1 Introduction

2.1.1 Background

Tanzania is one of the countries that has been and still is heavly affected by plague disease for over 127 years. In most parts of Tanzania, the disease is still endemic and some tangible efforts need to be made to be able to eradicate this historical threat (Kilonzo *et al.*, 1992; Ziwa *et al.*, 2014). In this chapter, we study the dynamics of bubonic plague Bubonic plague diseases which occurs when the bacteria (Yersinia pestis) infects the lymphatic system (immune system), causing inflammation of lymphoid organs such as the spleen and the thymus (Crook and Tempest, 1992; Stenseth *et al.*, 2008).

[1]This chapter is based on the research paper: Ngeleja, R. C., Luboobi, L. S., & Nkansah-Gyekye, Y. (2016). Modelling the dynamics of bubonic plague with Yersinia pestis in the environment. *Communications in Mathematical Biology and Neuroscience, 2016,* Article-ID 10.

Bubonic plague is the most common form of plague disease. It is a severe infectious feverish disease characterized by chills, prostration, delirium, and formation of buboes. It is transmitted to humans mainly by the bite of a flea that has bitten an infected rodent or human being and very rarely when infected rodent bite a susceptible human being (Parmenter *et al.*, 1999).

In a few other cases, one can get the bacteria from the environment by touching and/or eating infected material and contaminated undercooked food or animals that have come into contact with an infected individual (Scott and Duncan, 2001). If not treated, the bacteria causing bubonic plague, may move into the blood and cause septicemic plague, or to the lungs, causing pneumonic plague (Emmeluth and Alcamo, 2009; Benedict, 1996).

Symptoms of bubonic plague generally appear within two to seven days after exposure and include: Fever and chills, headache, muscle pain, general weakness and seizures. Infected individuals may also experience painful swollen lymph glands called buboes, these typically appear in the groin, armpits, neck, or site of the insect bite or scratch. The buboes are what give bubonic plague its name (Wingfield and Palmer, 2009).

2.1.2 Transmission and infection

When the *Yersinia pestis* are in the flea's stomach, they multiply themselves making millions of copies, which in due course block the flea's digestive system. This makes it incapable of swallowing the blood it feeds on and as a result it gradually causes the hungry flea to become a ravenous biter. Due to this, the flea will attempt to feed on any warm-blooded animal that it can possibly reach and it switches hosts frequently as it searches for a blood meal. Every time it bites, it swallows some blood, but since the flea's stomach is so full of Yersinia pestis, it vomits up the blood along with some Yersinia cells and as a result the cells get inserted right into the new host (Moore, 2007).

During plague epizootics, many rodents die, causing hungry fleas to seek other sources of blood. Thus, people and other animals like Mice, rats, rabbits, squirrels, chipmunks, and prairie dogs that visit places where rodents have recently died from plague are at risk of being infected from flea bites (Eisen and Gage, 2009; Drancourt *et al.*, 2006; Perry and Fetherston, 1997; Echenberg, 2007). Bubonic plague can lead to gangrene if blood vessels in an individual's fingers and toes disrupt blood flow and cause death to the tissue. In rare cases, any form of plague disease may cause meningitis, which is an inflammation of membranes that surround the individual's spinal cord and brain (Antolin *et al.*, 2002).

Although plague disease (bubonic plague) is historical disease, it is still endemic in different

communities around the world. This persistence feature of plague disease makes it different from many historical diseases and thus arouse the need for different studies of the same. Sebbane *et al.* (2005) developed a model of bubonic plague using the inbred Brown Norway strain of *Rattus norvegicus* to characterize the development and dynamics of infection and the host immune response after intradermal inoculation of Yersinia pestis. The model was also used to characterize the temporal development of histopathology and cellular immune response in the spleen and lymph nodes, and thus evaluate hypothesized mechanisms of Y. pestis pathogenesis and immune evasion during infection. The study made a milestone for studies that relate to microbial pathogenesis, host response, and the efficacy of new medical countermeasures against plague.

Keeling and Gilligan (2000*b*) also developed a stochastic, spatial metapopulation model to study the dynamic of plague disease by proposing that bubonic plague is driven by the disease dynamics in the rat population. The study further postulates that bubonic plague can continue in relatively small rodent populations from which rare human being epidemics arise, this is why historically the plague persisted despite long disease-free periods and why the disease reappears in cities even those with tight quarantine control. The study based its findings in the rodent population and specifically the metapopulation behavior of rodent population.

Keeling and Gilligan (2000*a*) developed a model for bubonic plague that includes the disease dynamics in rat, flea and human populations. The spread of infections depends on the force of infection to humans, variation in the flea searching efficiency and the movement rates of rats and flea. The study also discussed the stochastic behaviour of the corresponding metapopulation model. They intended to study the dynamics of rats and the force of infection at the local spatial scale and identify the criteria for the spread to human populations in terms of the rat density. The study found that, Short-lived local epidemics in rats govern the transmission and spread and the endemic behavior in a few rat sub-populations allows the disease to persist for many years.

In this research work we study the dynamics of bubonic plague and the effect of survival of bacteria in the environment, the study uses deterministic mathematical modeling approach, in which the bubonic plague disease model is formulated and analyzed with the ultimate goal of understanding the dynamics of bubonic plague disease and its force of infection to human beings, rodents and fleas.

2.2 Material and Methods

The basic SEIR (Susceptible-Exposed-Infectious-Recovered) model is used with modification depending on the characteristics of the considered population and transmission network of bubonic plague disease. The model has four general groups; the human population, flea population, rodent population and pathogens in the environment. In all four groups, the model assume that all individuals from each population are born susceptible, there is no recovery for non-human host and the recovered individuals are conferred temporary immunity and return to be susceptible.

2.2.1 Description of the dynamics of bubonic plague in interactive population

We consider four populations namely Human beings, Fleas, Rodents and the pathogens in the environment. Within human beings the population is divided into four sub-groups: the group of people who have not contracted the disease but may get it if they get in contact with the infectious agent (susceptible) S_H, people who have the disease but have not shown any symptom and are incapable of transmitting the disease(Exposed) denoted by E_H, people who are infected and are capable of transmitting the disease (Infective) denoted by I_H and people who are removed from population I_H through recovery denoted R_H. Fleas are divided into two sub-groups: those who have not contracted the disease but may get it if they get in contact with infectious rodents or human beings (susceptible) S_F and those who are infected and are capable of transmitting the disease (Infective) denoted by I_F. The rodent population is also divided into three sub-groups: those who have not contracted the disease but may get it if they get in contact with infectious agent (susceptible) S_R, those who have the disease but have not shown any symptom and are incapable of transmitting the disease (Exposed) denoted by E_R and those who are infected and are capable of transmitting the disease (Infective) denoted by I_R.

The infection begins when flea in sub-group S_F gets *Yersinia pestis* bacteria by either biting the infected rodent who are the primary reservoir of the bacteria at a rate Γ_{rf} or biting the infected human being at the rate Γ_{hf} with the proportional of ρ and $(1-\rho)$ respectively. The susceptible flea then become infected I_F, and may cause the disease through biting the susceptible human being S_H and the susceptible rodent S_R at the rate Γ_{fh} and Γ_{fr} respectively. The probability of human beings and rodents to become latent to the disease thus progresses to be exposed human E_H and exposed rodent E_R are α_1 and γ_1 respectively. After two to seven days, the sub-groups E_H and E_R become infected and capable of transmitting the disease and thus progress to sub-group I_H and I_R at the rate α_2 and γ_2 respectively.

A fraction of infected human beings I_H may recover and attain temporary immunity at a rate α_3 and thus progress to a sub-group R_H which thereafter return to a sub-group S_H at the rate ϖ. Those who do not recover die either for natural death at the rate μ_1 and due to the disease at the rate δ_1. After the infection, all the infected rodents I_R die out due to disease at the rate δ_3 and naturally at a rate μ_3. The pathogen within the environment will upon interaction with S_H and S_R cause infections at the rate ω_1 and ω_2 respectively. However, they are recruited through birth at the rate λ_4 and they suffer natural mortality at a rate μ_4. The human population in sub-groups S_H and E_H , flea population in sub-group S_F and rodent population in sub-groups S_R and E_R all suffer natural mortality at a rate μ_1, μ_2 and μ_3 respectively.

The compartments I_H, I_F and I_R suffer both natural death at the rate μ_1, μ_2 and μ_3 and disease induced mortality at rates δ_1, δ_2 and δ_3 respectively. The Human beings, rodents and fleas are recruited through immigration at the rates ψ_1, ψ_{2s} and ψ_3 respectively.

2.2.2 Variables and Parameters

The variables and parameters used in the model are summarized in Tables 1 and 2 respectively.

Table 1: Variables and their description for bubonic plague.

Variable	**Description**
S_H	Susceptible individuals
E_H	Exposed individuals
I_H	Infected individuals
R_H	Recovered individuals
S_R	Susceptible rodents
E_R	Exposed rodents
I_R	Infected rodents
S_F	Susceptible fleas
I_F	Infected fleas
A	Pathogens in the environment

Table 2: Parameters and their description for bubonic plague.

Parameters	**Description**
Γ_{rf}	Adequate contact rate: rodent to flea
Γ_{fh}	Adequate contact rate: flea to human
Γ_{fr}	Adequate contact rate: flea to rodent
α_1	Probability that human progress from S_H to E_H
γ_1	Probability that rodent progress from S_R to E_R
Γ_{hf}	Adequate contact rate: human to flea
λ_4	Recruitment rate of pathogens
α_2	Progression rate of exposed human to infected
γ_2	Progression rate of exposed rodent to infected
α_3	Human recovery rate
ϖ	Progression rate of recovered human to susceptible
μ_1	Natural death rate for Human
δ_1	Disease induced death rate for Human
δ_3	Disease induced death rate for rodent
μ_3	Natural death rate for rodent
ω_1	Adequate contact rate: Pathogens to human
ω_2	Adequate contact rate: Pathogens to rodent
μ_4	Natural death rate for Pathogens
μ_2	Natural death rate for flea
δ_2	Disease induced death rate for flea
ψ_1	Immigration rate of human
ψ_{2s}	Immigration rate of Susceptible flea
ψ_3	Immigration rate of rodent
β	The probability at which fleas become infected

Using the description of the dynamics of bubonic plague and the assumptions, we construct the compartmental diagram that capture the interaction between the human beings, rodents, fleas and pathogens in the environment that dictate the dynamics of bubonic plague disease as given in Fig 2.

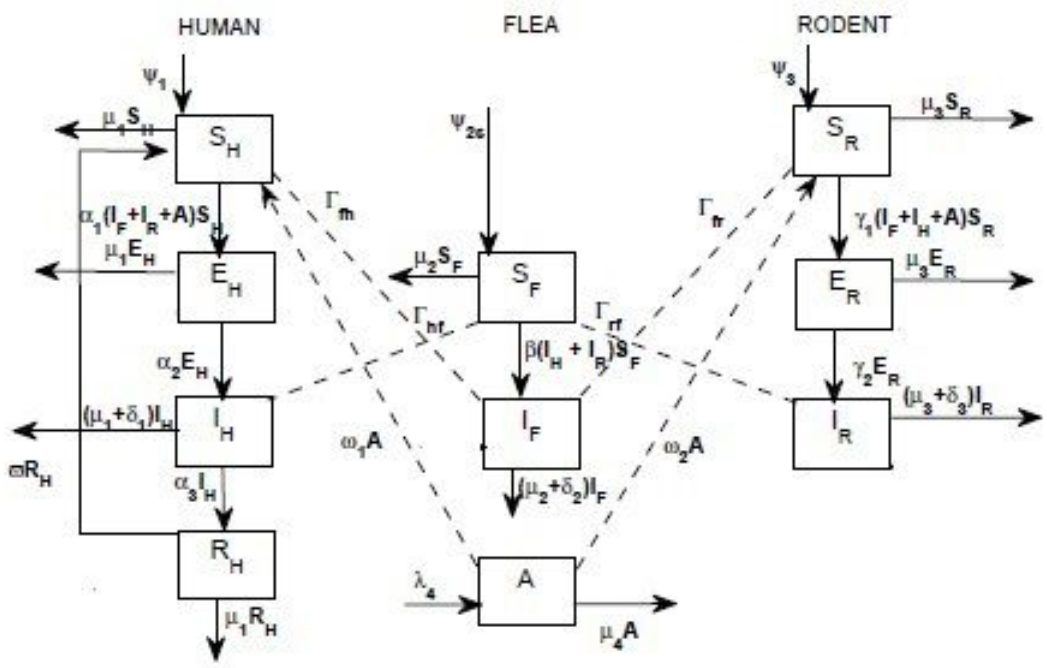


Figure 2: Compartmental model for bubonic plague

2.2.3 Model Equations for bubonic Plague

From the compartmental diagram in Fig 2 we derive the following equations;

Human beings

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \mu_1 S_H, \tag{1a}$$

$$\frac{dE_H}{dt} = \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \alpha_2 E_H - \mu_1 E_H, \tag{1b}$$

$$\frac{dI_H}{dt} = \alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1)I_H, \tag{1c}$$

$$\frac{dR_H}{dt} = \alpha_3 I_H - \varpi R_H - \mu_1 R_H. \tag{1d}$$

Rodents

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \mu_3 S_R \tag{2a}$$

$$\frac{dE_R}{dt} = \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \gamma_2 E_R - \mu_3 E_R \tag{2b}$$

$$\frac{dI_R}{dt} = \gamma_2 E_R - (\mu_3 + \delta_3)I_R \tag{2c}$$

Flea

$$\frac{dS_F}{dt} = \psi_{2s} - \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - \mu_2 S_F \tag{3a}$$

$$\frac{dI_F}{dt} = \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - (\mu_2 + \delta_2)I_F \tag{3b}$$

Pathogens in the environment

$$\frac{dA}{dt} = \lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A \tag{4}$$

2.3 Basic properties of the model

2.3.1 Positivity of the solution and Invariant regions

Solving the equations of the system in their patches for testing the positivity, we found that by letting the initial values of the system (1,2,3 and 4) be: ($S_H(0)$, $S_R(0)$,$S_F(0)$, $A(0)) > 0$ and ($E_H(0)$,$I_H(0)$,$R_H(0)$,$E_R(0)$, $I_R(0)$, $I_F(0)) \geq 0$ then the solution set $S_H(t)$, $S_R(t)$, $S_F(t)$, $A(t)$, $E_H(t)$, $I_H(t)$, $R_H(t)$, $E_R(t)$, $I_R(t)$ and $I_F(t)$ are non-negative $\forall$ t≥ 0.

Since the system is modeling populations, we assume that all state variables and parameters of the model are non-negative $\forall t \geq 0$. The bubonic plague disease model has four compartments which are analyzed separately. The model system is analyzed in suitable feasible region where all state variables are positive. This region is obtained by considering the following theorem:

Theorem 2.1
All forward solutions in R_+^{10} of the system are feasible $\forall t \geq 0$ if they enter the invariant region Φ for $\Phi = \Omega_H \times \Omega_R \times \Omega_F \times \Omega_A$

where

$$\Omega_H = (S_H, E_H, I_H, R_H) \in R_+^4 : S_H + E_H + I_H + R_H \leq N_1$$
$$\Omega_R = (S_R, E_R, I_R) \in R_+^3 : S_R + E_R + I_R \leq N_3$$
$$\Omega_F = (S_F, I_F) \in R_+^2 : S_F + I_F \leq N_2$$
$$\Omega_A = A \in R_+^1$$

and Φ is the positive invariant region of the whole system.

Proof. **For human population**
We need to prove that the solutions of the system (1) are feasible $\forall t > 0$ as they enter the invariant region Ω_H.

We now let $\Omega_H = (S_H, E_H, I_H, R_H) \in R^4$ be the solution space of the system (1) with non-negative initial conditions.

The total human population is

$$N_1 = S_H + E_H + I_H + R_H$$

Then

$$\frac{dN_1}{dt} = \frac{dS_H}{dt} + \frac{dE_H}{dt} + \frac{dI_H}{dt} + \frac{dR_H}{dt} \tag{5}$$

Adding up the system (1a) - (1d) we get,

$$\frac{dN_1}{dt} = \psi_1 - \mu_1 N_1 - \delta_1 I_H \quad \Rightarrow \quad \tfrac{dN_1}{dt} \leq \psi_1 - \mu_1 N_1$$

Now integrating this and applying the initial condition $t = 0, N_1(t = 0) = N_{10}$ we find that;

$$N_1 \leq \frac{\psi_1}{\mu_1} + (N_{10} - \frac{\psi_1}{\mu_1})e^{-\mu_1 t} \tag{6}$$

Figure 3a illustrates that, considering expression (6) when $N_{10} > \frac{\psi_1}{\mu_1}$ the population decreases asymptotically to $\frac{\psi_1}{\mu_1}$ and when $N_{10} < \frac{\psi_1}{\mu_1}$ the population increases asymptotically to $\frac{\psi_1}{\mu_1}$.
Now applying Birkhof and Rota's theorem on differential inequality for equation (6), as $t \to \infty$, in the case when $N_{10} > \frac{\psi_1}{\mu_1}$ or when $N_{10} < \frac{\psi_1}{\mu_1}$ we obtain $0 \leq N_1 \leq \frac{\psi_1}{\mu_1}$ Hence all the feasible solutions of the system enter the region

$$\Omega_H = \left\{ (S_H, E_H, I_H, R_H) : N_1 \leq Max \left\{ N_{10}, \frac{\psi_1}{\mu_1} \right\} \right\}$$

For rodent population

We need to prove that the solutions of the system (2) are feasible $\forall t > 0$ as they enter invariant region Ω_R.
We now let $\Omega_R = (S_R, E_R, I_R) \in R^3$ be any solution of the system with non-negative initial conditions.
Using the procedures stated in subsection (2.3.1) we find that

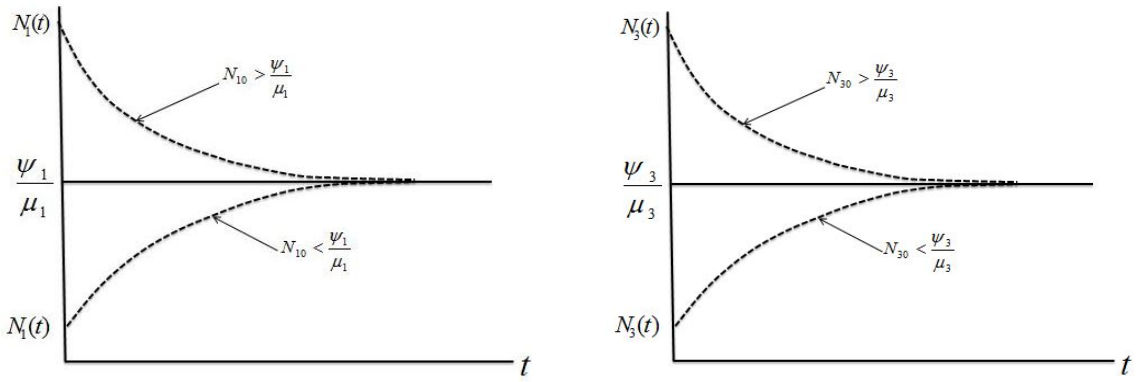
$$N_3 \leq \frac{\psi_3}{\mu_3} + (N_{30} - \frac{\psi_3}{\mu_3})e^{-\mu_3 t} \tag{7}$$

Figure 3b shows that, for expression (7), when $N_{30} > \frac{\psi_3}{\mu_3}$ the population decreases asymptotically to $\frac{\psi_3}{\mu_3}$ and when $N_{30} < \frac{\psi_3}{\mu_3}$ the rodent population increases asymptotically to $\frac{\psi_3}{\mu_3}$. Now applying Birkhof and Rota's theorem on differential inequality for equation (7), as $t \to \infty$, in the case when $N_{30} > \frac{\psi_3}{\mu_3}$ or when $N_{30} < \frac{\psi_3}{\mu_3}$ we obtain $0 \leq N_3 \leq \frac{\psi_3}{\mu_3}$. Hence all the feasible solutions of the system enter the region

$$\Omega_R = \left\{ (S_R, E_R, I_R) : N_3 \leq Max \left\{ N_{30}, \frac{\psi_3}{\mu_3} \right\} \right\}$$

. **For flea population**

We need to prove that the solutions of the system (3) are feasible $\forall t > 0$ as they enter invariant region Ω_F.
We now let $\Omega_F = (S_F, I_F) \in R^2$ be any solution of the system with non-negative initial



(a) **(b)**

Figure 3: Feasible region for Human and Rodent systems

conditions.

We also employ the procedures stated in subsection $(2.3.1)$ and find that

$$N_2 \leq \frac{\psi_{2s}}{\mu_2} + (N_{20} - \frac{\psi_{2s}}{\mu_2})e^{-\mu_2 t} \tag{8}$$

Figure 4a shows that, for expression (8) when $N_{20} > \frac{\psi_{2s}}{\mu_2}$ the population decreases asymptotically to $\frac{\psi_{2s}}{\mu_2}$ and when $N_{20} < \frac{\psi_{2s}}{\mu_2}$ the flea population increases asymptotically to $\frac{\psi_{2s}}{\mu_2}$.

Now applying Birkhof and Rota's theorem on differential inequality for equation (8), as $t \to \infty$ in the case when $N_{20} > \frac{\psi_{2s}}{\mu_2}$ or when $N_{20} < \frac{\psi_{2s}}{\mu_2}$ we obtain $0 \leq N_2 \leq \frac{\psi_{2s}}{\mu_2}$ Hence all the feasible solution of the system enter the region

$$\Omega_F = \left\{ (S_F, I_F) : N_2 \leq Max \left\{ N_{20}, \frac{\psi_{2s}}{\mu_2} \right\} \right\}.$$

For pathogens in the environment

We need to prove that the solutions of the system (4) are feasible $\forall t > 0$ as they enter invariant region Ω_A.

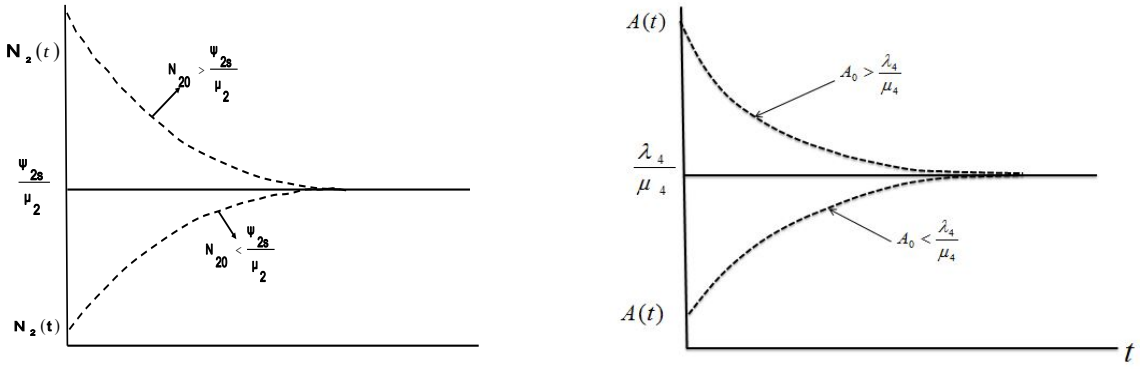
We now let $\Omega_A = A \in R_+^1$ be any solution of the system with non-negative initial conditions. Now integrating this and applying the initial condition $t = 0, A(t = 0) = A_0$ we find that;

$$A(t) \leq \frac{\lambda_4}{\mu_4} + (A_0 - \frac{\lambda_4}{\mu_4})e^{-\mu_4 t}. \tag{9}$$

Figure 4b shows that, for expression (9), when $A_0 > \frac{\lambda_4}{\mu_4}$ the pathogens decrease asymptotically to $\frac{\lambda_4}{\mu_4}$ and when $N_{30} < \frac{\lambda_4}{\mu_4}$ pathogens increase asymptotically to $\frac{\lambda_4}{\mu_4}$. Now applying Birkhof and Rota's theorem on differential inequality for equation (9), as $t \to \infty$ in the case when $A_0 > \frac{\lambda_4}{\mu_4}$ or when $N_{30} < \frac{\lambda_4}{\mu_4}$ we obtain $0 \leq A \leq \frac{\lambda_4}{\mu_4}$. Hence the feasible solution of the system enter the region

$$\Omega_A = \left\{ A : A \leq Max \left\{ A_0, \frac{\lambda_4}{\mu_4} \right\} \right\}.$$

□



(a) **(b)**

Figure 4: Feasible region for Flea and Pathogens in the Environment systems

2.3.2 Positivity of the solution

For the bubonic plague disease model system (1) - (4) to be epidemiologically meaningful and well posed, we need to prove that all state variables are non-negative $\forall t \geq 0$. We now solve the equations of the system in their patches for testing the positivity.

Theorem 2.2
Let the initial values of the system (1,2,3 and 4) be: $(S_H(0),\ S_R(0),\ S_F(0),\ A_0) > 0$ and $(E_H(0),\ I_H(0),\ R_H(0),\ E_R(0),\ I_R(0),\ I_F(0)) \geq 0$. Then the solution set $S_H(t)$, $S_R(t)$, $S_F(t)$, $A(t)$, $E_H(t)$, $I_H(t)$, $R_H(t)$, $E_R(t)$, $I_R(t)$ and $I_F(t)$ are positive $\forall t \geq 0$.

Proof. We use the equations of the system (1)-(4) in their subgroups for testing the positivity

For human population
Using the first equation in human system we have

$$S_H \geq S_{H0} e^{-\int_0^t (\alpha_1(\Gamma_{fh}\frac{I_F}{N_2}+\omega_1 A)+\mu_1)d\tau} > 0 \text{ since } (\alpha_1(\Gamma_{fh}\frac{I_F}{N_2}+\omega_1 A)+\mu_1) > 0$$

From the second equation we have

$$E_H \geq E_{H0} e^{-(\alpha_2+\mu_1)t} > 0 \quad \text{since} \quad (\alpha_2+\mu_1) > 0.$$

Third equation of system (1) we have

$$I_H \geq I_{H0} e^{-(\alpha_3+\mu_1+\delta_1)t} > 0 \quad \text{since} \quad (\alpha_3 I_H+\mu_1+\delta_1) > 0.$$

And the last equation in system (1) we have

$$R_H \geq R_{H0}e^{-(\varpi+\mu_1)t} > 0 \quad \text{since} \quad (\varpi + \mu_1) > 0.$$

For rodent population

Using equation one from system (2) we have

$$S_R \geq S_{R0}e^{-\int_0^t(\gamma_1(\Gamma_{fr}\frac{I_F}{N_2}+\omega_2 A)+\mu_3)d\tau} > 0 \quad \text{since} \quad (\gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A) + \mu_3) > 0.$$

From the second equation of the system (2) we have

$$E_R \geq E_{R0}e^{-(\gamma_2+\mu_3)t} > 0 \quad \text{since } (\gamma_2 + \mu_3) > 0.$$

And the from the third equation of system (2) we have

$$I_R \geq I_{R0}e^{-(\mu_3+\delta_3)t} > 0 \quad \text{since} \quad (\mu_3 + \delta_3) > 0.$$

For flea population

Now from the first equation of system (3) we have

$$S_F \geq S_{F0}e^{-\int_0^t(\beta(\rho\Gamma_{hf}\frac{I_H}{N_1}+(1-\rho)\Gamma_{rf}\frac{I_R}{N_3})+\mu_2)d\tau} > 0 \quad \text{since} \quad (\beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3}) + \mu_2) > 0.$$

Taking the second equation we have

$$I_F \geq I_{F0}e^{-(\mu_2+\delta_2)t} > 0 \quad \text{since} \quad (\mu_2 + \delta_2) > 0.$$

For pathogens in the environment

The sub-group has only one equation so using equation (4) we have

$$A \geq A_0e^{-\int_0^t(\omega_1 S_H+\omega_2 S_R+\mu_4)d\tau} > 0 \quad \text{since} \quad (\omega_1 S_H + \omega_2 S_H + \mu_4) > 0.$$

□

2.4 Model analysis

In this section, we assess existence of equilibrium states, reproduction number and stability of the equilibrium states.

2.4.1 Disease Free Equilibrium

The model has disease free equilibrium which is obtained by setting $I_H = E_H = R_H = 0$, $I_R = E_R = 0$,$I_F = 0$ and $A = 0$ for human , Rodent, Flea and pathogen system respectively. We then substitute the above into the new system obtained by setting the derivatives of (1) - (4) equal to zero such that:

Human

$$\psi_1 + \varpi R_H - \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \mu_1 S_H = 0 \tag{10a}$$

$$\alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \alpha_2 E_H - \mu_1 E_H = 0 \tag{10b}$$

$$\alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1)I_H = 0 \tag{10c}$$

$$\alpha_3 I_H - \varpi R_H - \mu_1 R_H = 0 \tag{10d}$$

Rodent

$$\psi_3 - \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \mu_3 S_R = 0 \tag{11a}$$

$$\gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \gamma_2 E_R - \mu_3 E_R = 0 \tag{11b}$$

$$\gamma_2 E_R - (\mu_3 + \delta_3)I_R = 0 \tag{11c}$$

Flea

$$\psi_{2s} - \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - \mu_2 S_F = 0 \tag{12a}$$

$$\beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - (\mu_2 + \delta_2)I_F = 0 \tag{12b}$$

Pathogens

$$\lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A = 0 \tag{13}$$

Then we have the disease free-equilibrium point given as $E_H^0 = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0\right)$, $E_R^0 = \left(\frac{\psi_3}{\mu_3}, 0, 0\right)$, $E_F^0 = \left(\frac{\psi_{2s}}{\mu_2}, 0\right)$ and $E_A^0 = 0$ for human, Rodent, Flea and pathogen respectively.
Then the disease free equilibrium of the entire system

$$E^0(S_H^0, E_H^0, I_H^0, R_H^0, S_R^0, E_R^0, I_R^0, S_F^0, I_F^0, A^0) = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0, \frac{\psi_3}{\mu_3}, 0, 0, \frac{\psi_{2s}}{\mu_2}, 0, 0\right).$$

2.4.2 Basic Reproduction Number R_0 for bubonic plague

Basic reproduction number is the expected number of secondary cases produced by a single infectious individual during the entire infectious period of that particular individual in a completely susceptible population. The epidemiological criterion of R_0 is that if $R_0 < 1$, then

the single infected individual in entirely susceptible population infects less than one individual. Hence the disease may be eradicated from the population and the disease-free equilibrium point is asymptotically stable.That is the disease cannot invade the population. If $R_0 > 1$ it means that a single infected individual in entirely susceptible population infects more than one individuals. Hence the disease may persist in the population, and the disease free equilibrium point is unstable. In this case the disease can invade the population and persist for a long time If $R0 = 1$ it means that a single infected individual in entirely susceptible population infects one new individuals. Hence the disease will stay alive in the population without an epidemic (Allen *et al.*, 2008).

We use next generation method as described by Van den Driessche and Watmough (2002) to find the basic reproductive number. Consider a heterogeneous population whose individuals are distinguishable by stage of the disease, and hence identifiable and put into epidemiological compartments $S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F$ and A. By first re-arranging the system to have the infection classes come first, we sort the compartments so that the first m compartments correspond to infected individuals.

We now let $F_i(x)$ be the rate of appearance of new infections in compartment i, $V_i^+(x)$ be the rate of transfer of individuals into compartment i by all other means except the epidemic and $V_i^-(x)$ be the rate of transfer of individuals out of compartment i.

The disease transmission model consists of the system of equations $x_i^{'} = F_i(x) - V_i(x)$
where $V_i(x) = V_i^-(x) - V_i^+(x)$.
Since we already have the disease free equilibrium x_0, we then compute matrices F and V which are $m \times m$ matrices defined by:

$$F = \left(\frac{\partial F_i}{\partial x_j}(x_0)\right), V = \left(\frac{\partial V_i}{\partial x_j}(x_0)\right)$$

with $1 \leq i, j \leq m$.

Since F is non-negative and V is a non-singular matrix then V^{-1} is non-negative and also FV^{-1} is non-negative. Matrix FV^{-1}, is defined as the next generation matrix (Diekmann *et al.*, 1990). Therefore the basic reproductive number is defined as:

$$R_0 = \rho(FV^{-1})$$

where $\rho(FV^{-1})$ is the maximum modulus of the eigenvalues of the non-negative matrix FV^{-1}.

We first re-arrange the system to have the infection classes come first:

$$\frac{dE_H}{dt} = \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \alpha_2 E_H - \mu_1 E_H, \tag{14a}$$
$$\frac{dI_H}{dt} = \alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1)I_H, \tag{14b}$$
$$\frac{dE_R}{dt} = \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \gamma_2 E_R - \mu_3 E_R \tag{14c}$$
$$\frac{dI_R}{dt} = \gamma_2 E_R - (\mu_3 + \delta_3)I_R \tag{14d}$$
$$\frac{dI_F}{dt} = \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - (\mu_2 + \delta_2)I_F \tag{14e}$$
$$\frac{dA}{dt} = \lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A \tag{14f}$$
$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \mu_1 S_H, \tag{14g}$$
$$\frac{dR_H}{dt} = \alpha_3 I_H - \varpi R_H - \mu_1 R_H. \tag{14h}$$
$$\frac{dS_R}{dt} = \psi_3 - \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \mu_3 S_R \tag{14i}$$
$$\frac{dS_F}{dt} = \psi_{2s} - \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - \mu_2 S_F \tag{14j}$$

Now from the system (14) the infectious classes are (14a) to (14f) with compartment E_H, I_H, E_R, I_R and A , this will now yield

$$\mathbf{F_i} = \begin{pmatrix} \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H \\ 0 \\ \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R \\ \psi_3 \\ \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F \\ 0 \end{pmatrix} \tag{15}$$

And

$$\mathbf{V_i} = \begin{pmatrix} \alpha_2 E_H + \mu_1 E_H \\ \alpha_3 I_H + (\mu_1 + \delta_1)I_H - \alpha_2 E_H \\ \mu_3 E_R + \gamma_2 E_R \\ (\mu_3 + \delta_3)I_R - \gamma_2 E_R \\ (\mu_2 + \delta_2)I_F \\ \omega_1 A S_H + \omega_2 A S_R + \mu_4 A - \lambda_4 \end{pmatrix}. \tag{16}$$

We compute Jacobian matrices of F and V at x_0
For F we will have;

$$\frac{\partial F_i}{\partial x_j} = \begin{pmatrix} \frac{\partial F_1}{\partial E_H} & \frac{\partial F_1}{\partial I_H} & \frac{\partial F_1}{\partial E_R} & \frac{\partial F_1}{\partial I_R} & \frac{\partial F_1}{\partial I_F} & \frac{\partial F_1}{\partial A} \\ \frac{\partial F_2}{\partial E_H} & \frac{\partial F_2}{\partial I_H} & \frac{\partial F_2}{\partial E_R} & \frac{\partial F_2}{\partial I_R} & \frac{\partial F_2}{\partial I_F} & \frac{\partial F_2}{\partial A} \\ \frac{\partial F_3}{\partial E_H} & \frac{\partial F_3}{\partial I_H} & \frac{\partial F_3}{\partial E_R} & \frac{\partial F_3}{\partial I_R} & \frac{\partial F_3}{\partial I_F} & \frac{\partial F_3}{\partial A} \\ \frac{\partial F_4}{\partial E_H} & \frac{\partial F_4}{\partial I_H} & \frac{\partial F_4}{\partial E_R} & \frac{\partial F_4}{\partial I_R} & \frac{\partial F_4}{\partial I_F} & \frac{\partial F_4}{\partial A} \\ \frac{\partial F_5}{\partial E_H} & \frac{\partial F_5}{\partial I_H} & \frac{\partial F_5}{\partial E_R} & \frac{\partial F_5}{\partial I_R} & \frac{\partial F_5}{\partial I_F} & \frac{\partial F_5}{\partial A} \\ \frac{\partial F_6}{\partial E_H} & \frac{\partial F_6}{\partial I_H} & \frac{\partial F_6}{\partial E_R} & \frac{\partial F_6}{\partial I_R} & \frac{\partial F_6}{\partial I_F} & \frac{\partial F_6}{\partial A} \end{pmatrix} = \begin{pmatrix} 0 & 0 & 0 & 0 & \frac{\alpha_1 \Gamma_{fh} S_H}{N_2} & \alpha_1 \omega_1 S_H \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\gamma_1 \Gamma_{fr} S_R}{N_2} & \gamma_1 \omega_2 S_R \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta \rho \Gamma_{hf} S_F}{N_1} & 0 & \frac{\beta(1-\rho)\Gamma_{rf} S_F}{N_3} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}.$$

Now at x_0 we will have

$$\mathbf{F} = \begin{pmatrix} 0 & 0 & 0 & 0 & \frac{\alpha_1 \psi_1 \mu_2 \Gamma_{fh}}{\mu_1 \psi_{2s}} & \frac{\alpha_1 \psi_1 \omega_1}{\mu_1} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\gamma_1 \psi_3 \mu_2 \Gamma_{fr}}{\mu_3 \psi_{2s}} & \frac{\gamma_1 \psi_3 \omega_2}{\mu_3} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta \psi_{2s} \mu_1 \rho \Gamma_{hf}}{\mu_2 \psi_1} & 0 & \frac{\beta \psi_{2s} \mu_3 (1-\rho) \Gamma_{rf}}{\mu_2 \psi_3} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}. \tag{17}$$

and for V we will have;

$$V = \frac{\partial V_i}{\partial x_j}(x_0) = \begin{pmatrix} \frac{\partial V_1}{\partial E_H} & \frac{\partial V_1}{\partial I_H} & \frac{\partial V_1}{\partial E_R} & \frac{\partial V_1}{\partial I_R} & \frac{\partial V_1}{\partial I_F} & \frac{\partial V_1}{\partial A} \\ \frac{\partial V_2}{\partial E_H} & \frac{\partial V_2}{\partial I_H} & \frac{\partial V_2}{\partial E_R} & \frac{\partial V_2}{\partial I_R} & \frac{\partial V_2}{\partial I_F} & \frac{\partial V_2}{\partial A} \\ \frac{\partial V_3}{\partial E_H} & \frac{\partial V_3}{\partial I_H} & \frac{\partial V_3}{\partial E_R} & \frac{\partial V_3}{\partial I_R} & \frac{\partial V_3}{\partial I_F} & \frac{\partial V_3}{\partial A} \\ \frac{\partial V_4}{\partial E_H} & \frac{\partial V_4}{\partial I_H} & \frac{\partial V_4}{\partial E_R} & \frac{\partial V_4}{\partial I_R} & \frac{\partial V_4}{\partial I_F} & \frac{\partial V_4}{\partial A} \\ \frac{\partial V_5}{\partial E_H} & \frac{\partial V_5}{\partial I_H} & \frac{\partial V_5}{\partial E_R} & \frac{\partial V_5}{\partial I_R} & \frac{\partial V_5}{\partial I_F} & \frac{\partial V_5}{\partial A} \\ \frac{\partial V_6}{\partial E_H} & \frac{\partial V_6}{\partial I_H} & \frac{\partial V_6}{\partial E_R} & \frac{\partial V_6}{\partial I_R} & \frac{\partial V_6}{\partial I_F} & \frac{\partial V_6}{\partial A} \end{pmatrix}$$

$$\mathbf{V} = \begin{pmatrix} \alpha_2 + \mu_1 & 0 & 0 & 0 & 0 & 0 \\ -\alpha_2 & \alpha_3 + \mu_1 + \delta_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_3 + \gamma_2 & 0 & 0 & 0 \\ 0 & 0 & -\gamma_2 & \mu_3 + \delta_3 & 0 & 0 \\ 0 & 0 & 0 & 0 & \mu_2 + \delta_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & \omega_1 S_H + \omega_2 S_R + \mu_4 \end{pmatrix}. \tag{18}$$

For simplicity we now let;

$$\begin{aligned} z_1 &= \alpha_2 + \mu_1 \\ z_2 &= \alpha_3 + \mu_1 + \delta_1 \\ z_3 &= \mu_3 + \gamma_2 \\ z_4 &= \mu_3 + \delta_3 \\ z_5 &= \mu_2 + \delta_2 \\ z_6 &= \tfrac{\omega_1 \psi_1}{\mu_1} + \tfrac{\omega_2 \psi_3}{\mu_3} + \mu_4. \end{aligned}$$

And thus matrix V become

$$V = \begin{pmatrix} z_1 & 0 & 0 & 0 & 0 & 0 \\ -\alpha_2 & z_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & z_3 & 0 & 0 & 0 \\ 0 & 0 & -\gamma_2 & z_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & z_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & z_6 \end{pmatrix}$$

We now compute V^{-1} and FV^{-1} using maple we will have;

$$\mathbf{V^{-1}} = \begin{pmatrix} \frac{1}{z_1} & 0 & 0 & 0 & 0 & 0 \\ \frac{\alpha_2}{z_2 z_1} & \frac{1}{z_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{z_3} & 0 & 0 & 0 \\ 0 & 0 & \frac{\gamma_2}{z_4 z_3} & \frac{1}{z_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{z_5} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{z_6} \end{pmatrix} \tag{19}$$

We again have;

$$\mathbf{FV^{-1}} = \begin{pmatrix} 0 & 0 & 0 & 0 & \frac{\alpha_1\psi_1\mu_2\Gamma_{fh}}{\mu_1\psi_{2s}z_5} & \frac{\alpha_1\psi_1\omega_1}{\mu_1 z_6} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\gamma_1\psi_3\mu_2\Gamma_{fr}}{\mu_3\psi_{2s}z_5} & \frac{\gamma_1\psi_3\omega_2}{\mu_3 z_6} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{\beta\psi_{2s}\mu_1\rho\Gamma_{hf}\alpha_2}{\mu_2\psi_1 z_2 z_1} & \frac{\beta\psi_{2s}\mu_1\rho\Gamma_{hf}}{\mu_2\psi_1 z_2} & \frac{\beta\psi_{2s}\mu_3(1-\rho)\Gamma_{rf}\gamma_2}{\mu_2\psi_3 z_4 z_3} & \frac{\beta\psi_{2s}\mu_3(1-\rho)\Gamma_{rf}}{\mu_2\psi_3 z_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{20}$$

From (20) the basic reproduction number R_0 is computed by finding the spectral radius $\rho(FV^{-1})$ of the next generation matrix in which the dominant eigenvalue of matrix (20) will be the required R_0 . Now using maple software we get the following eigenvalues:
$\lambda_1 = \lambda_2 = \lambda_3 = \lambda_4 = 0$ and

$$\lambda_5 = \frac{\sqrt{z_4 z_3 \psi_{2s} z_5 z_2 z_1 \beta(z_1 z_2 \psi_{2s}(1-\rho)\Gamma_{rf}\gamma_2\gamma_1\Gamma_{fr} + \rho\Gamma_{hf}\alpha_2\alpha_1\Gamma_{fh} z_4 z_3 \psi_{2s})}}{z_4 z_3 \psi_{2s} z_5 z_2 z_1}$$

$$\lambda_6 = -\frac{\sqrt{z_4 z_3 \psi_{2s} z_5 z_2 z_1 \beta(z_1 z_2 \psi_{2s}(1-\rho)\Gamma_{rf}\gamma_2\gamma_1\Gamma_{fr} + \rho\Gamma_{hf}\alpha_2\alpha_1\Gamma_{fh} z_4 z_3 \psi_{2s})}}{z_4 z_3 \psi_{2s} z_5 z_2 z_1}$$

From the above eigenvalues we take the basic reproduction number as:

$$R_0 = \frac{\sqrt{z_4 z_3 \psi_{2s} z_5 z_2 z_1 \beta(z_1 z_2 \psi_{2s}(1-\rho)\Gamma_{rf}\gamma_2\gamma_1\Gamma_{fr} + \rho\Gamma_{hf}\alpha_2\alpha_1\Gamma_{fh} z_4 z_3 \psi_{2s})}}{z_4 z_3 \psi_{2s} z_5 z_2 z_1}$$

Simplifying and substituting the expressions for z_1, z_2, z_3, z_4 and z_5 we will get:

$$R_0 = \sqrt{\frac{\beta}{(\mu_2+\delta_2)}\left(\frac{\gamma_2\gamma_1\Gamma_{rf}\Gamma_{fr}(1-\rho)}{(\mu_3+\gamma_2)(\mu_3+\delta_3)} + \frac{\rho\alpha_2\alpha_1\Gamma_{hf}\Gamma_{fh}}{(\alpha_2+\mu_1)(\alpha_3+\mu_1+\delta_1)}\right)}$$

This dimensionless quantity measures the average number of secondary infection produced when a typical infectious individual enters an entirely susceptible population. Since our model has multiple transmission routes which are from flea to rodent, flea to human, pathogens in the environment to rodent and human, rodent to flea and human to flea transmissions, then the basic reproductive number obtained via next-generation method does not give the number of host infected by a single individual (as there are more than one agents for transmission), rather it gives the geometric mean of the number of infections per generation (Li and Blakeley, 2011). It depends on the probability at which fleas gets infected β, flea's infectious period $\frac{1}{\mu_2+\delta_2}$, probability that rodent survive the infected class $\frac{\gamma_2}{\mu_3+\gamma_2}$, rodent's infectious period $\frac{1}{\mu_3+\delta_3}$, the proportion that flea gets the disease from the rodent or human which are $(1-\rho)\Gamma_{rf}$ or $\rho\Gamma_{hf}$ respectively, human's infectious period $\frac{1}{\mu_1+\delta_1+\alpha_3}$, probability that human survive the infectious class $\frac{\alpha_2}{\mu_1+\alpha_2}$, the adequate contact rate flea to human Γ_{fh}, the adequate contact rate flea to rodent Γ_{fr} and the probability at which human and rodent become exposed to the the disease which are α_1 and γ_1 respectively.

2.5 Sensitivity analysis, Simulation and Discussion

Sensitivity analysis is used to determine the strength of the dependence of model predictions on parameter values. In this section, we use sensitivity analysis to determine the impact of the parameters on R_0. In order to determine an effective way that can reduce mortality and morbidity due to bubonic plague disease in human beings and rodents (domestic animals). It is important to deeply understand the comparative importance of factors that are responsible for the transmission and prevalence of the disease (Cohen and Murray, 2004).

2.5.1 Numerical Simulation

Parameter values

Table 3 shows the values of the parameters of bubonic plague disease model. The parameters are taken from previous studies that relate to this study, existing information from literature and through estimation using sensitivity analysis and simulations.

Table 3: Parameter values for Bubonic plague disease model

Parameter	**Value**	**Reference/Source**
Γ_{rf}	0.6	Estimated
Γ_{fh}	0.09	Benkirane *et al.* (2009)
Γ_{fr}	4.7	Li (1993)
α_1	0.9	Estimated
γ_1	0.9	Estimated
Γ_{hf}	0.28	Benkirane *et al.* (2009)
λ_4	0.89	Estimated
α_2	0.04	Keeling and Gilligan (2000*a*)
γ_2	0.05	Keeling and Gilligan (2000*a*)
α_3	0.1	Keeling and Gilligan (2000*a*)
ϖ	0.1	Keeling and Gilligan (2000*a*)
μ_1	0.04	Keeling and Gilligan (2000*a*)
δ_1	0.04	Keeling and Gilligan (2000*a*)
δ_3	0.05	Keeling and Gilligan (2000*b*)
μ_3	0.2	Galtier and Mouchiroud (1998)
ω_1	0.01	Keeling and Gilligan (2000*a*)
ω_2	0.073	Benkirane *et al.* (2009)
μ_4	0.1	Estimated
μ_2	0.07	Benkirane *et al.* (2009)
δ_2	0.03	Benkirane *et al.* (2009)
ψ_1	0.09	Estimated
ψ_{2S}	0.008	Keeling and Gilligan (2000*b*)
ψ_3	0.03	Keeling and Gilligan (2000*a*)
β	0.99	Estimated

Figure 5, Fig. 6, Fig. 7 and Fig. 8 show the dynamics of the compartments in human being, rodent, flea and Pathogens populations respectively. In human population, it can be seen that there is an increase in susceptible and infected human beings for a short period of time, then it decreases to the endemic equilibrium point. However due to natural recovery, the population of susceptible human beings is higher than the infectious human beings. The exposed human beings and recovered human beings experience the exponential decay to the endemic equilibrium

point due to due to progression from E_H to I_H and from R_H to S_H respectively

In rodent population, we note that there is a fast increase of infected rodent, it then undergoes exponential decay together with susceptible and Exposed rodent to the endemic point. In flea population there is increase of infected flea for the short time before it decays together with susceptible flea class to the endemic point. The Pathogens in the environment experience a rapid decay to the endemic point.

The features displayed by all groups are realistic and biologically relevant as there is no any intervention to combat the disease, the little recovery rate that is seen in human group is to those who are lucky enough to get treatment. Thus it is fact that the compartment in all groups will eventually decrease to the endemic points.

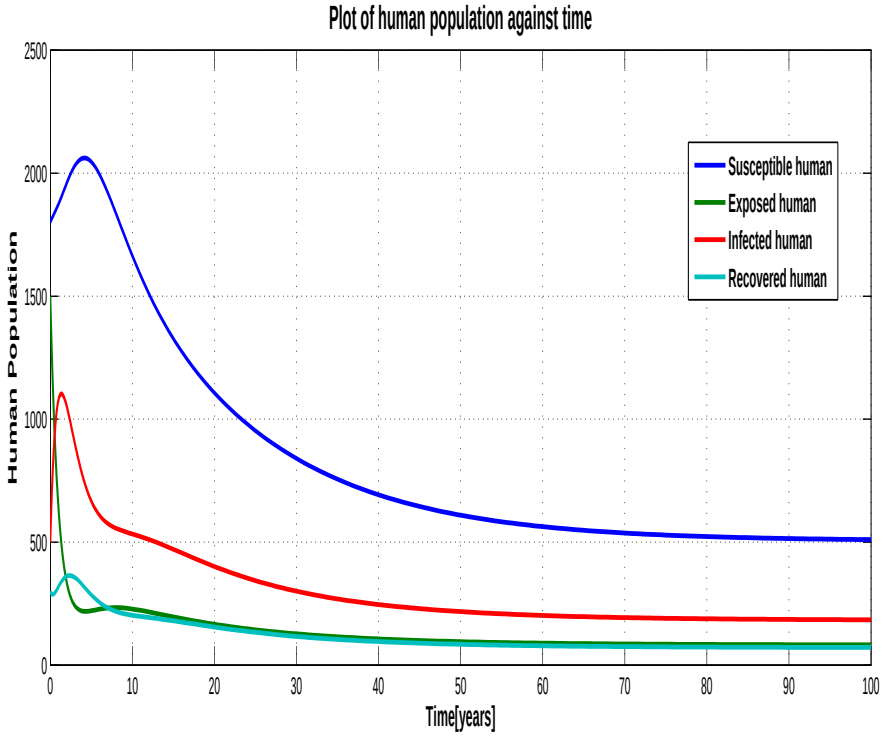


Figure 5: The dynamics of Susceptible, Exposed, Infected and Recovered human from sub-model (1) with baseline parameter values given in Table 3. These parameters correspond to $R0 = 3.2$.

2.5.2 Sensitivity analysis of R_0 for bubonic plague disease

The sensitivity analysis of R_0 for plague disease helps to determine the impact of various parameters on R_0 and thus the parameters' effect on the prevalence and transmission of bubonic plague disease (Chitnis *et al.*, 2008). In this section, we analyze the bubonic plague model by

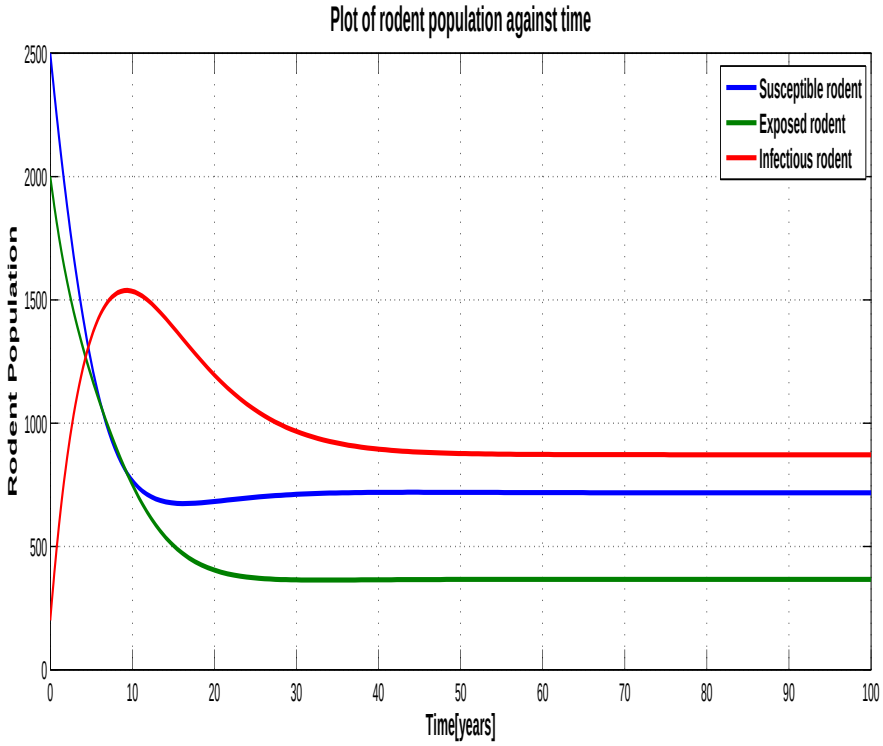


Figure 6: The dynamics of Susceptible, Exposed and Infected rodent from sub-model (2) with baseline parameter values given in Table 3. These parameters correspond to $R_0 = 3.2$.

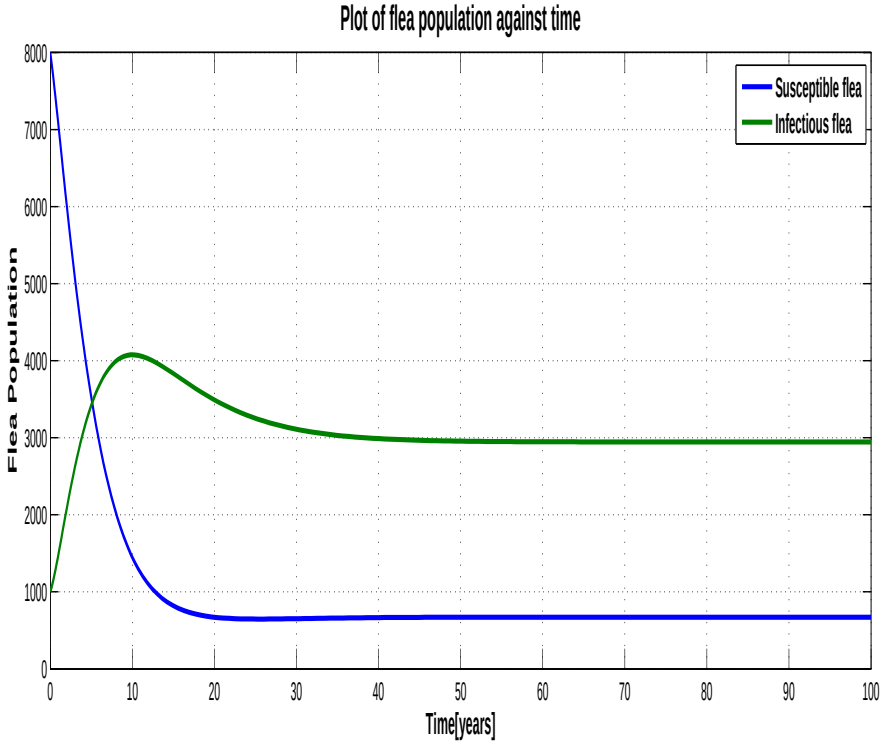


Figure 7: The dynamics of Susceptible and Infected flea from sub-model (3) with baseline parameter values given in Table 3. These parameters correspond to $R_0 = 3.2$.

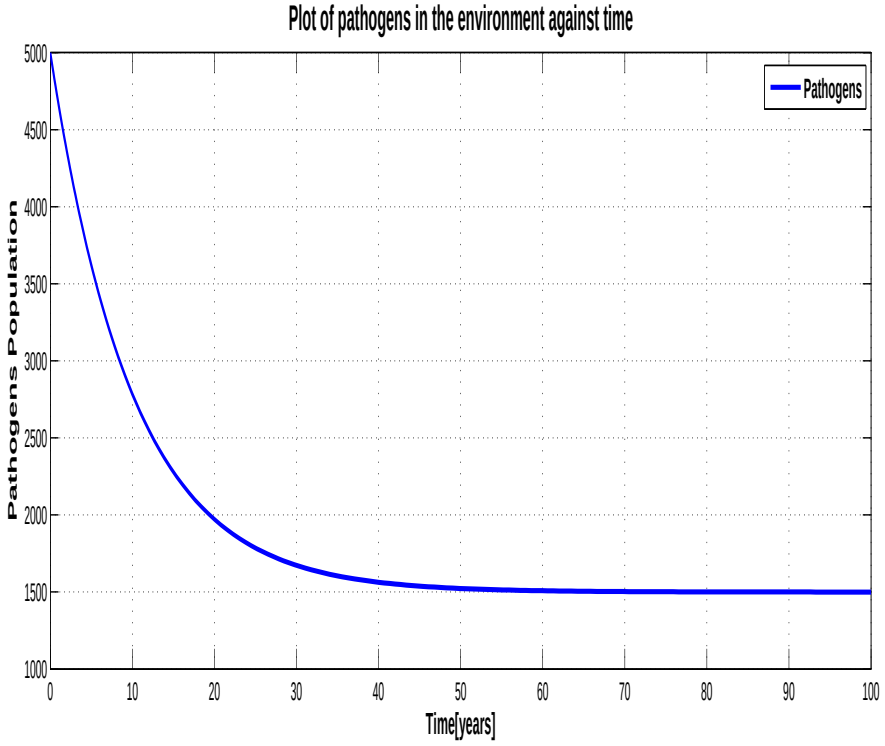


Figure 8: The dynamics of pathogens from sub-model (4) with baseline parameter values given in Table 3. These parameters correspond to $R_0 = 3.2$.

evaluating the sensitivity indices of the basic reproductive number, R_0, to model parameters using the baseline values given in Table 3. The basic reproduction number R_0 of bubonic plague depends on seventeen parameters, applying the method used by Chitnis *et al.* (2008) we derive an analytical expression for its sensitivity to each parameter using the normalized forward sensitivity indices of R_0 with respect to parameters n_i involved in R_0 as given below:

$$\Upsilon_{n_i}^{R_0} = \frac{\partial R_0}{\partial n_i} \times \frac{n_i}{R_0}$$

For example, the sensitivity indices of R_0 with respect to β and δ_2 are given respectively by:

$$\Upsilon_{\beta}^{R_0} = \frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0} = \frac{1}{2} \quad \text{and} \quad \Upsilon_{\delta_2}^{R_0} = \frac{\partial R_0}{\partial \delta_2} \times \frac{\delta_2}{R_0} = \frac{-\beta}{2(\mu_2 + \delta_2)}$$

Now using the same procedure we can find the indices for $\Upsilon_{\Gamma_{fh}}^{R_0}$, $\Upsilon_{\Gamma_{hf}}^{R_0}$, $\Upsilon_{\Gamma_{fr}}^{R_0}$, $\Upsilon_{\Gamma_{rf}}^{R_0}$, $\Upsilon_{\alpha_1}^{R_0}$, $\Upsilon_{\alpha_2}^{R_0}$, $\Upsilon_{\alpha_3}^{R_0}$, $\Upsilon_{\delta_1}^{R_0}$, $\Upsilon_{\delta_3}^{R_0}$, $\Upsilon_{\gamma_1}^{R_0}$, $\Upsilon_{\gamma_2}^{R_0}$, $\Upsilon_{\mu_1}^{R_0}$, $\Upsilon_{\mu_2}^{R_0}$ and $\Upsilon_{\mu_3}^{R_0}$ as tabulated in Table 4;

From Table 4 we observe that the most influential parameter is the probability that susceptible flea become infected (β), the indices of adequate contact rate from infectious flea to susceptible human being (Γ_{fh}), adequate contact rate infectious human being to susceptible flea (Γ_{hf}), probability that human progress from susceptible to exposed (α_1), adequate contact rate infectious flea to susceptible rodent (Γ_{fr}), adequate contact rate infectious rodent to susceptible

Table 4: Sensitivity indices evaluated at baseline parameter values for plague disease.

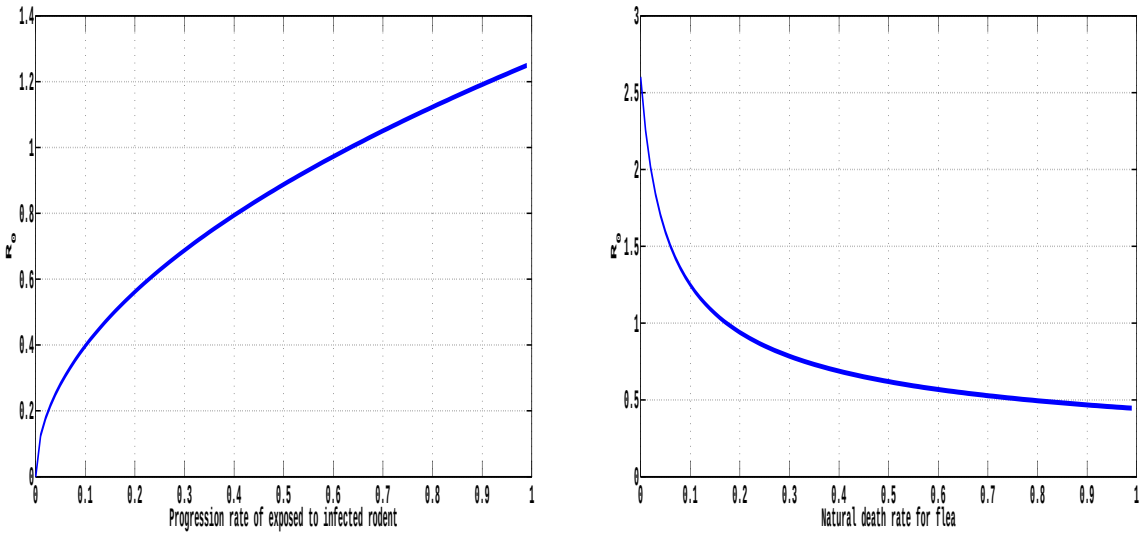
Parameter	**Sensitivity Index**	**Parameter**	**Sensitivity Index**
Γ_{rf}	+0.4986	δ_3	-0.0100
Γ_{fh}	+0.0014	μ_3	-0.3144
Γ_{fr}	+0.4986	μ_2	-0.8846
α_1	+0.0014	δ_2	-0.1154
γ_1	+0.4986	α_2	+0.0006
Γ_{hf}	+0.0014	γ_2	+0.4155
α_3	-0.0005	δ_1	-0.0004
μ_1	-0.0011	β	+0.5
ρ	+0.1232		

flea (Γ_{rf}), progression rate of exposed human being to infected human being (α_2), probability that rodent progress from susceptible to exposed (γ_1) and progression rate of exposed rodent to infected rodent (γ_2) are positive. The positive sign of the indices of the mentioned parameters imply that increasing (decreasing) one of these parameters while keeping others constant increases (decreases) the value of the basic reproduction number. For example the sensitivity indices of R_0 with respect to β given by

$$\Upsilon_{\beta}^{R_0} = \frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0} = \frac{1}{2}$$

implies that the increase of the probability that flea become infectious by 10%, increases the value of basic reproduction number by 5% and hence increases the chance of persistence of the disease; the vice versa is also true. Additionally, the indices of human recovery rate (α_3), disease induced death rate for human being (δ_1), disease induced death rate for flea (δ_2), disease induced death rate for rodent (δ_3), natural death rate for human being (μ_1), natural death rate for flea (μ_2) and natural death rate for rodent (μ_3) are negative. This implies that increasing (decreasing) one of these parameters while keeping the other constant decreases (increases) the value of basic reproduction number R_0 and hence decreases (increases) the chance of persistence of bubonic plague.

Figure 9 illustrates the effect of the most influential positive index (the probability that flea become infected (β)) and the most influential negative index (flea's natural death rate (μ_2)) on the basic reproduction number. In Fig. 9a we note that the increase of the probability at which fleas become infectious result in the rapid increase of the basic reproduction number. Figure 9b shows a quite significant exponential decrease of the basic reproduction number as we increase flea's natural death rate (μ_2). The behavior that is seen in Fig. 9b echoes that depict in Fig. 9a and shows that since fleas are the major player in the transmission and spread of plague disease.



(a) **(b)**

Figure 9: The effect of progression rate of exposed flea to infected and flea's natural death rate on the basic reproduction number

Hence the increase of flea's death rate will reduce the flea's population and thus automatically reduce the transmission rate of the bacteria causing bubonic plague disease in human beings, rodents and to the environment.

McNeill (2010) postulates that as the number of infected flea increases the disease transmission into the rodent and human populations increase as well, this is due to the significant role played by infected flea in the transmission of bubonic plague disease as demonstrated in Fig. 10. The parameters that increases the basic reproduction number proportionally increase the endemicity of the disease (Hartemink *et al.*, 2008).

In the basic reproduction number, the contribution of the pathogens in the environment is negligible, this is caused by the nature of bubonic plague (when the Yersinia pestis affect the lymphatic system) the transmission from the environment to human being and rodent population is very rare due to the effect of weather conditions (temperature, precipitation and humidity). For instance the studies by Shrewsbury (2005) and Armon and Cheruti (2012) postulate that *Yersinia pestis* survives at the temperature between $4°C$ to $8\ °C$. Under normal circumstances, taking Tanzania as an example, it is not common to find an area with such temperature. The absence of weather conditions that favors survival and growth of pathogens, leads to enormous loss of pathogens from the environment which as a result leads to its poor contribution to the transmission and spread of Bubonic Plague. However, if we assume the availability of the favorable condition for pathogen's growth and survival. The result will be the enormous increase in the population of pathogens in the environment. This will as a result increases the possibility of the disease transmission from the pathogens in the environment to the human beings and

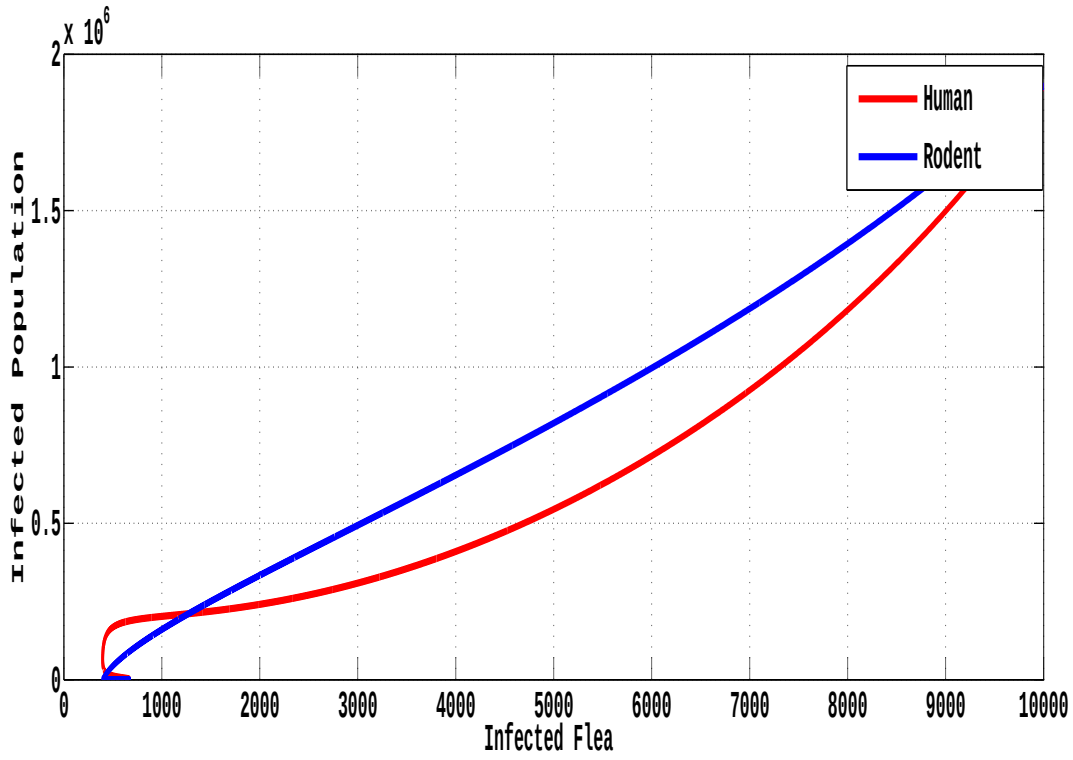


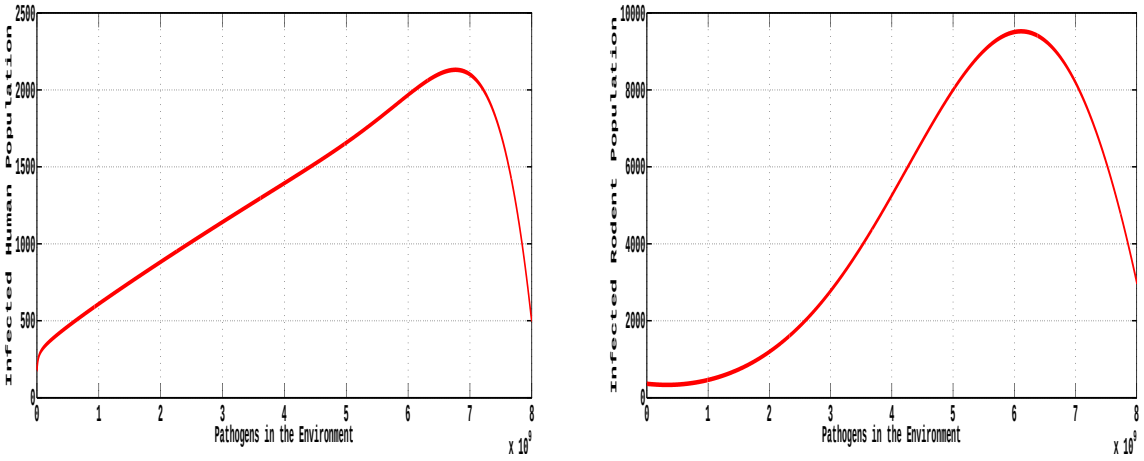
Figure 10: Variation of Infected Human and Rodent with Infected Flea population

rodents.

Figure 11a and Fig. 11b illustrate the effect of increasing number of pathogens in the environment on the infected human and rodent population respectively. The figures depict an increase in the number of infected human beings and rodents with the increase in the number of pathogens in the environment to their maximum which is the point where all human and rodent become infectious. The populations then decline due to natural and disease induced death.

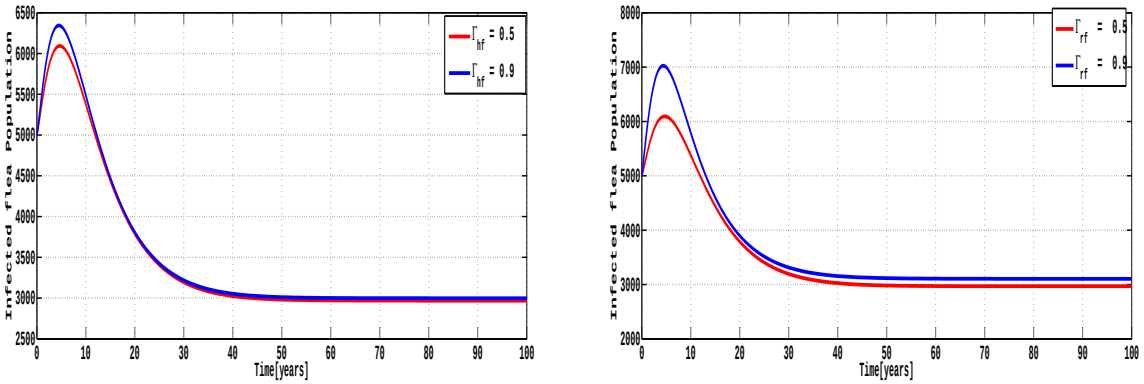
Transmission of the disease occurs after adequate contact between the infected flea with either the human being or the rodent and the vise versa. As seen in Table 4 adequate contact rates is very significant in the transmission and spread of bubonic plague disease. Figure 12a, Fig. 12b, Fig. 13a and Fig. 13b respectively show the effect of contact rate between human to flea, rodent to flea, and flea to human and rodent. We note that in all cases the increase of contact rate between the infected and the susceptible results in the number infected.

Therefore any mechanism/strategy of controlling bubonic plague disease must put into consideration the parameters that have shown a great influence in the transmission and spread of bubonic plague disease. Most of the parameters may be reduced by reducing the number of infected fleas and rodent population and disinfecting the contaminated environment by using various ways that will kill the pathogens. The analysis shows that the best control measure of



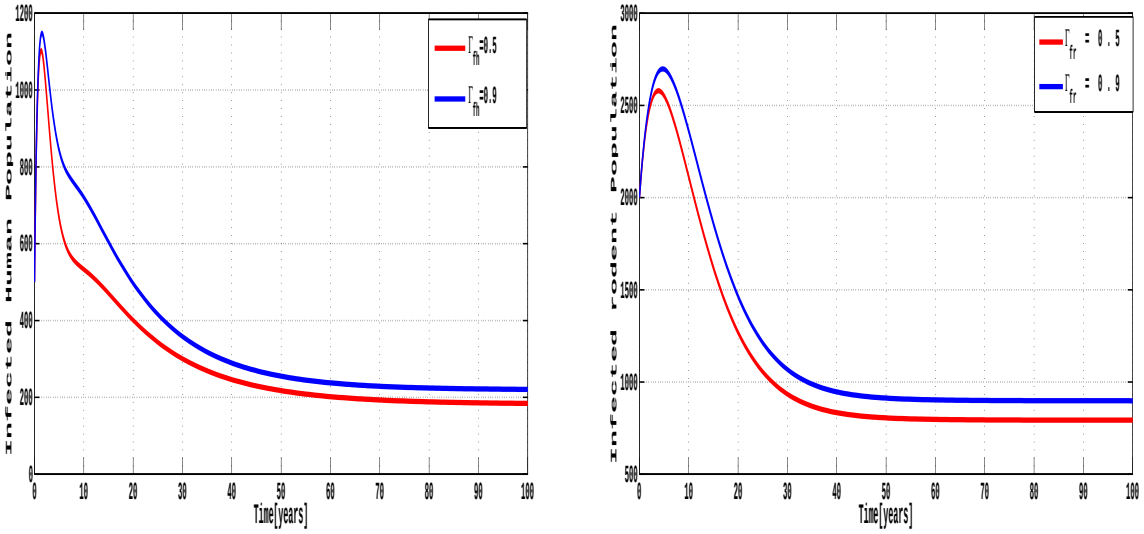
(a) **(b)**

Figure 11: Variation of Infected Human and Rodent with the increase in the number of Pathogens in the Environment



(a) Human to Flea **(b)** Rodent to Flea

Figure 12: The effect of contact rate on the infected flea population



(a) Flea to Human **(b)** Flea to Rodent

Figure 13: The effect of contact rate on the infected Human and Rodent population

the bubonic plague disease outbreak will be the one that will reduce the probability at which flea become infected(β). This will as a result reduce the number of infected fleas which are the major players in the transmission and spread of bubonic plague disease in human and rodent population. Although susceptible human beings and rodents may get the disease through the adequate interaction with the infected environment, to large extent infected flea carries the significant contribution in the transmission and spread of bubonic plague disease.

Also, there are parameters whose increase reduces the initial diseases transmission. These are natural and disease induced death rate for human, flea and rodent and human recovery rate. The increase of disease induced death rates in human, rodent and flea will reduce the population of infectious classes as a result hinders the occurrence of new infection and thus reduce initial bubonic plague transmission. The natural death rates for human, rodent and flea reduces the general population but most importantly it reduces the infectious and exposed classes which in turn reduce the transmission force of the disease. The human recovery rate reduces the number of infected human population and as a result it reduces the transmission force of the disease.

To effectively guide public policy and public health decision making, the mentioned factors that affect the parameter values must be highly considered. Using the values of the parameters used in this study the value of R_0 exceeds one, this tells us that the disease will persist within the community and thus various control measures should be taken to control and/or eliminate the disease.

2.6 Discussion and Conclusion

The SEIR model with modification was developed and analyzed to study the dynamics of bubonic plague disease, the model includes four populations which are human beings, rodents who are also the primary reservoir of Yesinia pestis, flea and pathogens within the environment. The analytical results show that bubonic plague transmission to both human and rodent population depends largely on the infected flea population. Moreover infected rodents and human beings are the major transmission agents of bubonic plague to flea population.

The basic reproduction number R_0 is computed and discussed. Using the sensitivity analysis, we obtain the parameter which are most, medium and least sensitive to the initial transmission of bubonic plague. The rate at which the infected flea are recruited and the adequate contact rates between susceptible and infected individuals have shown to have a significant positive contribution in the transmission and spread of bubonic plague disease as seen in Fig 9a and Fig 13. Other parameters like Fleas, Rodent and Human natural and disease induced death rate

contribute negatively on the bubonic plague transmission as in Fig 9b. These parameters are vital in determining where and how to implement the control strategies for the eradication of the disease.

The numerical solutions show that without the intervention, the populations ultimately go/approach to endemic points. This study recommends that for the sustainable control of bubonic plague any intervention strategy should put into consideration the parameter that have shown to be very influential (negatively and positively) to the basic reproduction number in order to reduce the endemicity of the disease or if possible eradicate the disease whenever an outbreak occur.

CHAPTER THREE

Stability Analysis of Bubonic Plague Model with the Causing Pathogen *Yersinia pestis* in the Environment [2]

Abstract: Bubonic plague is a serious bacterial disease, mainly transmitted to human beings and rodents through flea bite. However the disease may also be transmitted upon the interaction with the infected materials or surfaces in the environment. In this study, a deterministic model for bubonic plague disease with *yersinia pestis* in the environment is developed and analyzed. Conditions for existence and stability of the equilibrium points are established. Using the Jacobian method, disease free equilibrium (DFE) point, E^0 was proved to be locally asymptotically stable. The Metzler matrix method was used to prove that the DFE is globally asymptotically stable when $R_0 < 1$. By applying Lyapunov stability theory and LaSalle's invariant principle, we prove that the endemic equilibrium point of system is globally asymptotically stable when $R_0 > 1$. Numerical simulations are done to verify the analytical predictions. The results show that bubonic plague can effectively be controlled or even be eradicated if efforts are made to ensure that there is effective and timely control strategies.

Keywords: Disease free equilibrium; Endemic Equilibrium; Stability analysis; Bubonic Plague; Pathogens in the environment.

3.1 Introduction

Bubonic plague is a bacterial infection caused by *Yersinia pestis* when the bacteria infects lymphatic system (Gonzalez and Miller, 2016). It is characterised by geographical foci and extraordinarily adaptation capability which gives it ability to re-emerge even after decades of silence. Thus even though the disease is historic, it still infects and kills thousands of people around the world (Guinet *et al.*, 2015).

The disease mainly affects wild rodents, it can also be transmitted to human and other domestic animals through flea bites. Bubonic plague causes fever and very throbbing swelling of the lymph glands also called buboes, which is the reason why the disease is called bubonic plague.

When the flea is infested with pathogens causing bubonic plague, the bacteria multiply in the proventriculus (foregut) of the flea (Eisen *et al.*, 2015). The bacteria has the tendency of block-

[2]This chapter is based on the research paper: Ngeleja, R. C., Luboobi, L., & Nkansah-Gyekye, Y. (2016). Stability Analysis of Bubonic Plague Model with the Causing Pathogen Yersinia pestis in the Environment. *Advances in Infectious Diseases, 6*(03), 120.

ing the flea's bloodsucking apparatus which consequently lead to the inability of flea to pump blood into the midgut for digestion. This makes the flea to become ravenous and as a result it bites the host repetitively while vomiting the bacteria causing disease into the host. When a host dies, fleas moves off the body to seek another live warm-blooded host (Ayyadurai *et al.*, 2008).

Although it is not yet clearly known how, Yersinia pestis may survive in the soil and remain viable and fully virulent for 40 weeks in the environment and can cause the infection upon the adequate interaction with the susceptible individual. This is believed to be the reason for possible mechanism of interepizootic persistence, epizootic spread, and as a factor defining plague foci (Eisen *et al.*, 2008).

In this chapter, we discuss the stability analysis of the bubonic plague epidemic model in human, rodent and flea population. The model includes the transmission from the environment to the susceptible human or rodent. We also discuss the disease-free equilibrium point, endemic equilibrium point of the model and analyze the local and global stability of these steady states. We finally use numerical simulations to support our analytical results.

3.2 Model Formulation

This chapter presents the stability analysis of the bubonic plague epidemic model developed by Ngeleja *et al.* (2016). The model includes four interacting populations which are: human population, Flea population, Rodent population and pathogens in the environment is developed. We use S_H, E_H, I_H and R_H to represent Susceptible human beings, Exposed human beings, Infected human beings and Recovered human beings respectively; S_R, E_R and I_R for Susceptible rodents, Exposed rodents and Infected rodents respectively. The Susceptible and the Infectious flea are denoted by S_F and I_F respectively. The pathogens in the environment are denoted by A. The total population for human being, rodent and flea population are given by

$$N_1 = S_H + E_H + I_H + R_H \tag{1a}$$

$$N_2 = S_F + I_F \tag{1b}$$

$$N_3 = S_R + E_R + I_R \tag{1c}$$

The parameters used in the model are described in Table 5

Table 5: Parameters and their description for bubonic plague

Parameter	Description .
Γ_{rf}	Adequate contact rate: infected rodent to flea
Γ_{fh}	Adequate contact rate: infected flea to human
Γ_{fr}	Adequate contact rate: infected flea to rodent
α_1	The probability that human progress from susceptible to exposed
γ_1	Probability that rodent progress from susceptible to exposed
Γ_{hf}	Adequate contact rate: infected human to flea
λ_4	Recruitment rate of pathogens
α_2	Progression rate of exposed human to infected
γ_2	Progression rate of exposed rodent to infected
α_3	Human recovery rate
ϖ	Progression rate of recovered human to susceptible
μ_1	Natural death rate for Human
δ_1	Disease induced death rate for Human
δ_3	Disease induced death rate for rodent
μ_3	Natural death rate for rodent
ω_1	Adequate contact rate: Pathogens to human
ω_2	Adequate contact rate: Pathogens to rodent
μ_4	Natural death rate for Pathogens
μ_2	Natural death rate for flea
δ_2	Disease induced death rate for flea
ψ_1	Immigration rate of human
ψ_{2s}	Immigration rate of Susceptible flea
ψ_3	Immigration rate of rodent
β	The probability at which fleas become infected

3.2.1 Model Equations for bubonic Plague

Since we allow the population in and out of the compartments(i.e., the population is not fixed), the rate at which new infections occur in a population will depend on the fraction of the population that is infected (disease prevalence) (i.e., frequency-dependent formulation). The infection rate in human beings depends on the probability that a contact between infectious flea and sus-

ceptible human and between infectious environment and susceptible human leads to infection. For the rodent, infection depends on the probability that a contact between infectious flea and susceptible rodent and between infectious environment and susceptible rodent leads to infection. For the flea, infection depends on the probability that a contact between infectious human and susceptible flea and between infectious rodent and susceptible flea leads to infection. Therefore the infection rates of susceptible humans, rodent population and flea population are as given in (2a), (2b) and (2c) respectively.

$$\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A \tag{2a}$$

$$\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A \tag{2b}$$

$$\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_r}{N_3} \tag{2c}$$

Pathogens in the environment are recruited at a constant rate λ_4 and they are removed through natural death μ_4 or removed when they come into contact with susceptible human and rodent at the rates ω_1 and ω_2 respectively.

Using the definition of variables and parameters stated in Table 5, we derive the model for the dynamics of bubonic plague disease in human, rodent, flea and pathogens in the environment as given in (3), (4), (5) and (6) respectively.

Human

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \mu_1 S_H, \tag{3a}$$

$$\frac{dE_H}{dt} = \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \alpha_2 E_H - \mu_1 E_H, \tag{3b}$$

$$\frac{dI_H}{dt} = \alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1)I_H, \tag{3c}$$

$$\frac{dR_H}{dt} = \alpha_3 I_H - \varpi R_H - \mu_1 R_H. \tag{3d}$$

Rodent

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \mu_3 S_R \tag{4a}$$

$$\frac{dE_R}{dt} = \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \gamma_2 E_R - \mu_3 E_R \tag{4b}$$

$$\frac{dI_R}{dt} = \gamma_2 E_R - (\mu_3 + \delta_3)I_R \tag{4c}$$

Flea

$$\frac{dS_F}{dt} = \psi_{2s} - \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - \mu_2 S_F \tag{5a}$$

$$\frac{dI_F}{dt} = \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - (\mu_2 + \delta_2)I_F \tag{5b}$$

Pathogens

$$\frac{dA}{dt} = \lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A \tag{6}$$

3.3 Steady State and Local Stability of the Critical Points

In this section, we assess the existence of equilibrium states and stability of the equilibrium states of the system (3) - (6).

3.3.1 Disease Free Equilibrium

The model has a disease free equilibrium which is obtained by setting $I_H = E_H = R_H = 0$, $I_R = E_R = 0$, $I_F = 0$ and $A = 0$ and the derivatives equal to zero into the system (3) - (6).

Then we have the disease free-equilibrium point given as $E_H^0 = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0\right)$, $E_R^0 = \left(\frac{\psi_3}{\mu_3}, 0, 0\right)$, $E_F^0 = \left(\frac{\psi_{2s}}{\mu_2}, 0\right)$ and $E_A^0 = 0$ for Human, Rodent, Flea and Pathogen respectively.

Then the disease free equilibrium of the entire system is

$$E^0(S_H^0, E_H^0, I_H^0, R_H^0, S_R^0, E_R^0, I_R^0, S_F^0, I_F^0, A^0) = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0, \frac{\psi_3}{\mu_3}, 0, 0, \frac{\psi_{2s}}{\mu_2}, 0, 0\right)$$

3.3.2 Local Stability of the Disease-free Equilibrium Point

In this section, we examine the local stability analysis of the disease free equilibrium point of the bubonic plague disease system (3) - (6). We analyze the local stability of the disease free equilibrium point using the Jacobian method in which all equations in system (3) - (6) are considered and analyzed at the disease free equilibrium E^0. In this method, we compute and examine the eigenvalues of Jacobian matrix of the system (3) - (6) to prove that the DFE is locally and asymptotically stable. We are required to show that all real parts of the eigenvalues at E^0 are negative. Now, in order to attest that the eigenvalues are negative, we need to prove the general condition that the determinant and the trace of the Jacobian matrix are positive and negative respectively (Martcheva, 2015).

Now the Jacobian matrix of the system (3) - (6) at E^0 is given by:

$$\mathbf{J}(\mathbf{E^0}) = \begin{pmatrix} -\mu_1 & 0 & 0 & \varpi & 0 & 0 & 0 & 0 & -k_3 & \frac{-\alpha_1\psi_1\omega_1}{\mu_1} \\ 0 & -k_7 & 0 & 0 & 0 & 0 & 0 & 0 & k_3 & \frac{\alpha_1\psi_1\omega_1}{\mu_1} \\ 0 & \alpha_2 & -k_6 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_3 & -k_9 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_3 & 0 & 0 & 0 & -k_4 & \frac{-\gamma_1\psi_3\omega_2}{\mu_3} \\ 0 & 0 & 0 & 0 & 0 & -k_{10} & 0 & 0 & k_4 & \frac{\gamma_1\psi_3\omega_2}{\mu_3} \\ 0 & 0 & 0 & 0 & 0 & \gamma_2 & -k_{11} & 0 & 0 & 0 \\ 0 & 0 & -k_1 & 0 & 0 & 0 & -k_2 & -\mu_2 & 0 & 0 \\ 0 & 0 & k_1 & 0 & 0 & 0 & k_2 & 0 & -k_8 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -k_5 \end{pmatrix} \tag{7}$$

where

$$\begin{aligned} k_1 &= \tfrac{\beta\rho\Gamma_{hf}\psi_{2s}\mu_1}{\psi_1\mu_2} & k_2 &= \tfrac{\beta(1-\rho)\Gamma_{rf}\psi_{2s}\mu_3}{\psi_3\mu_2} & k_3 &= \tfrac{\alpha_1\psi_1\mu_2\Gamma_{fh}}{\mu_1\psi_{2s}} \\ k_4 &= \tfrac{\gamma_1\psi_3\mu_2\Gamma_{fr}}{\mu_3\psi_{2s}} & k_5 &= \omega_1+\omega_2+\mu_4 & k_6 &= \alpha_3+\mu_1+\delta_1 \\ k_7 &= \alpha_2+\mu_1 & k_8 &= \mu_2+\delta_2 & k_9 &= \varpi+\mu_1 \\ k_{10} &= \gamma_2+\mu_3 & k_{11} &= \mu_3+\delta_3 \end{aligned}$$

We now use trace and determinant method to check the stability of the disease free equilibrium point E^0 in which we need to prove that the trace and the determinant of matrix (7) are negative and positive respectively.

Then using mathematica software we prove that trace of the matrix (7) is given by

$$\mathbf{Trace} = -\mu_1-(\alpha_2+\mu_1)-k_6-(\varpi+\mu_1)-\mu_3-(\gamma_2+\mu_3)-(\mu_3+\delta_3)-\mu_2-(\mu_2+\delta_2)-k_5$$

where

$$k_5 = \omega_1+\omega_2+\mu_4 \quad k_6 = \alpha_3+\mu_1+\delta_1$$

It is clear that the trace of the matrix (7) in negative. Then using the same software (mathematica) we are able to prove that the determinant of the matrix (7) is positive provided:

$$\sqrt{\frac{\beta}{(\mu_2+\delta_2)}\left(\frac{\gamma_2\gamma_1\Gamma_{rf}\Gamma_{fr}(1-\rho)}{(\mu_3+\gamma_2)(\mu_3+\delta_3)}+\frac{\rho\alpha_2\alpha_1\Gamma_{hf}\Gamma_{fh}}{(\alpha_2+\mu_1)(\alpha_3+\mu_1+\delta_1)}\right)} < 1$$

where

$$\sqrt{\frac{\beta}{(\mu_2+\delta_2)}\left(\frac{\gamma_2\gamma_1\Gamma_{rf}\Gamma_{fr}(1-\rho)}{(\mu_3+\gamma_2)(\mu_3+\delta_3)}+\frac{\rho\alpha_2\alpha_1\Gamma_{hf}\Gamma_{fh}}{(\alpha_2+\mu_1)(\alpha_3+\mu_1+\delta_1)}\right)} \tag{8}$$

is the basic reproduction number, R_0.

R_0 measures the average number of secondary infection produced by a typical infectious individual in an entirely susceptible population. In our case, due to the presence of multiple transmission cycles the basic reproductive number does not give the number of cases infected by a single individual rather it gives the geometric mean of the number of infections per generation (Li and Blakeley, 2011).

Referring to (8), the geometric mean of the number of infections per generation depends on: rodent's infective period $\frac{1}{\mu_3+\delta_3}$, the probability that flea gets the disease from the rodent or

human which are $(1-\rho)\Gamma_{rf}$ or $\rho\Gamma_{hf}$ respectively. The human infectious period $\frac{1}{\mu_1+\delta_1+\alpha_3}$, probability that human survive the infected class $\frac{\alpha_2}{\mu_1+\alpha_2}$, the probability at which fleas gets infected β, flea's infective period $\frac{1}{\mu_2+\delta_2}$, probability that rodent survive the infected class $\frac{\gamma_2}{\mu_3+\gamma_2}$, the adequate contact rate flea to human Γ_{fh}, the adequate contact rate flea to rodent Γ_{fr} and the probability at which human and rodent become exposed to the disease which are α_1 and γ_1 respectively.

Thus disease free equilibrium point E^0 is therefore locally asymptotically stable and leads to the following theorem:

Theorem 3.3
The Disease Free Equilibrium E^0 of bubonic plague is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

3.3.3 Global Stability of the Disease-free Equilibrium Point

In this section, we analyze the global stability of the disease free equilibrium point using Metzler matrix method as stated by Castillo-Chavez *et al.* (2002). To do this, we first sub-divide the general system (3) - (6) of bubonic plague disease into transmitting and non-transmitting components.

Now let $\mathbf{Y_n}$ be the vector for non-transmitting compartment, $\mathbf{Y_i}$ be the vector for transmitting compartment and $\mathbf{Y_{E_0,n}}$ be the vector of disease free point. Then

$$\begin{cases} \dfrac{d\mathbf{Y_n}}{dt} &= A_1(\mathbf{Y_n} - \mathbf{Y_{E_0,n}}) + A_2\mathbf{Y_i} \\ \\ \dfrac{d\mathbf{Y_i}}{dt} &= A_3\mathbf{Y_i} \end{cases} \tag{9}$$

We then have

$$\mathbf{Y_n} = (S_H, R_H, S_R, S_F)^T \quad \mathbf{Y_i} = (E_H, I_H, E_R, I_R, I_F, A) \quad \mathbf{Y_{E_0,n}} = (\tfrac{\psi_1}{\mu_1}, 0, \tfrac{\psi_3}{\mu_3}, \tfrac{\psi_{2s}}{\mu_2})$$

$$\mathbf{Y_n} - \mathbf{Y_{E_0,n}} = \begin{pmatrix} S_H - \frac{\psi_1}{\mu_1} \\ R_H \\ S_R - \frac{\psi_3}{\mu_3} \\ S_F - \frac{\psi_{2s}}{\mu_2} \end{pmatrix}$$

Now to prove the global stability of the DFE we need to show that Matrix A_1 has real negative eigenvalues and A_3 is a Metzler matrix in which all off diagonal element must be non-negative.

Referring to (9), we write the general model as below

$$\begin{pmatrix} \psi_1 + \varpi R_H - \alpha_1 k S_H - \mu_1 S_H, \\ \alpha_3 I_H - \varpi R_H - \mu_1 R_H. \\ \psi_3 - \gamma_1 M S_R - \mu_3 S_R \\ \psi_{2s} - \beta Y S_F - \mu_2 S_F \end{pmatrix} = A_1 \begin{pmatrix} S_H - \frac{\psi_1}{\mu_1} \\ R_H \\ S_R - \frac{\psi_3}{\mu_3} \\ S_F - \frac{\psi_{2s}}{\mu_2} \end{pmatrix} + A_2 \begin{pmatrix} E_H \\ I_H \\ E_R \\ I_R \\ I_F \\ A \end{pmatrix}$$

and

$$\begin{pmatrix} \alpha_1 k S_H - \alpha_2 E_H - \mu_1 E_H, \\ \alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1) I_H, \\ \gamma_1 M S_R - \gamma_2 E_R - \mu_3 E_R \\ \gamma_2 E_R - (\mu_3 + \delta_3) I_R \\ \beta Y S_F - (\mu_2 + \delta_2) I_F \\ \lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A \end{pmatrix} = A_3 \begin{pmatrix} E_H \\ I_H \\ E_R \\ I_R \\ I_F \\ A \end{pmatrix}$$

For

$$k = (\Gamma_{fh} \tfrac{I_F}{N_2} + \omega_1 A) \quad M = (\Gamma_{fr} \tfrac{I_F}{N_2} + \omega_2 A) \quad Y = (\rho \Gamma_{hf} \tfrac{I_H}{N_1} + (1-\rho) \Gamma_{rf} \tfrac{I_R}{N_3})$$

Now using the transmitting and non-transmitting element on the general system we will have the matrices below:

$$\mathbf{A_1} = \begin{pmatrix} -\mu_1 & \varpi & 0 & 0 \\ 0 & -(\varpi + \mu_1) & 0 & 0 \\ 0 & 0 & -\mu_3 & 0 \\ 0 & 0 & 0 & -\mu_2 \end{pmatrix} \tag{10}$$

$$\mathbf{A_2} = \begin{pmatrix} 0 & 0 & 0 & 0 & \frac{-\alpha_1 \psi_1 \mu_2 \Gamma_{fh}}{\mu_1 \psi_{2s}} & \frac{-\alpha_1 \psi_1 \omega_1}{\mu_1} \\ 0 & \alpha_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{-\gamma_1 \psi_3 \mu_2 \Gamma_{fr}}{\mu_3 \psi_{2s}} & \frac{-\gamma_1 \psi_3 \omega_2}{\mu_3} \\ 0 & \frac{-\beta \psi_{2s} \mu_1 \rho \Gamma_{hf}}{\mu_2 \psi_1} & 0 & \frac{-\beta \psi_{2s} \mu_3 (1-\rho) \Gamma_{rf}}{\mu_2 \psi_3} & 0 & 0 \end{pmatrix} \tag{11}$$

$$\mathbf{A_3} = \begin{pmatrix} -(\alpha_2 + \mu_1) & 0 & 0 & 0 & \frac{\alpha_1 \psi_1 \mu_2 \Gamma_{fh}}{\mu_1 \psi_{2s}} & \frac{\alpha_1 \psi_1 \omega_1}{\mu_1} \\ \alpha_2 & -\zeta_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\gamma_2 + \mu_3) & 0 & \frac{\gamma_1 \psi_3 \mu_2 \Gamma_{fr}}{\mu_3 \psi_{2s}} & \frac{\gamma_1 \psi_3 \omega_2}{\mu_3} \\ 0 & 0 & \gamma_2 & -(\mu_3 + \delta_3) & 0 & 0 \\ 0 & \zeta_3 & 0 & \frac{\beta(1-\rho) \Gamma_{rf} \psi_{2s} \mu_3}{\psi_3 \mu_2} & -(\mu_2 + \delta_2) & 0 \\ 0 & 0 & 0 & 0 & 0 & -\zeta_2 \end{pmatrix} \tag{12}$$

where $\zeta_1 = (\alpha_3 + \mu_1 + \delta_1)$, $\zeta_2 = (\omega_1 S_H + \omega_2 S_R + \mu_4)$ and $\zeta_3 = \frac{\beta\rho\Gamma_{hf}\psi_{2s}\mu_1}{\psi_1\mu_2}$
Now when we consider matrix A_1, the computation shows that the eigenvalues are real and negative, which now confirms that the system

$$\frac{d\mathbf{Y_n}}{dt} = A_1(\mathbf{Y_n} - \mathbf{Y_{E_0,n}}) + A_2\mathbf{Y_i}$$

is globally and asymptotically stable at $\mathbf{Y_{E_0}}$. And for matrix A_3 we find that all its off-diagonal elements are non-negative and thus A_3 is a Metzler stable matrix.Therefore Disease Free Equilibrium point for the general bubonic plague system is globally asymptotically stable and as a result we have the following theorem:

Theorem 3.4
The disease-free equilibrium point is globally asymptotically stable in E_0 if $R_0 < 1$ and unstable if $R_0 > 1$.

3.3.4 Existence of Endemic Equilibrium

Here, we consider the situation in which the disease persists in a population. We investigate conditions for existence of the endemic equilibrium point of the system (3)-(6). The endemic equilibrium point $E^*(S_H^*, E_H^*, I_H^*, R_H^*, S_R^*, E_R^*, I_R^*, S_F^*, I_F^*, A^*)$ is obtained by solving the equations obtained by setting the derivatives of (3)-(6) equal to zero as in (13)-(16) which exist for $R_O > 1$.

Human

$$\psi_1 + \varpi R_H - \alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \mu_1 S_H = 0 \tag{13a}$$

$$\alpha_1(\Gamma_{fh}\frac{I_F}{N_2} + \omega_1 A)S_H - \alpha_2 E_H - \mu_1 E_H = 0 \tag{13b}$$

$$\alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1)I_H = 0 \tag{13c}$$

$$\alpha_3 I_H - \varpi R_H - \mu_1 R_H = 0 \tag{13d}$$

Rodent

$$\psi_3 - \gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \mu_3 S_R = 0 \tag{14a}$$

$$\gamma_1(\Gamma_{fr}\frac{I_F}{N_2} + \omega_2 A)S_R - \gamma_2 E_R - \mu_3 E_R = 0 \tag{14b}$$

$$\gamma_2 E_R - (\mu_3 + \delta_3)I_R = 0 \tag{14c}$$

Flea

$$\psi_{2s} - \beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - \mu_2 S_F = 0 \tag{15a}$$

$$\beta(\rho\Gamma_{hf}\frac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\frac{I_R}{N_3})S_F - (\mu_2 + \delta_2)I_F = 0 \tag{15b}$$

Pathogens

$$\lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A = 0 \tag{16}$$

Since it is difficult to obtain explicitly the endemic equilibrium points of the model, we will prove its existence using the approach described in the studies by Tumwiine *et al.* (2007) and Massawe *et al.* (2015). For the endemic equilibrium to exist it must satisfy the condition $E_H \neq 0$ or $I_H \neq 0$ or $E_R \neq 0$ or $I_R \neq 0$ or $I_F \neq 0$ or $A \neq 0$ that is $S_H > 0$ or $E_H > 0$ or $I_H > 0$ or $S_R > 0$ or $I_R > 0$ or $E_R > 0$ or $S_F > 0$ or $I_F > 0$ or $A > 0$ must be satisfied. Now adding system (13)-(16) we have

$$\begin{aligned} &\psi_1 + \psi_{2s} + \psi_3 + \lambda_4 - \mu_1(S_H + E_H + I_H + R_H) - \mu_2(S_F + I_F) \\ &- \mu_3(S_R + E_R + I_R) - \delta_1 I_H - \delta_2 I_F - \delta_3 I_R - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A = 0 \end{aligned} \tag{17}$$

Substituting $N_1 = S_H + E_H + I_H + R_H$, $N_2 = S_F + I_F$ and $N_3 = S_R + E_R + I_R$ in (17) we have

$$\psi_1 + \psi_{2s} + \psi_3 - \mu_1 N_1 - \mu_2 N_2 - \mu_3 N_3 - \delta_1 I_H - \delta_2 I_F - \delta_3 I_R + \lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A = 0 \tag{18}$$

But from equation (16), we have $\lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A = 0$
It follows that

$$\mu_1 N_1 + \mu_2 N_2 + \mu_3 N_3 + \delta_1 I_H + \delta_2 I_F + \delta_3 I_R = \psi_1 + \psi_{2s} + \psi_3$$

Since $\psi_1 + \psi_{2s} + \psi_3 > 0$, $\mu_1 > 0$, $\mu_2 > 0$, $\mu_3 > 0$, $\delta_1 > 0$, $\delta_2 > 0$ and $\delta_3 > 0$ we can discern that $\mu_1 N_1 > 0$, $\mu_2 N_2 > 0$, $\mu_3 N_3 > 0$, $\delta_1 I_H > 0$, $\delta_2 I_F > 0$ and $\delta_3 I_R > 0$ implying that $S_H > 0$, $E_H > 0$, $I_H > 0$, $S_F > 0$, $I_F > 0$, $S_R > 0$, $E_R > 0$ and $I_R > 0$.
Hence endemic equilibrium point of the bubonic plague disease model in human, rodent, flea and pathogens in the environment exists.

Since the endemic equilibrium points exist, we now determine the conditions under which they are stable or unstable. We prove whether the solution starting sufficiently close to the equilibrium remains close to the equilibrium and approaches the equilibrium as $t \to \infty$, or if there are solutions starting arbitrary close to the equilibrium which do not approach it respectively.

3.3.5 Global stability of Endemic equilibrium point

Using the idea from the study by Van den Driessche and Watmough (2002), we assert that the local stability of the Disease Free Equilibrium advocates for local stability of the Endemic Equilibrium for the reverse condition. We then work to find the global stability of Endemic equilibrium using a Korobeinikov approach as stipulated in Van den Driessche and Watmough (2002), Korobeinikov (2004) and Korobeinikov (2007) by forming a suitable Lyapunov function

for our general model as given below:
We construct the Lyapunov function as given in the form:

$$V = \sum a_i(y_i - y_i^* \ln y_i)$$

where a_i is defined as a properly selected positive constant, y_i defines the population of the i^{th} compartment, and y_i^* is the equilibrium point.
We will have the following Lyapunov function,

$$\begin{aligned} V = \; & W_1(S_H - S_H^* \ln S_H) + W_2(E_H - E_H^* \ln E_H) + W_3(I_H - I_H^* \ln I_H) \\ & + W_4(R_H - R_H^* \ln R_H) + W_5(S_R - S_R^* \ln S_R) + W_6(E_R - E_R^* \ln E_R) \\ & + W_7(I_R - I_R^* \ln I_R) + W_8(S_F - S_F^* \ln S_F) + W_9(I_F - I_F^* \ln I_F) \\ & + W_{10}(A - A^* \ln A) \end{aligned}$$

The constants W_i are non-negative in Φ such that $W_i > 0$ for $i = 1, 2, 3...10$. The Lyapunov function V together with its constants $W_1, W_2, ..., W_{10}$ chosen in such a way that V is continuous and differentiable in a space.

We then compute the time derivative of V from which we get:

$$\begin{aligned} \frac{dV}{dt} = \; & W_1(1 - \tfrac{S_H^*}{S_H})\tfrac{dS_H}{dt} + W_2(1 - \tfrac{E_H^*}{E_H})\tfrac{dE_H}{dt} + W_3(1 - \tfrac{I_H^*}{I_H})\tfrac{dI_H}{dt} \\ & + W_4(1 - \tfrac{R_H^*}{R_H})\tfrac{dR_H}{dt} + W_5(1 - \tfrac{S_R^*}{S_R})\tfrac{dS_R}{dt} + W_6(1 - \tfrac{E_R^*}{E_R})\tfrac{dE_R}{dt} \\ & + W_7(1 - \tfrac{I_R^*}{I_R})\tfrac{dI_R}{dt} + W_8(1 - \tfrac{S_F^*}{S_F})\tfrac{dS_F}{dt} + W_9(1 - \tfrac{I_F^*}{I_F})\tfrac{dI_F}{dt} \\ & + W_{10}(1 - \tfrac{A^*}{A})\tfrac{dA}{dt} \end{aligned}$$

Now using the general system (3)-(6) we will have

$$\begin{aligned} \frac{dV}{dt} = \; & W_1(1 - \tfrac{S_H^*}{S_H})[\psi_1 + \varpi R_H - \alpha_1(\Gamma_{fh}\tfrac{I_F}{N_2} + \omega_1 A)S_H - \mu_1 S_H] \\ & + W_2(1 - \tfrac{E_H^*}{E_H})[\alpha_1(\Gamma_{fh}\tfrac{I_F}{N_2} + \omega_1 A)S_H - \alpha_2 E_H - \mu_1 E_H] \\ & + W_3(1 - \tfrac{I_H^*}{I_H})[\alpha_2 E_H - \alpha_3 I_H - (\mu_1 + \delta_1)I_H] \\ & + W_4(1 - \tfrac{R_H^*}{R_H})[\alpha_3 I_H - \varpi R_H - \mu_1 R_H] \\ & + W_5(1 - \tfrac{S_R^*}{S_R})[\gamma_1(\Gamma_{fr}\tfrac{I_F}{N_2} + \omega_2 A)S_R - \mu_3 S_R] \\ & + W_6(1 - \tfrac{E_R^*}{E_R})[\gamma_1(\Gamma_{fr}\tfrac{I_F}{N_2} + \omega_2 A)S_R - \gamma_2 E_R - \mu_3 E_R] \\ & + W_7(1 - \tfrac{I_R^*}{I_R})[\gamma_2 E_R - (\mu_3 + \delta_3)I_R] \\ & + W_8(1 - \tfrac{S_F^*}{S_F})[\psi_{2s} - \beta(\rho\Gamma_{hf}\tfrac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\tfrac{I_R}{N_3})S_F - \mu_2 S_F] \\ & + W_9(1 - \tfrac{I_F^*}{I_F})[\beta(\rho\Gamma_{hf}\tfrac{I_H}{N_1} + (1-\rho)\Gamma_{rf}\tfrac{I_R}{N_3})S_F - (\mu_2 + \delta_2)I_F] \\ & + W_{10}(1 - \tfrac{A^*}{A})[\lambda_4 - \omega_1 A S_H - \omega_2 A S_R - \mu_4 A] \end{aligned}$$

At endemic equilibrium point we have

Human

$$\psi_1 = -\varpi R_H^* + \alpha_1(\Gamma_{fh}\frac{I_F^*}{N_2^*} - \omega_1 A^*)S_H^* + \mu_1 S_H^*, \tag{19a}$$

$$(\alpha_2 + \mu_1) = \frac{1}{E_H^*}\alpha_1(\Gamma_{fh}\frac{I_F^*}{N_2^*} + \omega_1 A^*)S_H^*, \tag{19b}$$

$$\alpha_2 = \frac{1}{E_H^*}(\alpha_3 I_H^* + (\mu_1 + \delta_1)I_H^*) \tag{19c}$$

$$\alpha_3 = \frac{1}{I_H^*}(\varpi + \mu_1)R_H^* \tag{19d}$$

Rodent

$$\psi_3 = \gamma_1(\Gamma_{fr}\frac{I_F^*}{N_2^*} - \omega_2 A^*)S_R^* + \mu_3 S_R^* \tag{20a}$$

$$(\gamma_2 + \mu_3) = \frac{1}{E_R^*}\left(\gamma_1(\Gamma_{fr}\frac{I_F^*}{N_2^*} - \omega_2 A^*)S_R^*\right) \tag{20b}$$

$$\gamma_2 = \frac{1}{E_R^*}\left(\mu_3 + \delta_3\right) I_R^* \tag{20c}$$

Flea

$$\psi_{2s} = \beta(\rho\Gamma_{hf}\frac{I_H^*}{N_1^*} - (1-\rho)\Gamma_{rf}\frac{I_R^*}{N_3^*})S_F^* + \mu_2 S_F^* \tag{21a}$$

$$(\mu_2 + \delta_2) = \frac{1}{I_F^*}\beta(\rho\Gamma_{hf}\frac{I_H^*}{N_1^*} - (1-\rho)\Gamma_{rf}\frac{I_R^*}{N_3^*})S_F^* \tag{21b}$$

Pathogens

$$\lambda_4 = \omega_1 A^* S_H^* + \omega_2 A^* S_R^* + \mu_4 A^* \tag{22}$$

We use equations (19),(20),(21) and (22) into time derivative of V, after simplification we get:

$$\begin{aligned}\tfrac{dV}{dt} = \quad & -W_1(1-\tfrac{S_H^*}{S_H})^2 - W_2(1-\tfrac{E_H^*}{E_H})^2 - W_3(1-\tfrac{I_H^*}{I_H})^2 \\ & -W_4(1-\tfrac{R_H^*}{R_H})^2 - W_5(1-\tfrac{S_R^*}{S_R})^2 - W_6(1-\tfrac{E_R^*}{E_R})^2 \\ & -W_7(1-\tfrac{I_R^*}{I_R})^2 - W_8(1-\tfrac{S_F^*}{S_F})^2 - W_9(1-\tfrac{I_F^*}{I_F})^2 \\ & -W_{10}(1-\tfrac{A^*}{A})^2 + F(S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A)\end{aligned}$$

where the function $F(S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A)$ is non positive, Now following the procedures by McCluskey (2006) and Korobeinikov and Wake (2002). We have $F(S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A) \leq 0$ for all $S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A$, Then $\frac{dV}{dt} \leq 0$ for all $S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A$ and it is zero when $S_H = S_H^*, E_H = E_H^*, I_H = I_H^*, R_H = R_H^*, S_R = S_R^*, E_R = E_R^*, I_R = I_R^*, S_F = S_F^*, I_F = I_F^*, A = A^*$ Hence the largest compact invariant set in $S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A$ such that $\frac{dV}{dt} = 0$ is the singleton E^* which is Endemic Equilibrium point of the model system (3) - (6).

LaSalles's invariant principle by La Salle (1976) then implies that E^* is globally asymptotically stable in the interior of the region of $S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A$ and thus leads to the Theorem 3.5

Theorem 3.5
If $R_0 > 1$ then the bubonic plague disease model system (3) - (6) has a unique endemic equilibrium point E^* which is globally asymptotically stable in $S_H, E_H, I_H, R_H, S_R, E_R, I_R, S_F, I_F, A$

3.4 Numerical Simulations

Numerical simulations are carried out in order to study and understand the dynamics of bubonic plague disease and demonstrate analytical results. In particular, we illustrate through numerical simulations the stability of the endemic equilibrium states in human, rodent, flea and pathogens in the environment.

3.4.1 Parameter values

The values of the parameters used in bubonic plague disease model are shown in Table 6. The parameters are taken from the previous studies that relate to this study, existing information and through estimation using sensitivity analysis and simulations.

Table 6: Parameter values for Bubonic Plague disease model.

Parameter	Value	Reference/Source
Γ_{rf}	0.6	Estimated
Γ_{fh}	0.09	Benkirane *et al.* (2009)
Γ_{fr}	4.7	Li (1993)
α_1	0.9	Estimated
γ_1	0.9	Estimated
Γ_{hf}	0.28	Benkirane *et al.* (2009)
λ_4	0.89	Estimated
α_2	0.04	Keeling and Gilligan (2000*a*)
γ_2	0.05	Keeling and Gilligan (2000*a*)
α_3	0.1	Keeling and Gilligan (2000*a*)
ϖ	0.1	Keeling and Gilligan (2000*a*)
μ_1	0.04	Keeling and Gilligan (2000*a*)

Continued on next page

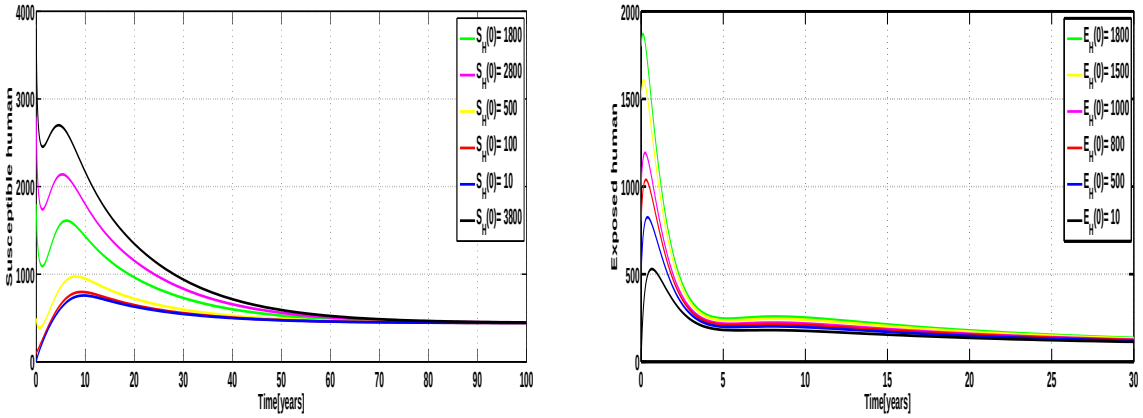
Table 6 – *Continued from previous page*

Parameter	**Value**	**Reference/Source**
δ_1	0.04	Keeling and Gilligan (2000*a*)
δ_3	0.05	Keeling and Gilligan (2000*b*)
μ_3	0.2	Galtier and Mouchiroud (1998)
ω_1	0.01	Keeling and Gilligan (2000*a*)
ω_2	0.073	Benkirane *et al.* (2009)
μ_4	0.1	Estimated
μ_2	0.07	Benkirane *et al.* (2009)
δ_2	0.03	Benkirane *et al.* (2009)
ψ_1	0.09	Estimated
ψ_{2S}	0.008	Keeling and Gilligan (2000*b*)
ψ_3	0.03	Keeling and Gilligan (2000*a*)
β	0.99	Estimated

In the simulation, we assume different cases where each sub-population starts at different initial values (six different initial values) and ultimately returns to its endemic point. We thus justify that a solution that starts sufficiently close to the equilibrium remains close to it and it eventually approaches the equilibrium as $t \to \infty$.

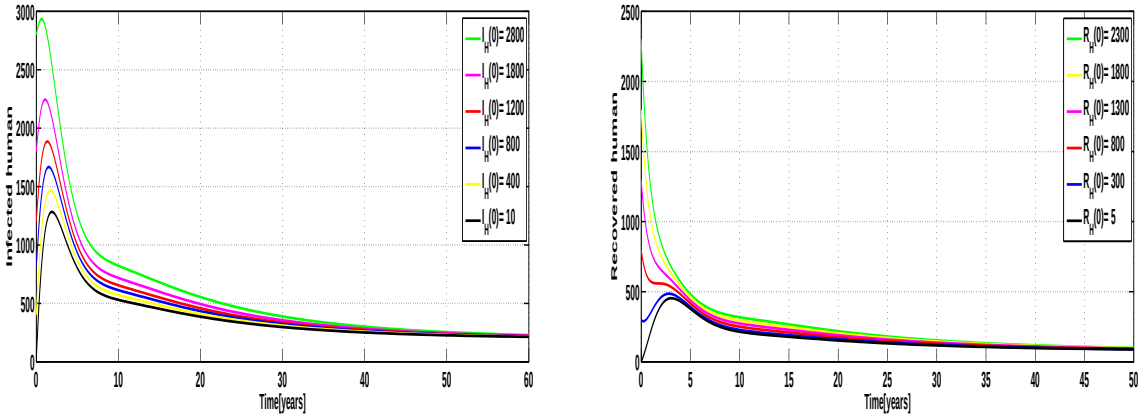
Figures 14 and 15 shows the dynamical behavior of the human population. The Fig. 14a shows a marginal increase in number of susceptible human as people moves in through migration. When the disease becomes endemic, the number of susceptible human decreases as they becomes exposed to the disease due to the increase of force of infection which resembles to the general scenario of vector borne infection as depicted in Lemon *et al.* (2008). Given that the model assumes no treatment nor vaccination is applied, it thus justifies the behavior illustrated in Fig. 14b. The figure shows the very slight increase of a exposed human beings before it drops to its endemic level as the large number of exposed human progresses and become infected human. The increase of number of infected human beings from the exposed class is depicted in Fig. 15a. We can see that in the first five years the number infected human subgroup experience a substantial increase before it decreases to its endemic level. The decrease in number of infected human is mainly through natural death and disease induced death whereas very few will recover and join a recovery class. The number of recovery human shows a slightly increase before it decreases and reaches its endemic level as illustrated in Fig. 15b (McNeill, 2010; Poland and

Dennis, 1998).



(a) **(b)**

Figure 14: Simulation of the model's solution trajectories to show stability of the endemic points S_H and E_H.



(a) **(b)**

Figure 15: Simulation of the model's solution trajectories to show stability of the endemic points I_H and R_H.

Figure 16 shows the dynamics in rodent population. The results depict in this figure also agree with the findings by Gage and Kosoy (2005) and Scott and Duncan (2001). We can see from Fig. 16a that the susceptible rodent population drops very fast within the first years, before it slightly rises due to migration at the rate ψ_3 , to its endemic equilibrium level. The quick drop of susceptible rodent may be due to the fact that rodents are the primary victim of bubonic plague, so that when the disease is endemic, most of them are infected and become exposed to the disease (Dennis and Staples, 2009). The increase of the rate of infection in susceptible rodent population proportionally increases the number of exposed rodent (Davis and Calvet, 2005). After the significant increase of the exposed rodent population within the first five years, it then

drops to its endemic level. It takes only 2 to 6 days for an exposed rodent to become infectious (Putzker *et al.*, 2000) which is the reason for a quick decrease of exposed rodent as seen in Fig. 16b. The infectious rodent population increases as the number of rodent progressing from exposed class to infectious increase. I_R then drops to its endemic level as it experience both natural and disease induced death as in Fig. 16c.

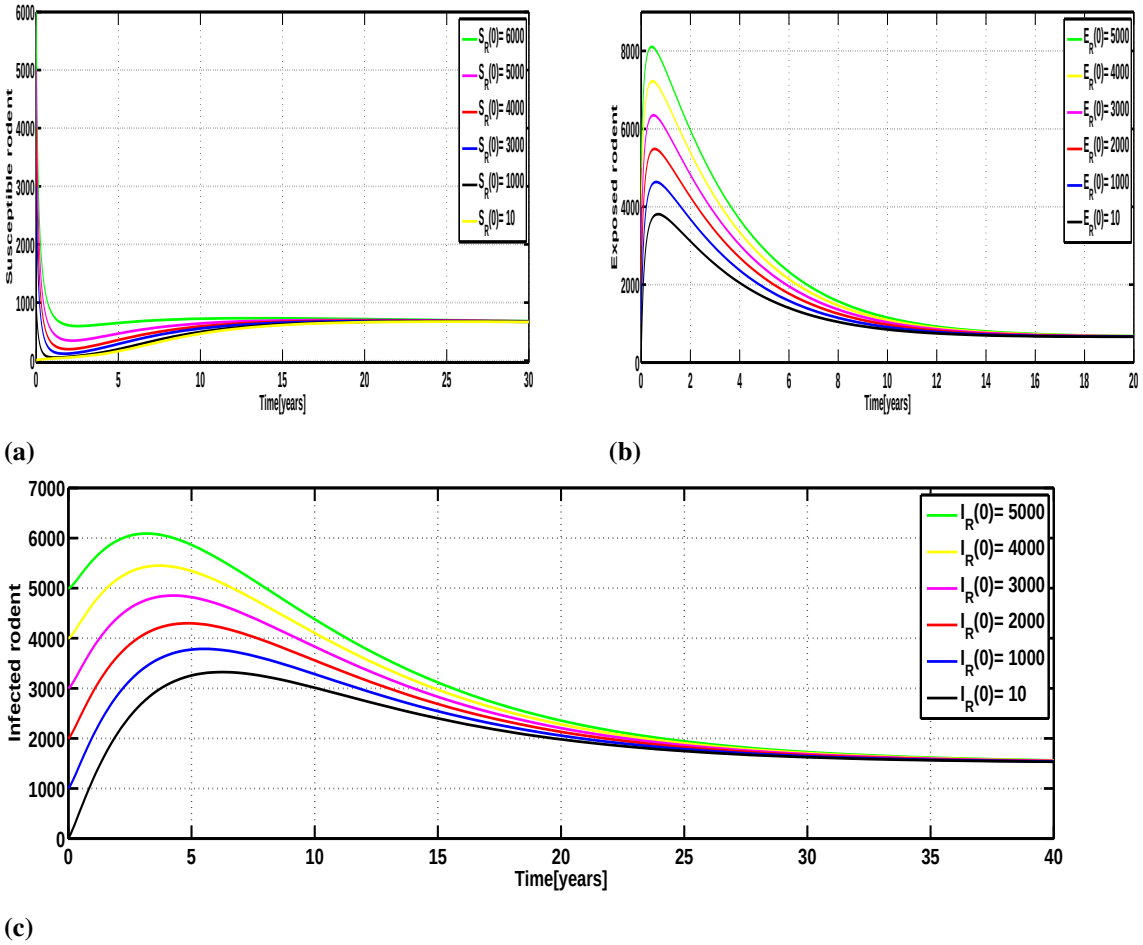
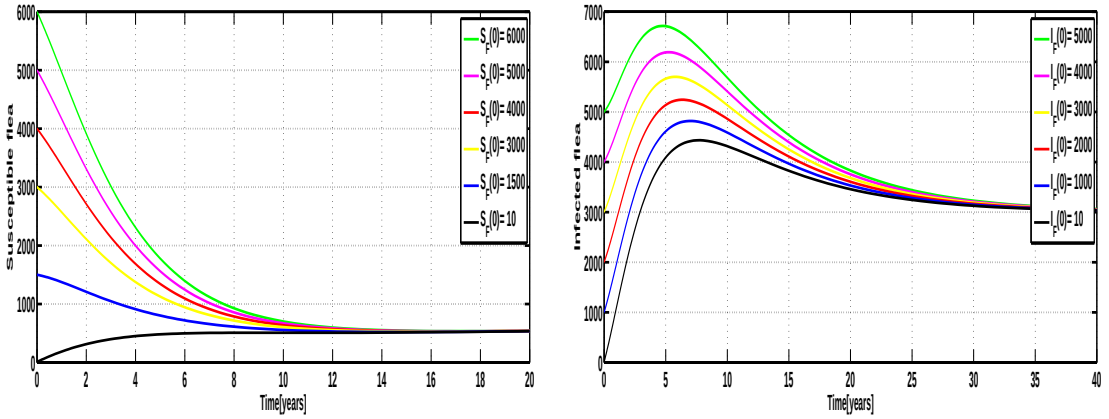


Figure 16: Simulation of the model's solution trajectories to show stability of the endemic point in subsystem (4).

The number of susceptible flea decreases exponentially as they die naturally or acquire infection from the infected rodent or human at the rate Γ_{hf} or Γ_{rf} respectively see Fig. 17a. The increased death of rodent due to the endemicity of the disease, will as a result lead to scarcity of hosts for flea to feed on and thus die (Gage and Kosoy, 2005). The addition of natural and disease induced death in infected flea population will lead to a quick drops to its endemic level as illustrated in Fig. 17b (this agrees with the findings in the studies by Keeling and Gilligan (2000*a*) and Samia *et al.* (2011)).



(a) **(b)**

Figure 17: Simulation of the model's solution trajectories to show stability of the endemic point of subsystem (4).

The pathogens in the environment are removed when they come into contact with the susceptible human and rodent at the rate ω_1 and ω_2 respectively and due to natural death at the rate μ_4. Since we assume that human and rodent infectious classes have a negligible contribution in increasing the number of pathogens in the environment (*Equation (6)*), then as the disease becomes endemic, the rates ω_1 and ω_2 increase which in turn decrease the number of pathogens in the environment. Pathogens are also highly affected by the conditions in the environment (temperature, humidity and precipitation). Most of the time, this leads to a massive decay of the pathogens population in the environment as the environment is not favorable for their survival and growth (Ari *et al.*, 2011). Consequently the number of pathogens in the environment will gradually decrease to its endemic level as in Fig 18.

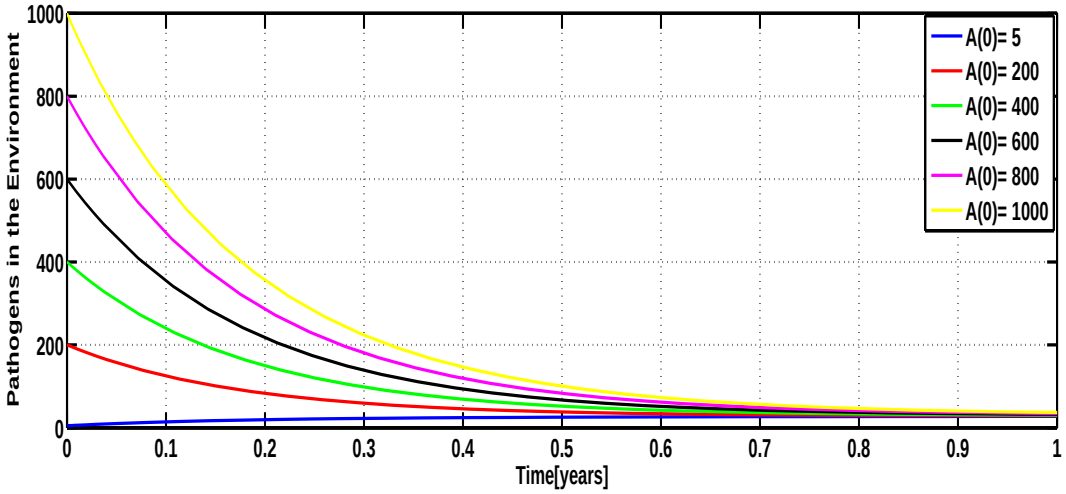


Figure 18: Solution trajectories to show stability of the endemic point in (6).

3.5 Conclusion

In this chapter, we considered a bubonic plague in human, rodent and flea with *yersinia pestis* in the environment. We carried out the stability analysis of the equilibrium states in which the analytical results show that the disease free equilibrium point is locally and globally asymptotically stable when $R_0 < 0$ and unstable when $R_0 > 0$. This result necessitates that the basic reproduction number, is a key non-dimension parameter that dictates whether the disease will spread or die out. When R_0 is increased or decreased above or below unity compels to the persistence or eradication of bubonic plague disease respectively. The decrease or increase of the basic reproduction number will as a result affects negatively or positively the flea's infectious period $\frac{1}{\mu_2+\delta_2}$, probability that rodent survive the infectious class $\frac{\gamma_2}{\mu_3+\gamma_2}$, the adequate contact rate flea to human Γ_{fh}, rodent's infective period $\frac{1}{\mu_3+\delta_3}$, the probability that flea gets the disease from the rodent or human which are $(1-\rho)\Gamma_{rf}$ or $\rho\Gamma_{hf}$ respectively The human infectious period $\frac{1}{\mu_1+\delta_1+\alpha_3}$, probability that human survive the infectious class $\frac{\alpha_2}{\mu_1+\alpha_2}$, the probability at which fleas gets infected β, the adequate contact rate flea to rodent Γ_{fr} and the probability at which human and rodent become exposed to the the disease which are α_1 and γ_1 respectively. The endemic equilibrium point is also found to be locally and globally asymptotically stable whenever they exist. Using the model's parameter values from literature reviewed in this chapter and some estimated we use the simulation to show the endemic equilibrium points are stable thus supports the analytical results. We observe that without intervention that controls the value of R_0 to less than a unity, bubonic plague may be very fatal and a life threatening disease whenever it occurs.

CHAPTER FOUR

Modeling the Dynamics of Pneumonic Plague [3]

Abstract: A deterministic mathematical model to study the dynamics of pneumonic plague is developed and analyzed. We compute the basic reproduction number using the next generation matrix method and use it to derive and establish the condition for local and global asymptotic stability of equilibrium points. Sensitivity and elasticity analysis is used to determine the effect (positive or negative) of parameters on the basic reproduction number. The results show that R_0 is most sensitive to expected number of new cases of pathogens in the environment caused by one rodent infected with pneumonic plague and it is least sensitive to expected number of new cases of human beings infected with pneumonic plague caused by pathogens in the environment. We then use numerical simulations to show the dynamical behavior of pneumonic plague disease in the compartments. The results show clearly the vital role played by fleas, human beings and rodents with bubonic plague in the increase of the number of individuals with pneumonic plague. The result also show that the increase of the number of individuals with pneumonic plague is greatly influenced by the pair k_{ij} (expected number of new cases of i caused by one infected individual of j) that constitute the basic reproduction number which should also be highly considered when planning for any control strategies against the disease.

Key words: Pneumonic plague; Pathogens in the environment; airborne transmission; Yersinia pestis.

4.1 Introduction

Pneumonic plague arises when Yersinia Pestis infects the lungs. It is an extreme type of lung infection, exceedingly contagious and incurable unless identified within the first twenty-four hours (Gamsa, 2006). Among all three main types of plague namely Bubonic plague, septicemic plague and pneumonic plague, it is the most serious and deadliest form of a plague epidemic. The symptoms normally come abruptly and are very severe, characterized by rapid prostration; shallow, distressed and very rapid breathing; individual coughing watery and bloody sputum which contain bacteria (yersinia pestis); high body temperature and bleeding. Individuals with Bubonic or Septicemic plague get the disease from the bite of an infected flea that is primarily infected by the wild rats which are the primary reservoir of *Yersinia pestis*. If not treated, Y. pestis reaches the lungs and thus develops pneumonic plague (Scott and Duncan, 2001).

[3] This chapter is based on a manuscript: Modeling the Dynamics of Pneumonic Plague

Agar *et al.* (2009) examined the progression of infection in rats that were exposed to aerosolized Yersinia Pestis in a whole body. The study was able to demonstrate direct transmission of Yersinia pestis from infected to a susceptible animals (rats) held in the same cage. The infection transpired via aerosol droplets produced when pneumonic plague infected rat coughs. These findings extend to all animals including human beings, rodents and other domestic animals with lungs. When an individual (human beings or rodents and other domestic animals) with pneumonic plague coughs, the bacteria are released into the air. Then when an individual with lungs breathes in the aerosolized bacteria, there is a high possibility that this particular individual may get pneumonic plague (Prentice and Rahalison, 2007).

Ge *et al.* (2015) investigated the case where the patient died after contact with a dog that had captured pneumonic plague infected marmot. In this case, the infection was a result of exposure to Yersinia pestis aerosols from sputum and throat samples. In their study, they found that all of the dogs that ate the marmot were infected with Y. pestis without symptoms. The disease was also detected in the serum of the doctors and in people who had been in contact with the patient for a long period of time in which the transmission may be associated to wearing of masks. The study justify the possibility of rodent to rodent, rodent to human and human to human transmission of pneumonic plague as a result of physical contact or through eating or biting the infected individual.

Pneumonic plague has a tremendous transmission capability from one individual to another. It is a highly contagious disease which is the feature that makes it very dangerous when it enters in a community. It is also the reason why pneumonic plague disease appears on the top list of the diseases that can be used as a bioweapon. Begier *et al.* (2006) conducted a study to investigate the communicability in a natural occurring pneumonic plague cluster. The cluster comprised of two simultaneous index patient's caregiver pairs. The result showed that both index patients transmitted pneumonic plague to only one caregiver each. It justify the possibility of the person to person transmission of pneumonic plague through respiratory droplets in which all individuals within droplet range became ill.

The rate of death due the disease for untreated individual with pneumonic plague increases to 100% within 2 to 7 days after infection. Richard *et al.* (2015) studied an outbreak of pneumonic plague occurred in Madagascar in the year 2011, the disease remained in the community for the period of over twenty seven (27) days. In those twenty seven days, there were seventeen (17) human beings suspected to have gotten the disease, two (2) cases were presumptive, and three were confirmed to have gotten the disease. The study postulates that there were fifteen (15) untreated patients and they all died due to the disease. The result shows that in this outbreak fatality rate was 100% for all non treated patients. This is to say that the rate of fatality in

Pneumonic plague is extreme, and it should therefore be given a special attention when it occurs.

Pneumonic plague is considered perilous mostly due to the fact that at present there is no effective vaccine. More over the instrument for diagnostic test especially the rapid diagnostic tests are scarce and the situation is even worse in African countries. Also it is the form of plague that its transmission capability is high as it can be transmitted directly between individuals (human and rodent or other domestic animal) and through the interaction with the infected environment (Zhou and Yang, 2014; Pechous *et al.*, 2015; Massin *et al.*, 2007). It is certain highly contagious infectious disease which is also listed as a leading critical biological agents with the high potential of being used as a bio weapon (Massin *et al.*, 2007).

The transmission and spreading capacity that characterize pneumonic plague signify that, extreme public health measures should be considered if this kind of disease occur in the community. There should be sustainable planning to do a very rapid evaluation of the outbreak to determine the extent of exposure and help develop the most effective disease containment strategies (Dembek, 2005). To do all of these, there is a need for public health authorities and all health stakeholders to conduct a thorough research on the subject.

In this study we formulate a mathematical model to enable us understand the dynamics of pneumonic plague. We compute the basic reproduction number, analyze the stability of equilibrium points, study the behaviour of the model through numerical simulation, discuss the results and then make conclusions and recommendations.

4.2 Material and Methods

4.2.1 Model Assumptions

We formulate a mathematical model to study the dynamics of pneumonic plague. The developed model rely on the following assumptions:

(i) Bubonic plague is the primary plague infection of pneumonic plague disease,

(ii) the primary infection of the disease is ignored when one gets the secondary infection of the same,

(iii) all individuals are born susceptible,

(iv) members of the population mix homogeneously,

(v) age, sex, social status, do not affect the probability of being infected,

(vi) on recovery human attain a temporary immunity,

(vii) there is no recovery in non-human host populations (they remain infected until they die),

(viii) the disease transmission from the soil/environment to either susceptible human being or rodent population at their respective adequate contact rates has a negligible effect to the dynamics of the pathogens population,

(ix) there is no vertical transmission, but only horizontal transmission is possible in all populations.

4.2.2 Description of pneumonic plague in various population groups

In the model, we have four populations namely the human population, fleas, rodents and the pathogens in the environment. The human population is divided into five sub-groups: the group of people who have not contracted the disease but may get it if they get in contact with infectious agent to be referred to as susceptibles and denoted as S_H; People who have the disease but have not shown any symptoms and are incapable of transmitting the disease i.e the Exposed denoted by E_H; those who are infected and are capable of transmitting the disease are divided into two sub-groups: there are those who have bubonic plague which, in this model, we regard as a primary stage of pneumonic plague denoted by I_{HA} and the others who have pneumonic plague disease denoted by I_{HB}. The fraction of the population in I_{HA} if treated may recover and move to sub-group R_H and if not, they either die or progress and become pneumonic plague disease infectives I_{HB}. The population in the sub-group I_{HB} then they recover and progress to the sub-group R_H if treated and otherwise they die.

The flea population is divided into two sub-groups: those who have not contracted the disease but may get it if they get in contact with infectious agent i.e. susceptible flea denoted by S_F and those who are infected and are capable of transmitting the disease i.e. infectious flea denoted by I_F.

The rodent population is divided into four sub-groups: those who have not contracted the disease but may get it if they get in contact with infectious agent i.e. susceptible rodent S_R, those who have the disease but have not shown any symptom and are incapable of transmitting the disease referred to as the exposed rodent denoted by E_R; those who are infected and are capable of transmitting the disease and these are divided into two subgroups: those who have bubonic plague denoted by I_{RA} and others who have pneumonic plague disease denoted by I_{RB}. To develop the model equations, we use the variables and parameters as described in Table 7 and Table 8.

4.2.3 Variables and Parameters used in the model and their description

Table 7: Variables and their description for pneumonic plague.

Variable	Description
S_H	Susceptible human beings
E_H	Exposed human beings
I_{HA}	Infectious human beings with bubonic plague
I_{HB}	Infectious human beings with pneumonic plague
R_H	Recovered human beings
S_R	Number of Susceptible rodents
E_R	Number of Exposed rodents
I_{RA}	Number of Infectious rodents with bubonic plague
I_{RB}	Number of Infectious rodents with pneumonic plague
S_F	Number of susceptible fleas
I_F	Number of infected fleas
A	Number of pathogens in the environment

Table 8: Parameters and their description for pneumonic plague.

Parameters	Description
Γ_{rf}	Adequate contact rate: rodent to flea
Γ_{fh}	Adequate contact rate: flea to human being
Γ_{fr}	Adequate contact rate: flea to rodent
α_1	Probability that human progress from susceptible to exposed
γ_1	Probability that rodent progress from susceptible to exposed
Γ_{hh}	Adequate contact rate: I_{HB} to S_H
Γ_{hr}	Adequate contact rate: I_{HB} to S_R
Γ_{rr}	Adequate contact rate: I_{RB} to S_R
Γ_{rh}	Adequate contact rate: I_{RB} to S_H
α_2	Progression rate of exposed human being to infected
γ_2	Progression rate of exposed rodent to infected
α_3	Human recovery rate from human being infected by bubonic
α_3	Progression rate from I_{HA} to I_{HB}
ϖ	Progression rate of recovered human being to susceptible

Continued on next page

Table 8 – *Continued from previous page*

Parameters	**Description**
κ_1	Burbonic plague Disease induced death rate for human being
δ_1	Pneumonic plague Disease induced death rate for human being
δ_2	Bubonic plague Disease induced death rate for flea
μ_1	Natural death rate for human being
μ_2	Natural death rate for flea
δ_3	Pneumonic plague Disease induced death rate for rodent
κ_2	Burbonic plague Disease induced death rate for rodent
μ_3	Natural death rate for rodent
ω_1	Adequate contact rate: Pathogens in the environment to human being
ω_2	Adequate contact rate: Pathogens in the environment to rodent
η_1	Transmission rate of pathogens to the environment by I_{HB}
η_2	Recruitment rate of pathogens to the environment by I_{RB}
μ_4	Natural death rate for pathogens
λ_4	Pathogens multiplication rate
ψ_1	Immigration rate of human beings
ψ_{2s}	Immigration rate of susceptible fleas
ψ_3	Immigration rate of rodent
ρ	The probability that I_{HA} progresses to either I_{HB} or R_H
τ_1	The probability that E_H progresses to either I_{HA} or I_{HB}
τ_2	The probability that E_R progresses to either I_{RA} or I_{RB}
ρ_1	The probability that flea gets infection from I_{HA}
ρ_2	The probability that flea gets infection from I_{HB}
ρ_3	The probability that flea gets infection from I_{RA}
ρ_4	The probability that flea gets infection from I_{RB}
π_1	The probability that migrant human beings are Susceptible
β	The probability at which fleas become infected.

4.2.4 Description of interactions

Fleas in sub-group S_F get *Yersinia pestis* bacteria through biting infected rodents who are the primary reservoir for the bacteria and/or infected human being at the rates Γ_{rf} and Γ_{hf} respectively, and become the infected flea I_F.

The groups S_H and S_R may get the disease in various ways; one is through the bites by the infected flea (I_F) at the rates Γ_{fh} and Γ_{fr} respectively and then become latently infected and thus progress to be exposed human population E_H and exposed rodent population E_R at the probability α_1 and γ_1 respectively. They may as well get the disease when they adequately contact the subgroups I_{HB} and I_{RB} who are infected by pneumonic plague. The transmission may be through airborne and/or physical contact (bloody sputum). The interaction may be in such a way that I_{HB} may come into contact and infect the subgroups S_H and S_R at the rate Γ_{hh} and Γ_{hr} respectively. Similarly, I_{RB} may come into contact and infect the sub-groups S_H and S_R at the rates Γ_{rh} and Γ_{rr} respectively.

After 2 to 7 days the sub-groups E_H and E_R become infectious and capable of transmitting the disease. The proportion τ_1 of exposed human beings (E_H) progress to subgroup I_{HA} and the other proportion $(1-\tau_1)$ to sub-group I_{HB} at the rate α_2, exposed rodents (E_R) progress to the sub-group I_{RA} and other $(1-\tau_1)$ to sub-group I_{RB} at the rate γ_2.

If treated the fraction of compartment I_{HA} recover and attain temporary immunity at a rate α_3 and thus progress to a subgroup R_H which then return to a sub-group S_H at a rate ϖ. Other human beings with bubonic plague (I_{HA}) progress to sub-group I_{HB} at a rate α_3 and the rest die either naturally or due to the disease at rates μ_1 and κ_1, respectively.

Individuals in compartment I_{HB} if treated they recover and progress to R_H at the rate α_4 which then return to a sub-group S_H at a rate ϖ. Otherwise they die either from the disease at a rate δ_1 or naturally at a rate of μ_1. After 2 to 7 days of infection the compartment I_{RA} may progress to subgroup I_{RB} at a rate γ_3 and the rest die either naturally or due to a disease at a rates μ_3 and κ_2 respectively. Subgroup I_{RB} die either from the disease at a rate δ_3 or naturally at a rate of μ_3.

The pathogen may survive in the environment if the conditions are favorable for their survival. Through airborne transmission or touching the contaminated soil/environment may cause infections to S_H and S_R at the rates of ω_1 and ω_2 respectively. Pathogens are constantly recruited into the environment at a rate λ_4. However the human beings and rodents infected with pneumonic plague (I_{HB} and I_{RB}) also shad yersinia pestis bacteria in the environment A at rates η_1 and η_2 respectively.

Pathogens in the environment suffer natural mortality at a rate μ_4. The human population in subgroups S_H and E_H, flea population in sub-group S_F and rodent population in sub-groups S_R and E_R suffer natural mortality at rates μ_1, μ_2 and μ_3 respectively. The compartments I_{HA}, I_{HB}, I_F, I_{RA} and I_{RB} suffer both natural death at rates μ_1, μ_2 and μ_3 and disease induced mortality at rates $\kappa_1, \delta_1, \delta_2, \kappa_2$ and δ_3, respectively. Human beings, fleas and rodents are recruited through immigration at rates ψ_1, ψ_2 and ψ_3 respectively.

Basing on the assumptions and the description of interactions stated above, the dynamics of pneumonic plague is as in Fig. 19.

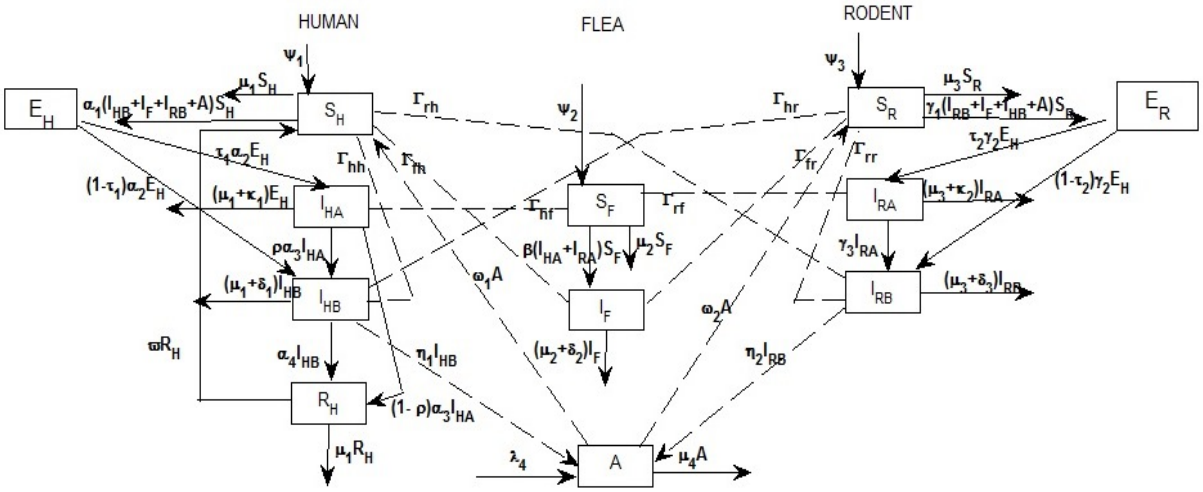


Figure 19: Compartmental model for pneumonic plague

4.2.5 Model Equations for Pneumonic Plague

Using the assumptions stated above, variables and parameters and their description in Tables 7 and 8, description of the dynamics and compartmental diagram in Fig. 19, the SEIR model for pneumonic plague is the following set of ordinary differential equations:

Humans

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A)S_H - \mu_1 S_H, \tag{1a}$$

$$\frac{dE_H}{dt} = \alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A)S_H - (\alpha_2 + \mu_1)E_H \tag{1b}$$

$$\frac{dI_{HA}}{dt} = \tau_1\alpha_2 E_H - \rho\alpha_3 I_{HA} - (1-\rho)\alpha_3 I_{HA} - (\mu_1 + \kappa_1)I_{HA} \tag{1c}$$

$$\frac{dI_{HB}}{dt} = (1-\tau_1)\alpha_2 E_H + \rho\alpha_3 I_{HA} - \alpha_4 I_{HB} - (\mu_1 + \delta_1)I_{HB} \tag{1d}$$

$$\frac{dR_H}{dt} = \alpha_4 I_{HB} + (1-\rho)\alpha_3 I_{HA} - \varpi R_H - \mu_1 R_H \tag{1e}$$

Rodents

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3} + \Gamma_{fr}\frac{I_F}{N_2} + \Gamma_{hr}\frac{I_{HB}}{N_1} + \omega_2 A)S_R - \mu_3 S_R \tag{2a}$$

$$\frac{dE_R}{dt} = \gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3} + \Gamma_{fr}\frac{I_F}{N_2} + \Gamma_{hr}\frac{I_{HB}}{N_1} + \omega_2 A)S_R - (\gamma_2 + \mu_3)E_R \tag{2b}$$

$$\frac{dI_{RA}}{dt} = \tau_2\gamma_2 E_R - \gamma_3 I_{RA} - (\mu_3 + \kappa_2)I_{RA} \tag{2c}$$

$$\frac{dI_{RB}}{dt} = (1-\tau_2)\gamma_2 E_R + \gamma_3 I_{RA} - (\mu_3 + \delta_3)I_{RB} \tag{2d}$$

Fleas

$$\frac{dS_F}{dt} = \psi_{2s} - \beta(\Gamma_{hf}\rho_1\frac{I_{HA}}{N_1} + \Gamma_{rf}(1-\rho_1)\frac{I_{RA}}{N_3})S_F - \mu_2 S_F \tag{3a}$$

$$\frac{dI_F}{dt} = \beta(\Gamma_{hf}\frac{\rho_1 I_{HA}}{N_1} + \Gamma_{rf}\frac{(1-\rho_1)I_{RA}}{N_3})S_F - (\mu_2 + \delta_2)I_F \tag{3b}$$

Pathogens

$$\frac{dA}{dt} = \lambda_4 + \eta_1\frac{I_{HB}}{N_1} + \eta_2\frac{I_{RB}}{N_3} - \mu_4 A \tag{4}$$

4.3 Basic properties of the model

4.3.1 Invariant region

Since pneumonic plague involves human being, rodent, vector and pathogens populations, then, in the modeling process, we assume that all state variables and parameters of the model are non-negative for $\forall t \geq 0$. The model system has four subgroups which are analyzed separately. The model system is analyzed in a suitable feasible region where all state variables are positive. This region will be obtained under the following theorem;

Theorem 4.6
All forward solutions in R_+^{12} of the system are feasible $\forall t \geq 0$ if they enter the invariant region Φ for $\Phi = \Omega_H \times \Omega_R \times \Omega_F \times \Omega_A$

where

$$\Omega_H = (S_H, E_H, I_{HA}, I_{HB}, R_H) \in R_+^5 : S_H + E_H + I_{HA} + I_{HB} + R_H \leq N_1$$
$$\Omega_R = (S_R, E_R, I_{RA}, I_{RB}) \in R_+^4 : S_R + E_R + I_{RA} + I_{RB} \leq N_3$$
$$\Omega_F = (S_F, I_F) \in R_+^2 : S_F + I_F \leq N_2$$
$$\Omega_A = A \in R_+^1$$

and Φ is the positive invariant region of the pneumonic plague system

Proof. We prove the theorem by considering each sub-population.

For human population:

We need to prove that the solution of the system (1) are feasible $\forall t > 0$ as they enter invariant region Ω_H. We now let $\Omega_H = (S_H, E_H, I_{HA}, I_{HB}, R_H) \in R^5$ be solution space of the system (1) with non-negative initial conditions.

The total human population is

$$N_1 = S_H + E_H + I_{HA} + I_{HB} + R_H.$$

Then,

$$\frac{dN_1}{dt} = \frac{dS_H}{dt} + \frac{dE_H}{dt} + \frac{dI_{HA}}{dt} + \frac{dI_{HB}}{dt} + \frac{dR_H}{dt} \tag{5}$$

Adding up the system (1) we get,

$$\frac{dN_1}{dt} = \psi_1 - \mu_1 N_1 - \delta_1 I_{HB} - \kappa_1 I_{HA}$$

We will then have

$$\frac{dN_1}{dt} \leq \psi_1 - \mu_1 N_1$$

We then get

$$\frac{dN_1}{dt} + \mu_1 N_1 \leq \psi_1$$

Finding the integrating factor $IF = e^{\mu_1 t}$ and multiplying it through out we get

$$e^{\mu_1 t}\frac{dN_1}{dt} + e^{\mu_1 t} N_1 \mu_1 \leq \psi_1 e^{\mu_1 t}$$

which gives

$$\frac{d(N_1 e^{\mu_1 t})}{dt} \leq \psi_1 e^{\mu_1 t}$$

Integrating on both sides yields

$$N_1 e^{\mu_1 t} \leq \frac{\psi_1}{\mu_1} e^{\mu_1 t} + C$$

Multiplying the equation by $e^{-\mu_1 t}$ we get

$$N_1 \leq \frac{\psi_1}{\mu_1} + C e^{-\mu_1 t}$$

Using the initial condition $t = 0, N_1(t = 0) = N_{10}$

then we will get

$$N_{10} - \frac{\psi_1}{\mu_1} \leq C$$

Substituting for the constant C we get

$$N_1 \leq \frac{\psi_1}{\mu_1} + (N_{10} - \frac{\psi_1}{\mu_1}) e^{-\mu_1 t}$$

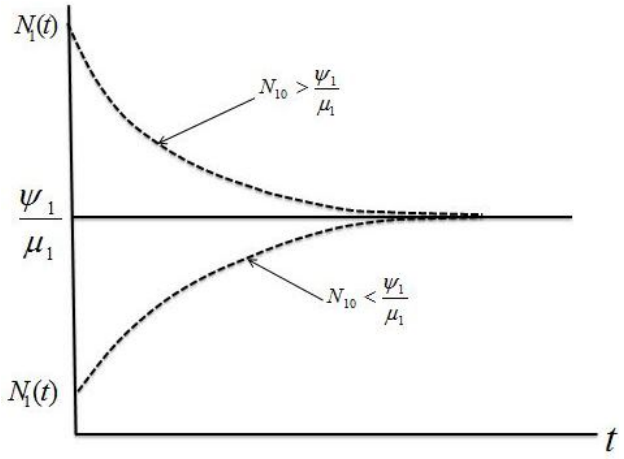


Figure 20: Feasible region for human system

When $N_{10} > \frac{\psi_1}{\mu_1}$, the population decreases asymptotically to $\frac{\psi_1}{\mu_1}$ and when $N_{10} < \frac{\psi_1}{\mu_1}$ the human population increases asymptotically to $\frac{\psi_1}{\mu_1}$ as in Fig. 20. Hence all the feasible solutions of the system enter the region

$$\Omega_H = \left\{ (S_H, E_H, I_{HA}, I_{HB}, R_H) : N_1 \leq Max \left\{ N_{10}, \frac{\psi_1}{\mu_1} \right\} \right\}$$

For rodent population:

We need to prove that the solutions of the system (rodent) are feasible $\forall t > 0$ as they enter invariant region Ω_R. We now let $\Omega_R = (S_R, E_R, I_{RA}, I_{RB}) \in R^4$ be solution space of the system with non-negative initial conditions.

The total rodent population is,

$$N_3 = S_R + E_R + I_{RA} + I_{RB}.$$

Then

$$\frac{dN_3}{dt} = \frac{dS_R}{dt} + \frac{dE_R}{dt} + \frac{dI_{RA}}{dt} + \frac{dI_{RB}}{dt}. \tag{6}$$

Adding up the system (2) we get,

$$\frac{dN_3}{dt} = \psi_3 - \mu_3 N_3 - \delta_3 I_{RB} - \kappa_2 I_{RA}.$$

We will then have

$$\frac{dN_3}{dt} \leq \psi_3 - \mu_3 N_3.$$

We then get

$$\frac{dN_3}{dt} + \mu_3 N_3 \leq \psi_3.$$

Finding the integrating factor $IF = e^{\mu_3 t}$ and multiplying it through out we get

$$e^{\mu_3 t} \frac{dN_3}{dt} + e^{\mu_3 t} N_3 \mu_3 \leq \psi_3 e^{\mu_3 t},$$

which gives

$$\frac{d(N_3 e^{\mu_3 t})}{dt} \leq \psi_3 e^{\mu_3 t}.$$

Integrating on both sides yields

$$N_3 e^{\mu_3 t} \leq \frac{\psi_3}{\mu_3} e^{\mu_3 t} + D,$$

multiplying the equation by $e^{-\mu_3 t}$ we get

$$N_3 \leq \frac{\psi_3}{\mu_3} + De^{-\mu_3 t}.$$

Using the initial condition $t = 0, N_3(t = 0) = N_{30}$ we get

$$N_{30} - \frac{\psi_3}{\mu_3} \leq D,$$

Substituting the constant we get

$$N_3 \leq \frac{\psi_3}{\mu_3} + (N_{30} - \frac{\psi_3}{\mu_3})e^{-\mu_3 t}.$$

When $N_{30} > \frac{\psi_3}{\mu_3}$, the population decreases asymptotically to $\frac{\psi_3}{\mu_3}$ and when $N_{30} < \frac{\psi_3}{\mu_3}$ the rodent population increases asymptotically to $\frac{\psi_3}{\mu_3}$ as in Fig. 21.

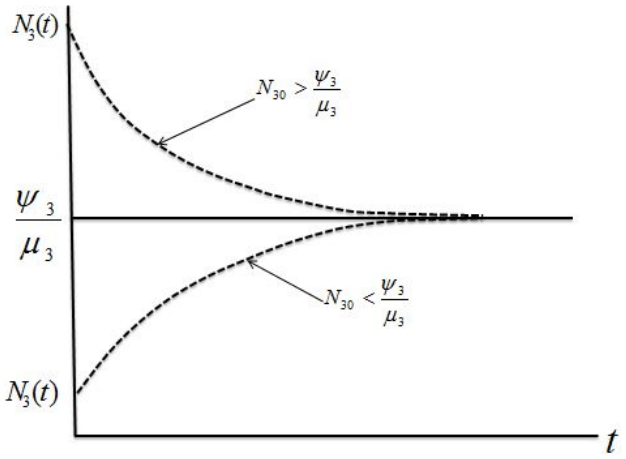


Figure 21: Feasible region for rodent system

Hence all the feasible solutions of the system enter the region

$$\Omega_R = \left\{ (S_R, E_R, I_{RA}, I_{RB}) : N_3 \leq Max \left\{ N_{30}, \frac{\psi_3}{\mu_3} \right\} \right\}$$

For flea population

We need to prove that the solutions of the system (Flea) are feasible $\forall t > 0$ as they enter invariant region Ω_F. We now let $\Omega_F = (S_F, I_F) \in R^2$ be solution space of the system with

non-negative initial conditions.
The total flea population is

$$N_2 = S_F + I_F$$

Then

$$\frac{dN_2}{dt} = \frac{dS_F}{dt} + \frac{dI_F}{dt} \tag{7}$$

Adding up the system (3) we get,

$$\frac{dN_2}{dt} = \psi_{2s} - \mu_2 N_2 - \delta_2 I_F$$

which can be written as

$$\frac{dN_2}{dt} \leq \psi_{2s} - \mu_2 N_2$$

We then get

$$\frac{dN_2}{dt} + N_2\mu_2 \leq \psi_{2s}$$

Finding the integrating factor $IF = e^{\mu_2 t}$ and multiplying it through out we get

$$e^{\mu_2 t}\frac{dN_2}{dt} + e^{\mu_2 t}N_2\mu_2 \leq (\psi_{2s})e^{\mu_2 t}$$

which gives

$$\frac{d(N_2 e^{\mu_2 t})}{dt} \leq (\psi_{2s})e^{\mu_2 t}$$

Integrating on both sides yields

$$N_2 e^{\mu_2 t} \leq \frac{\psi_{2s}}{\mu_2}e^{\mu_2 t} + E$$

Multiplying the equation by $e^{-\mu_2 t}$ we get

$$N_2 \leq \frac{\psi_{2s}}{\mu_2} + Ee^{-\mu_2 t}$$

Using the initial condition $t = 0, N_2(t = 0) = N_{20}$
then we will get

$$N_{20} - \frac{\psi_{2s}}{\mu_2} \leq E$$

Substituting the constant we get

$$N_2 \leq \frac{\psi_{2s}}{\mu_2} + (N_{20} - \frac{\psi_{2s}}{\mu_2})e^{-\mu_2 t}$$

When $N_{20} > \frac{\psi_{2s}}{\mu_2}$ the population decreases asymptotically to $\frac{\psi_{2s}}{\mu_2}$ and when $N_{20} < \frac{\psi_{2s}}{\mu_2}$ the flea population increases asymptotically to $\frac{\psi_{2s}}{\mu_2}$ as in Fig. 22. Hence all the feasible solutions of the system enter the region

$$\Omega_F = \left\{(S_F, I_F) : N_2 \leq Max\left\{N_{20}, \frac{\psi_{2s}}{\mu_2}\right\}\right\}$$

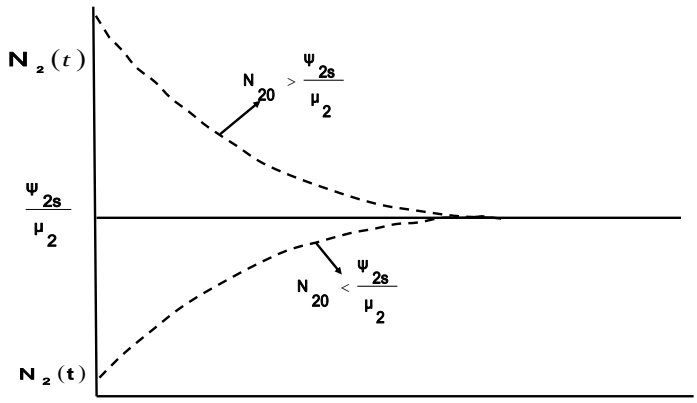


Figure 22: Feasible region for flea system

For pathogens population

We need to prove that the solutions of the system (pathogens) are feasible $\forall t > 0$ as they enter invariant region Ω_A we now let $\Omega_A = A \in R_+^1$ be any solution of the system with non-negative initial conditions.

The total pathogens population is A,
then from the equation (4)

$$\frac{dA}{dt} = \lambda_4 + \eta_1 \frac{I_{HB}}{N_1} + \eta_2 \frac{I_{RB}}{N_3} - \mu_4 A. \tag{8}$$

But

$$I_{HB} \leq N_1, I_{RB} \leq N_3.$$

Then this implies that

$$\frac{I_{HB}}{N_1} \leq 1, \frac{I_{RB}}{N_3} \leq 1.$$

The equation (8) becomes

$$\frac{dA}{dt} \leq \lambda_4 + \eta_1 + \eta_2 - \mu_4 A.$$

Then we will have

$$\frac{dA}{dt} + \mu_4 A \leq \eta_1 + \eta_2 + \lambda_4.$$

Finding the integrating factor $IF = e^{\mu_4 t}$ and multiplying it through out we get

$$e^{\mu_4 t}\frac{dA}{dt} + e^{\mu_4 t}\mu_4 A \leq e^{\mu_4 t}(\eta_1 + \eta_2 + \lambda_4).$$

Which gives

$$\frac{d(Ae^{\mu_4 t}}{dt} \leq (\eta_1 + \eta_2 + \lambda_4)e^{\mu_4 t}.$$

Integrating on both sides yields

$$Ae^{\mu_4 t} \leq \frac{\eta_1 + \eta_2 + \lambda_4}{\mu_4} e^{\mu_4 t} + B,$$

multiplying the equation by $e^{-\mu_4 t}$ we get

$$A(t) \leq \frac{\eta_1 + \eta_2 + \lambda_4}{\omega + \mu_4} + Be^{-\mu_4 t}.$$

Using the initial condition $t = 0, A(t = 0) = A_0$
then we will get

$$A_0 - \frac{\eta_1 + \eta_2 + \lambda_4}{\mu_4} \leq B,$$

substituting the constant we get

$$A(t) \leq \frac{\eta_1 + \eta_2 + \lambda_4}{\mu_4} + (A_0 - \frac{\eta_1 + \eta_2 + \lambda_4}{\mu_4})e^{-\mu_4 t}.$$

When $A_0 > \frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ pathogens decreases asymptotically to $\frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ and when $N_{30} < \frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ pathogens increases asymptotically to $\frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ as in Fig. 23. Hence the feasible

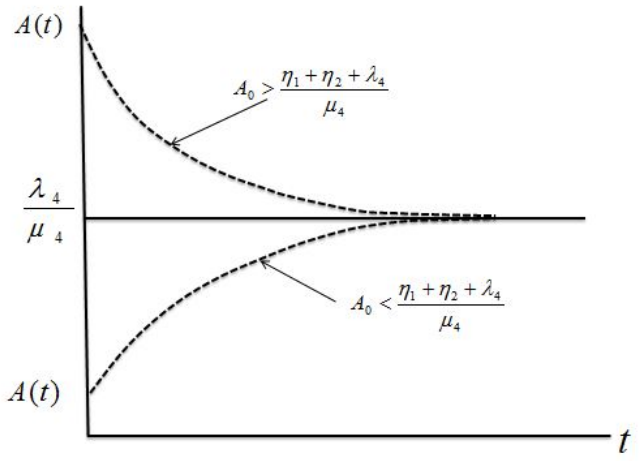


Figure 23: Feasible region for pathogens

solutions of the system enter the region

$$\Omega_A = \left\{ A : A \leq Max \left\{ A_0, \frac{\eta_1 + \eta_2 + \lambda_4}{\mu_4} \right\} \right\}$$

□

4.3.2 Positivity of the solution

All variables and parameters of the model must be non negative $\forall t \geq 0$. We now solve the equations of the system in their patches for testing the positivity.

Theorem 4.7
Let the initial values of the system (1), (2), (3) and (4) be: $(S_H(0)\, S_R(0), S_F(0), A_0) > 0$

and $(E_H(0), I_{HA}(0), I_{HB}(0), R_H(0), E_R(0), I_{RA}(0), I_{RB}(0), I_F(0)) \geq 0$. Then the solution set $S_H(t), S_R(t), S_F(t), A(t), E_H(t), I_{HA}(t), I_{HB}(t), R_H(t), E_R(t), I_{RA}(t), I_{RB}(t)$ and $I_F(t)$ are positive $\forall t \geq 0$.

Proof. We will prove each equation from all the four systems.

For human system

Using the first equation in the human system we have,

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A)S_H - \mu_1 S_H$$

$$\geq -\alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A)S_H - \mu_1 S_H.$$

$$\frac{dS_H}{dt} \geq -(\alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A) + \mu_1)S_H.$$

Integration yields

$$S_H \geq S_{H0}e^{-\int_0^t(\alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A) + \mu_1)d\tau} > 0$$

since

$$e^{-\int_0^t(\alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A) + \mu_1)d\tau} > 0.$$

From the second equation we have

$$\frac{dE_H}{dt} = \alpha_1(\Gamma_{hh}\frac{I_{HB}}{N_1} + \Gamma_{fh}\frac{I_F}{N_2} + \Gamma_{rh}\frac{I_{RB}}{N_3} + \omega_1 A)S_H - \tau_1\alpha_2 E_H - (1-\tau_1)\alpha_2 E_H - \mu_1 E_H.$$

Thus

$$\frac{dE_H}{dt} \geq -(\alpha_2 + \mu_1)E_H.$$

Integration yields

$$E_H \geq E_{H0}e^{-(\alpha_2+\mu_1)t} > 0$$

since

$$e^{-(\alpha_2+\mu_1)} > 0.$$

From the third equation of system (1) we have

$$\frac{dI_{HA}}{dt} = \tau_1\alpha_2 E_H - \rho\alpha_3 I_{HA} - (1-\rho)\alpha_3 I_{HA} - (\mu_1 + \delta_1)I_{HA}.$$

Thus

$$\frac{dI_{HA}}{dt} \geq -(\alpha_3 + \mu_1 + \delta_1)I_{HA}.$$

Integrating we get

$$I_H \geq I_{HA0}e^{-(\alpha_3+\mu_1+\delta_1)t} > 0.$$

since

$$e^{-(\alpha_3+\mu_1+\delta_1)t} > 0.$$

Fourth equation of the system we will have

$$\frac{dI_{HB}}{dt} = (1-\tau_1)\alpha_2 E_H + \rho\alpha_3 I_{HA} - \alpha_4 I_{HB} - (\mu_1+\delta_1)I_{HB}.$$

Thus

$$\frac{dI_{HA}}{dt} \geq -(\alpha_4+\mu_1+\delta_1)I_{HB}.$$

Integrating we get

$$I_H \geq I_{HA0}e^{-(\alpha_4+\mu_1+\delta_1)t} > 0,$$

since

$$e^{-(\alpha_4+\mu_1+\delta_1)} > 0.$$

And the last equation in system (1) we have

$$\frac{dR_H}{dt} = \alpha_4 I_{HB} + (1-\rho)\alpha_3 I_{HA} - \varpi R_H - \mu_1 R_H.$$

Thus

$$\frac{dR_H}{dt} \geq -(\varpi+\mu_1)R_H.$$

Integrating we get

$$R_H \geq R_{H0}e^{-(\varpi+\mu_1)t} > 0,$$

since

$$e^{-(\varpi+\mu_1)} > 0.$$

For rodent system

Using equation one from system (2) we have

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3} + \Gamma_{fr}\frac{I_F}{N_2} + \Gamma_{hr}\frac{I_{HB}}{N_1} + \omega_2 A)S_R - \mu_3 S_R.$$

Thus

$$\frac{dS_R}{dt} \geq -(\gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3} + \Gamma_{fr}\frac{I_F}{N_2} + \Gamma_{hr}\frac{I_{HB}}{N_1} + \omega_2 A) + \mu_3)S_R.$$

Integrating we get

$$S_R \geq S_{R0}e^{-\int_0^t(\gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3}+\Gamma_{fr}\frac{I_F}{N_2}+\Gamma_{hr}\frac{I_{HB}}{N_1}+\omega_2 A)+\mu_3)d\tau} > 0,$$

since

$$e^{-\int_0^t(\gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3}+\Gamma_{fr}\frac{I_F}{N_2}+\Gamma_{hr}\frac{I_{HB}}{N_1}+\omega_2 A)+\mu_3)d\tau} > 0.$$

From the second equation of the system (2) we have

$$\frac{dE_R}{dt} = \gamma_1(\Gamma_{rr}\frac{I_{RB}}{N_3} + \Gamma_{fr}\frac{I_F}{N_2} + \Gamma_{hr}\frac{I_{HB}}{N_1} + \omega_2 A)S_R - (1-\tau_2)\gamma_2 E_R - \tau_2\gamma_2 E_R - \mu_3 E_R,$$

from here we get

$$\frac{dE_R}{dt} \geq -(\gamma_2 + \mu_3)E_R.$$

Integrating we get

$$E_R \geq E_{R0}e^{-(\gamma_2+\mu_3)t} > 0,$$

since

$$e^{-(\gamma_2+\mu_3)t} > 0.$$

And from the third equation of system (2) we have

$$\frac{dI_{RA}}{dt} = \tau_2\gamma_2 E_H - \gamma_3 I_{RA} - (\mu_3 + \kappa_2)I_{RA}.$$

We will then have

$$\frac{dI_R}{dt} \geq -(\gamma_3 + \mu_3 + \kappa_2)I_{RA}.$$

Integrating we get

$$I_R \geq I_{R0}e^{-(\gamma_3+\mu_3+\kappa_2)t} > 0,$$

since

$$e^{-(\gamma_3+\mu_3+\kappa_2)t} > 0.$$

And from the last equation of system (2) we have

$$\frac{dI_{RB}}{dt} = (1-\tau_2)\gamma_2 E_H + \gamma_3 I_{RA} - (\mu_3 + \delta_3)I_{RB}.$$

We will then have

$$\frac{dI_{RB}}{dt} \geq -(\mu_3 + \delta_3)I_{RB}.$$

Integrating we get

$$I_R \geq I_{RB0}e^{-(\mu_3+\delta_3)t} > 0,$$

since

$$e^{-(\mu_3+\delta_3)t} > 0.$$

For flea system

Now from the first equation of system (3) we will have

$$\frac{dS_F}{dt} = \psi_{2s} - \beta(\Gamma_{hf}\frac{\rho_1 I_{HA} + \rho_2 I_{HB}}{N_1} + \Gamma_{rf}\frac{\rho_3 I_{RA} + \rho_4 I_{RB}}{N_3})S_F - \mu_2 S_F.$$

$$\frac{dS_F}{dt} \geq -(\beta(\Gamma_{hf}\frac{\rho_1 I_{HA} + \rho_2 I_{HB}}{N_1} + \Gamma_{rf}\frac{\rho_3 I_{RA} + \rho_4 I_{RB}}{N_3}) + \mu_2)S_F.$$

Integrating we get

$$S_F \geq S_{F0}e^{-\int_0^t(\beta(\Gamma_{hf}\frac{\rho_1 I_{HA}+\rho_2 I_{HB}}{N_1}+\Gamma_{rf}\frac{\rho_3 I_{RA}+\rho_4 I_{RB}}{N_3})+\mu_2)d\tau} > 0,$$

since

$$e^{-\int_0^t(\beta(\Gamma_{hf}\frac{\rho_1 I_{HA}+\rho_2 I_{HB}}{N_1}+\Gamma_{rf}\frac{\rho_3 I_{RA}+\rho_4 I_{RB}}{N_3})+\mu_2)d\tau} > 0.$$

Taking the second equation we have

$$\frac{dI_F}{dt} = \beta(\Gamma_{hf}\frac{\rho_1 I_{HA}+\rho_2 I_{HB}}{N_1}+\Gamma_{rf}\frac{\rho_3 I_{RA}+\rho_4 I_{RB}}{N_3})S_F-(\mu_2+\delta_2)I_F.$$

Then we have

$$\frac{dI_F}{dt} \geq -(\mu_2+\delta_2)I_F.$$

Integrating we have

$$I_F \geq I_{F0}e^{-(\mu_2+\delta_2)t} > 0,$$

since

$$e^{-(\mu_2+\delta_2)t} > 0.$$

For pathogens in the environment

The subgroup has only one equation so using equation (4) we will have

$$\frac{dA}{dt} = \lambda_4+\eta_1\frac{I_{HB}}{N_1}+\eta_2\frac{I_{RB}}{N_3}-\mu_4 A.$$

Then we will have

$$\frac{dA}{dt} \geq -\mu_4 A.$$

Integrating we get

$$A \geq A_0 e^{-\mu_4 t} > 0,$$

Since

$$e^{-\mu_4 t} > 0.$$

□

4.4 Model analysis

In this section, we examine the existence of equilibrium states, reproduction number and stability of the equilibrium states.

4.4.1 Disease Free Equilibrium

The model has a disease free equilibrium which is obtained by setting $I_{HA} = I_{HB} = E_H = R_H = 0$, $I_{RA} = I_{RB} = E_R = 0$, $I_F = 0$ and $A = 0$ for human beings, rodents, fleas and pathogens systems respectively. We substitute the above into the system (1) - (4) which are the

systems for human beings, rodents, fleas and pathogens in the environment respectively. Then we have the disease free-equilibrium point given as $E_H^0 = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0, 0\right)$, $E_R^0 = \left(\frac{\psi_3}{\mu_3}, 0, 0, 0\right)$, $E_F^0 = \left(\frac{\psi_{2s}}{\mu_2}, 0\right)$ and $E_A^0 = 0$ for human being, rodent, flea and pathogen, respectively.

Then the disease free equilibrium of the entire system

$$E^0(S_H^0, E_H^0, I_{HA}^0, I_{HB}^0, R_H^0, S_R^0, E_R^0, I_{RA}^0, I_{RB}^0, S_F^0, I_F^0, A^0) = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0, 0, \frac{\psi_3}{\mu_3}, 0, 0, 0, \frac{\psi_{2s}}{\mu_2}, 0, 0\right).$$

4.4.2 The next-generation matrix

We define the basic reproduction number as the expected number of secondary cases produced by a single infectious individual during the entire infectious period of that particular individual into a completely susceptible population. The value of this dimensionless quantity (R_0) dictate different epidemiological criteria such that: If $R_0 < 1$ then an infected individual in entirely susceptible population can produce less than one secondary cases of infection. This indicates that the disease cannot develop and may be eradicated from the population, which means that the disease-free equilibrium point is asymptotically stable. On the other hand, If $R_0 > 1$ it means that an infected individual in entirely susceptible population produce more than one secondary cases of infection. This indicates the persistence of the disease in the population for a long time and that the disease free equilibrium point is unstable (Allen *et al.*, 2008).

We compute the basic reproduction number R_0 using the next generation matrix as outlined by Heesterbeek (2000) and Mpeshe *et al.* (2014). We first categorize individuals by their state at the moment they become infected (type at infection). These types-at-infection refers specifically to the birth of the infection in the individual. These categories (types at infection) differ in the way they transmit disease and their ability to produce secondary cases.

For our case, we have six categories and we label them as follows: Human infected with bubonic plague (type 1), human infected with pneumonic plague (type 2), rodent infected with bubonic plague (type 3), rodent infected with pneumonic plague (type 4), flea infested with pathogens (type 5) and the pathogens in the environment (type 6). Since the system has six types-at-infection, the next-generation matrix, K, will be a 6×6 matrix with elements k_{ij},s. Each of the elements k_{ij} stands for expected number of new cases of i caused by one infected individual of j. We now define the next-generation matrix K whose entries are k_{ij}. This matrix is given as;

$$\mathbf{K} = \begin{pmatrix} k_{11} & k_{12} & k_{13} & k_{14} & k_{15} & k_{16} \\ k_{21} & k_{22} & k_{23} & k_{24} & k_{25} & k_{26} \\ k_{31} & k_{32} & k_{33} & k_{34} & k_{35} & k_{36} \\ k_{41} & k_{42} & k_{43} & k_{44} & k_{45} & k_{46} \\ k_{51} & k_{52} & k_{53} & k_{54} & k_{55} & k_{56} \\ k_{61} & k_{62} & k_{63} & k_{64} & k_{65} & k_{66} \end{pmatrix} \tag{9}$$

Then, $R_0 = \rho(K)$ where $\rho(K)$ is spectral radius of K.

The element k_{11} of the matrix 9 is the expected number of new cases of human beings infected with bubonic plague caused by one infected human beings with bubonic plague, k_{12} is the expected number of new cases of human beings infected with bubonic plague caused by one infected human beings with pneumonic plague, k_{13} is the expected number of new cases of human infected with bubonic plague caused by one infected rodent with bubonic plague, k_{14} is the expected number of new cases of human beings infected with bubonic plague caused by one infected rodent with pneumonic plague, k_{15} is the expected number of new cases of human beings infected with bubonic plague caused by one infected flea, k_{16} is the expected number of new cases of human beings infected with bubonic plague caused by infected environment.

k_{21} is the expected number of new cases of human beings infected with pneumonic plague caused by one infected human beings with bubonic plague, k_{22} is the expected number of new cases of human beings infected with pneumonic plague caused by one infected human beings with pneumonic plague, k_{23} is the expected number of new cases of human beings infected with pneumonic plague caused by one infected rodent with bubonic plague, k_{24} is the expected number of new cases of human beings infected with pneumonic plague caused by one infected rodent with pneumonic plague, k_{25} is the expected number of new cases of human beings infected with pneumonic plague caused by one infected flea, k_{26} is the expected number of new cases of human beings infected with pneumonic plague caused by infected environment.

k_{31} is the expected number of new cases of rodent infected with bubonic plague caused by one infected human beings with bubonic plague, k_{32} is the expected number of new cases of rodent infected with bubonic plague caused by one infected human beings with pneumonic plague, k_{33} is the expected number of new cases of rodent infected with bubonic plague caused by one infected rodent with bubonic plague, k_{34} is the expected number of new cases of rodent infected with bubonic plague caused by one infected rodent with pneumonic plague, k_{35} is the expected number of new cases of rodent infected with bubonic plague caused by one infected flea, k_{36} is the expected number of new cases of rodent infected with bubonic plague caused by infected environment.

k_{41} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected human beings with bubonic plague, k_{42} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected human beings with pneumonic plague, k_{43} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with bubonic plague, k_{44} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with pneumonic plague, k_{45} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected flea, k_{46} is the expected number of new cases of rodent infected with pneumonic plague caused by infected environment.

k_{51} is the expected number of new cases of infected flea caused by one infected human beings with bubonic plague, k_{52} is the expected number of new cases of infected flea caused by one infected human beings with pneumonic plague, k_{53} is the expected number of new cases of infected flea caused by one infected rodent with bubonic plague, k_{54} is the expected number of new cases of infected flea caused by one infected rodent with pneumonic plague, k_{55} is the expected number of new cases of infected flea caused by one infected flea, k_{56} is the expected number of new cases of infected flea caused by infected environment.

k_{61} is the expected number of new cases of infected environment caused by one infected human beings with bubonic plague, k_{62} is the expected number of new cases of infected environment caused by one infected human beings with pneumonic plague, k_{63} is the expected number of new cases of infected environment caused by one infected rodent with bubonic plague, k_{64} is the expected number of new cases of infected environment caused by one infected rodent with pneumonic plague, k_{65} is the expected number of new cases of infected environment caused by one infected flea and k_{66} is the expected number of new cases of infected environment caused by infected environment.

Some elements are equal to zero since not all type at infection individuals infect others. For example, human beings and rodent infected with bubonic and pneumonic do not cause new cases of infected human beings and rodent with bubonic plague, this means that k_{11}, k_{12}, k_{13} and k_{14} are equal to zero. There are no new cases of human beings infected with pneumonic plague caused by rodent infected with pneumonic plague and from the infected fleas, thus k_{23} and k_{25} are equal to zero. Human and rodent infected with bubonic and pneumonic do not cause new cases of infected rodent with bubonic plague, this means that k_{31}, k_{32}, k_{33} and k_{34} are equal to zero.

Also no single case of rodent with pnemonic plague is caused by a human beings or rodent infected with bubonic plague and from the infected fleas which again means k_{41}, k_{43} and k_{45} are equal to zero. A flea can neither infect itself nor by the environment and no new cases of

the infected environment (pathogens in the environment) is caused by human beings and rodent infected with bubonic plague, the infected flea or by itself which means k_{55}, k_{56}, k_{61}, k_{63}, k_{65} and k_{66} are equal to zero. There are no new cases of human beings and rodent infected with bubonic plague caused by infected environment (pathogens in the environment), and also no disease transmission from human beings and rodent with pneumonic plague to flea. This means k_{16}, k_{36}, k_{52} and k_{54} are equal to zero (McCray, 2006; Heroven and Dersch, 2014).

Now replacing in matrix K the k_{ij} elements with value zero, the matrix K becomes

$$\mathbf{K} = \begin{pmatrix} 0 & 0 & 0 & 0 & k_{15} & 0 \\ k_{21} & k_{22} & 0 & k_{24} & 0 & k_{26} \\ 0 & 0 & 0 & 0 & k_{35} & 0 \\ 0 & k_{42} & k_{43} & k_{44} & 0 & k_{46} \\ k_{51} & 0 & k_{53} & 0 & 0 & 0 \\ 0 & k_{62} & 0 & k_{64} & 0 & 0 \end{pmatrix} \tag{10}$$

The expected number of new cases of i caused by one infectious individual of j generally depends on the infectious period of individual of type j, the progression rate from one infective class to another within the individual type j, the probability that the individual of type j survives the incubation and the adequate contact rate: individual type j to individual type i depending on the particular type of infected individual j under consideration. For example, k_{15} depends on the infectious period of flea, probability that fleas survives the incubation period and the adequate contact rate: infected flea to human being. Using the method outlined by Gail and Benichou (2000), we now derive the expressions for k_{ij} basing on the adequate contact rate between the infected individual type j and the susceptible individual type i, the expected duration of infection of individual type j and the probability that the individual type j survive the duration between the latent stage to the time an individual experience the onset clinical disease as in (11)

$$\mathbf{K_{ij}} = \begin{pmatrix} \text{Effective} \\ \text{contact} \\ \text{Rate} \end{pmatrix} \times \begin{pmatrix} \text{Duration} \\ \text{of} \\ \text{infection} \end{pmatrix} \times \begin{pmatrix} \text{Probability that the} \\ \text{individual survive} \\ \text{the incubation period} \end{pmatrix} \tag{11}$$

we then have:

$$k_{15} = \left(\frac{\beta}{\beta + \mu_2}\right)\frac{\Gamma_{fh}}{\mu_2 + \delta_2}$$
$$k_{26} = \frac{\omega_1 \lambda_4}{\mu_4(\mu_4 + \lambda_4)}$$

$$k_{22} = \frac{(1-\tau_1)\alpha_2\Gamma_{hh}}{((1-\tau_1)\alpha_2 + \mu_1)(\mu_1 + \delta_1 + \alpha_4)}$$
$$k_{24} = \frac{(1-\tau_2)\gamma_2\Gamma_{rh}}{((1-\tau_2)\gamma_2 + \mu_3)(\mu_3 + \delta_3)}$$

$$k_{21} = \left(\frac{\tau_1\alpha_2}{\tau_1\alpha_2 + \mu_1}\right)\frac{\rho\alpha_3}{\mu_1 + \kappa_1 + \alpha_3}$$
$$k_{46} = \frac{\omega_2 \lambda_4}{\mu_4(\mu_4 + \lambda_4)}$$

$$k_{35} = \left(\frac{\beta}{\beta + \mu_2}\right)\frac{\Gamma_{fr}}{\mu_2 + \delta_2}$$
$$k_{44} = \frac{(1-\tau_2)\gamma_2\Gamma_{rr}}{((1-\tau_2)\gamma_2 + \mu_3)(\mu_3 + \delta_3)}$$

$$k_{43} = \left(\frac{\tau_2\gamma_2}{\tau_2\gamma_2 + \mu_3}\right)\frac{\gamma_3}{\gamma_3 + \mu_3 + \kappa_2}$$

$$k_{42} = \frac{(1-\tau_1)\alpha_2\Gamma_{hr}}{((1-\tau_1)\alpha_2 + \mu_1)(\mu_1 + \delta_1 + \alpha_4)}$$

$$k_{53} = \left(\frac{\tau_2\gamma_2}{\tau_2\gamma_2 + \mu_3}\right)\frac{\rho_3\Gamma_{rf}}{\gamma_3 + \mu_3 + \kappa_2}$$

$$k_{51} = \left(\frac{\tau_1\alpha_2}{\tau_1\alpha_2 + \mu_1}\right)\frac{\rho_1\Gamma_{hf}}{\mu_1 + \kappa_1 + \alpha_3}$$

$$k_{62} = \left(\frac{(1-\tau_1)\alpha_2}{(1-\tau_1)\alpha_2 + \mu_1} + \frac{\rho\alpha_3}{\rho\alpha_3 + \mu_1 + \kappa_1}\right)\frac{\eta_1}{\mu_1 + \delta_1 + \alpha_4}$$
$$k_{64} = \left(\frac{(1-\tau_2)\gamma_2}{(1-\tau_2)\gamma_2 + \mu_3} + \frac{\gamma_3}{\gamma_3 + \mu_3 + \kappa_2}\right)\frac{\eta_2}{\mu_3 + \delta_3}$$

Each element of the matrix K is the reproduction number for pairs of considered types (Hartemink *et al.*, 2008). The general interpretation of the matrix elements k_{ij} is that; the elements k_{11},k_{12}, k_{21}, k_{22} and k_{33}, k_{34}, k_{43}, k_{44} arise within human beings and rodents respectively as there are two groups of infectious classes which are those with bubonic plague I_{HA} and I_{RA} and those with pneumonic plague I_{HB} and I_{RB}. These two groups differ in the way they

transmit *Yersinia pestis*. The bubonic plague infectious cases occur when bacteria infect the lymphatic system and it is mainly transmitted through flea bite. In very rare cases the disease may be transmitted through the interaction with the environment, and in almost negligible cases the disease can be transmitted between human - human, human - rodent and rodent - rodent. These are the reasons why the value of k_{11}, k_{12}, k_{13}, k_{14} and k_{16} are zero. While the group of human beings and rodents infected with pneumonic plague occur when the bacteria infect the lungs, it is transmitted through airborne transmission.

Basic Reproduction Number R_0

Diekmann *et al.* (1990) and Heesterbeek (2000) postulates that we obtain the basic reproduction number R_0 by computing the maximum modulus of the eigenvalues of the next-generation matrix. Using mapple computing software package, the basic reproduction number is

$$R_0 = \frac{1}{6}\left(\nu_1 + \sqrt{\nu_2 - \nu_3}\right)^{\frac{1}{3}} + \frac{\nu_4}{\left(\nu_1 + \sqrt{\nu_2 - \nu_3}\right)^{\frac{1}{3}}} + \frac{1}{3}(k_{44} + k_{22})$$

for

$$\nu_2 - \nu_3 > 0$$

where

$$\begin{aligned}
\nu_1 = {} & 8k_{22}^3 - 12k_{44}k_{22}^2 + (36k_{62}k_{26} - 72k_{64}k_{46} + 36k_{42}k_{24} - 12k_{44}^2)k_{22} + 8k_{44}^3 + (36k_{64}k_{46} \\
& -72k_{62}k_{26} + 36k_{42}k_{24})k_{44} + 108k_{64}k_{42}k_{26} + 108k_{62}k_{24}k_{46} \\
\nu_2 = {} & (6{k_{44}}^3 + (6k_{42}k_{24} + 24k_{64}k_{46})k_{44} + 12\,k_{64}k_{42}k_{26} + 12\,k_{62}k_{24}k_{46})k_{22}{}^3 \\
& +24\,{k_{64}}^2{k_{46}}^2{k_{22}}^2 + ((6\,k_{42}k_{24} + 24\,k_{62}k_{26})k_{44}{}^3 + (30\,{k_{42}}^2{k_{24}}^2 + 6\,k_{42}(k_{62}k_{26} \\
& +k_{64}k_{46})k_{24} + 114\,k_{64}k_{46}k_{62}k_{26})k_{44} + 54\,(k_{62}k_{26} + k_{42}k_{24})(k_{64}k_{42}k_{26} \\
& +k_{62}k_{24}k_{46}))k_{22} + (12\,k_{64}k_{42}k_{26} + 12\,k_{62}k_{24}k_{46})k_{44}{}^3 + 24\,{k_{62}}^2{k_{26}}^2{k_{44}}^2 \\
& +54\,(k_{42}k_{24} + k_{64}k_{46})(k_{64}k_{42}k_{26} + k_{62}k_{24}k_{46})k_{44} + 81\,{k_{62}}^2{k_{24}}^2{k_{46}}^2 \\
& +90\,k_{64}k_{46}k_{62}k_{24}k_{42}k_{26} + 81\,{k_{64}}^2{k_{42}}^2{k_{26}}^2 \\
\nu_3 = {} & (-3\,{k_{44}}^2 - 12\,k_{64}k_{46})k_{22}{}^4 - 6\,k_{62}k_{22}{}^3k_{26}k_{44} + (-3\,k_{44}{}^4 + (-6\,k_{64}k_{46} - 24\,k_{42}k_{24} \\
& -6\,k_{62}k_{26})k_{44}{}^2 + (-18\,k_{62}k_{24}k_{46} - 18\,k_{64}k_{42}k_{26})k_{44} - 3\,(k_{62}k_{26} + k_{42}k_{24})(k_{42}k_{24} \\
& +20\,k_{64}k_{46} + k_{62}k_{26}))k_{22}{}^2 + (-6\,k_{64}k_{44}{}^3k_{46} + (-18\,k_{62}k_{24}k_{46} - 18\,k_{64}k_{42}k_{26})k_{44}{}^2 \\
& +(-24\,{k_{62}}^2{k_{26}}^2 - 24\,{k_{64}}^2{k_{46}}^2)k_{44} - 108\,k_{64}k_{46}(k_{64}k_{42}k_{26} + k_{62}k_{24}k_{46}))k_{22} \\
& -12\,k_{62}k_{26}k_{44}{}^4 - 3\,(k_{42}k_{24} + k_{64}k_{46})(k_{42}k_{24} + 20\,k_{62}k_{26} + k_{64}k_{46})k_{44}{}^2 \\
& -108\,k_{26}k_{62}(k_{64}k_{42}k_{26} + k_{62}k_{24}k_{46})k_{44} - 12\,k_{62}{}^3k_{26}{}^3 - 36\,k_{62}{}^2(k_{42}k_{24} \\
& +k_{64}k_{46})k_{26}{}^2 - 36\,k_{62}({k_{42}}^2{k_{24}}^2 + {k_{64}}^2{k_{46}}^2)k_{26} - 12\,(k_{42}k_{24} + k_{64}k_{46})^3 \\
\nu_4 = {} & 2k_{64}k_{46} + 2k_{62}k_{26} + 2k_{42}k_{24} + \tfrac{2}{3}k_{44}^2 + \tfrac{2}{3}k_{22}^2 - \tfrac{2}{3}k_{44}k_{22}
\end{aligned}$$

Since pneumonic plague has multiple transmission cycles, the next-generation matrix method gives the geometric mean of the number of infections per generation (Li and Blakeley, 2011).

It depends on the expected number of new cases of human beings infected with pneumonic plague caused by one infected human beings with pneumonic plague (k_{22}), the expected number of new cases of human beings infected with pneumonic plague caused by one infected rodent with pneumonic plague (k_{24}), the expected number of new cases of human beings infected with pneumonic plague caused by infected environment (k_{26}), the expected number of new cases of rodent infected with pneumonic plague caused by one infected human beings with pneumonic plague (k_{42}), the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with pneumonic plague (k_{44}), the expected number of new cases of rodent infected with pneumonic plague caused by infected environment (k_{46}), the expected number of new cases of infected environment caused by one infected human beings with pneumonic plague (k_{62}) and the expected number of new cases of infected environment caused by one infected rodent with pneumonic plague (k_{64}).

4.4.3 Local stability of the Disease Free Equilibrium point

In this section, we assess the local stability of the Disease Free Equilibrium (DFE) point of the pneumonic plague disease system, in which we prove that the trajectories start arbitrary close to the equilibrium point but do not precisely reach it. We do this by evaluating the Jacobian matrix of system (1) - (4) at DFE point:
Then we have

$$\mathbf{J}(\mathbf{E^0}) = \begin{pmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{pmatrix} \tag{12}$$

where J_{11}, J_{12}, J_{21} and J_{22} are (6×6) matrices given by;

$$\mathbf{J_{11}} = \begin{pmatrix} -\mu_1 & 0 & 0 & \frac{-\alpha_1\Gamma_{hh}S_H}{N_1} & \varpi & 0 \\ 0 & -(\alpha_2+\mu_1) & 0 & \frac{\alpha_1\Gamma_{hh}S_H}{N_1} & 0 & 0 \\ 0 & \tau_1\alpha_2 & -(\alpha_3+\mu_1+\kappa_1) & 0 & 0 & 0 \\ 0 & (1-\tau_1)\alpha_2 & \rho\alpha_3 & -(\alpha_4+\mu_1+\delta_1) & 0 & 0 \\ 0 & 0 & (1-\rho)\alpha_3 & \alpha_4 & -(\varpi+\mu_1) & 0 \\ 0 & 0 & 0 & \frac{-\gamma_1\Gamma_{hr}S_R}{N_1} & 0 & -\mu_3 \end{pmatrix} \tag{13}$$

$$\mathbf{J_{21}} = \begin{pmatrix} 0 & 0 & 0 & \frac{\gamma_1\Gamma_{hr}S_R}{N_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{-\beta\rho_1\Gamma_{hf}S_F}{N_1} & \frac{-\beta\rho_2\Gamma_{hf}S_F}{N_1} & 0 & 0 \\ 0 & 0 & \frac{\beta\rho_1\Gamma_{hf}S_F}{N_1} & \frac{\beta\rho_2\Gamma_{hf}S_F}{N_1} & 0 & 0 \\ 0 & 0 & 0 & \frac{\eta_1}{N_1} & 0 & 0 \end{pmatrix} \tag{14}$$

$$\mathbf{J_{12}} = \begin{pmatrix} 0 & 0 & \frac{-\alpha_1\Gamma_{rh}S_H}{N_3} & 0 & \frac{-\alpha_1\Gamma_{fh}S_H}{N_2} & -\alpha_1\omega_1 S_H \\ 0 & 0 & \frac{\alpha_1\Gamma_{rh}S_H}{N_3} & 0 & \frac{\alpha_1\Gamma_{fh}S_H}{N_2} & \alpha_1\omega_1 S_H \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{-\gamma_1\Gamma_{rr}S_R}{N_3} & 0 & \frac{-\gamma_1\Gamma_{fr}S_R}{N_2} & -\gamma_1\omega_2 S_R \end{pmatrix} \tag{15}$$

$$\mathbf{J_{22}} = \begin{pmatrix} -(\gamma_2+\mu_3) & 0 & \frac{\gamma_1\Gamma_{rr}S_R}{N_3} & 0 & \frac{\gamma_1\Gamma_{fr}S_R}{N_2} & \gamma_1\omega_2 S_R \\ \tau_2\gamma_2 & -(\gamma_3+\mu_3\kappa_2) & 0 & 0 & 0 & 0 \\ (1-\tau_2)\gamma_2 & \gamma_3 & -(\mu_3+\delta_3) & 0 & 0 & 0 \\ 0 & \frac{-\beta\rho_3\Gamma_{rf}S_F}{N_3} & \frac{-\beta\rho_4\Gamma_{rf}S_F}{N_3} & -\mu_2 & 0 & 0 \\ 0 & \frac{\beta\rho_3\Gamma_{rf}S_F}{N_3} & \frac{\beta\rho_4\Gamma_{rf}S_F}{N_3} & 0 & -(\mu_2+\delta_2) & 0 \\ 0 & 0 & \frac{\eta_2}{N_3} & 0 & 0 & -\mu_4 \end{pmatrix} \tag{16}$$

From the combined matrix $J(E^0)$, the diagonal entries from the first, fifth, sixth and tenth column makes the four eigenvalues of the matrix (12). These are $-\mu_1$, $-(\varpi+\mu_1)$, $-\mu_3$ and $-\mu_2$, now canceling their corresponding rows and columns we modify (12) and remain with an (8×8) matrix with the modified J_{11}, J_{12}, J_{21} and J_{22} as given in (17), (18), (19) and (20) respectively;

$$\mathbf{J_{11}} = \begin{pmatrix} -(\alpha_2+\mu_1) & 0 & \frac{\alpha_1\Gamma_{hh}S_H}{N_1} \\ \tau_1\alpha_2 & -(\alpha_3+\mu_1+\kappa_1) & 0 \\ (1-\tau_1)\alpha_2 & \rho\alpha_3 & -(\alpha_4+\mu_1+\delta_1) \end{pmatrix} \tag{17}$$

$$\mathbf{J_{21}} = \begin{pmatrix} 0 & 0 & \frac{\gamma_1 \Gamma_{hr} S_R}{N_1} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & \frac{\beta \rho_1 \Gamma_{hf} S_F}{N_1} & \frac{\beta \rho_2 \Gamma_{hf} S_F}{N_1} \\ 0 & 0 & \frac{\eta_1}{N_1} \end{pmatrix} \tag{18}$$

$$\mathbf{J_{12}} = \begin{pmatrix} 0 & 0 & \frac{\alpha_1 \Gamma_{rh} S_H}{N_3} & \frac{\alpha_1 \Gamma_{fh} S_H}{N_2} & \alpha_1 \omega_1 S_H \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{19}$$

$$\mathbf{J_{22}} = \begin{pmatrix} -(\gamma_2 + \mu_3) & 0 & \frac{\gamma_1 \Gamma_{rr} S_R}{N_3} & \frac{\gamma_1 \Gamma_{fr} S_R}{N_2} & \gamma_1 \omega_2 S_R \\ \tau_2 \gamma_2 & -(\gamma_3 + \mu_3 \kappa_2) & 0 & 0 & 0 \\ (1 - \tau_2)\gamma_2 & \gamma_3 & -(\mu_3 + \delta_3) & 0 & 0 \\ 0 & \frac{\beta \rho_3 \Gamma_{rf} S_F}{N_3} & \frac{\beta \rho_4 \Gamma_{rf} S_F}{N_3} & -(\mu_2 + \delta_2) & 0 \\ 0 & 0 & \frac{\eta_2}{N_3} & 0 & -\mu_4 \end{pmatrix} \tag{20}$$

Making further computation we find the other negative eigenvalues of the matrix 12 as $-\mu_4$, $-(\mu_2 + \delta_2)$, $-(\mu_3 + \delta_3)$, $-(\gamma_3 + \mu_3 + \kappa_2)$ and $-(\gamma_2 + \mu_2)$. Also there are complex eigenvalues with very long expressions and negative real part, we name them as $-p_1 + q_1 i$ and $-p_2 + q_2 i$ where p_1, p_2 and q_1, q_2 are real and imaginary part respectively. The computation show that the last eigenvalue is negative if and only if $R_0 < 1$. By Morand *et al.* (2011) these results prove that the equilibrium point E^0 is locally asymptotically stable. It then leads to Theorem 4.8.

Theorem 4.8

The Disease Free Equilibrium E^0 of pneumonic plague is locally asymptotically stable if $R_0 <$ 1and unstable if $R_0 > 1$.

4.4.4 Global stability of the disease-free equilibrium point

We employ the Metzler matrix method as described by Castillo-Chavez *et al.* (2002). We divide the general pneumonic plague system (1) - (4) into transmitting and non-transmitting components as stated below.

Let Y_n be the vector for non-transmitting compartments, Y_i be the vector for transmitting compartments and $Y_{E_0,n}$ be the vector of disease free point.

$$\begin{cases} \dfrac{dY_n}{dt} & = A_1(Y_n - Y_{E_0,n}) + A_2 Y_i \\ \\ \dfrac{dY_i}{dt} & = A_3 Y_i \end{cases} \tag{21}$$

We will then have

$$Y_n = (S_H, R_H, S_R, S_F)^T \qquad Y_i = (E_H, I_{HA}, I_{HB}, E_R, I_{RA}, I_{RB}, I_F, A)$$
$$Y_{E_0,n} = (\frac{\psi_1}{\mu_1}, 0, \frac{\psi_3}{\mu_3}, \frac{\psi_{2s}}{\mu_2})$$

$$\mathbf{Y_n} - \mathbf{Y_{E_0,n}} = \begin{pmatrix} S_H - \frac{\psi_1}{\mu_1} \\ R_H \\ S_R - \frac{\psi_3}{\mu_3} \\ S_F - \frac{\psi_{2s}}{\mu_2} \end{pmatrix}$$

In order to prove that the DFE point is globally and asymptotically stable, we are required to show that Matrix A_1 has real negative eigenvalues and A_3 is a Metzler matrix in which all off diagonal element must be non-negative. Referring to (29) we write the general model as given below;

$$\begin{pmatrix} \psi_1 + \varpi R_H - \alpha_1 k S_H - \mu_1 S_H, \\ \alpha_4 I_{HB} + (1-\rho)\alpha_3 I_{HA} - \varpi R_H - \mu_1 R_H, \\ \psi_3 - \gamma_1 M S_R - \mu_3 S_R \\ \psi_{2s} - \beta Y S_F - \mu_2 S_F \end{pmatrix} = \mathbf{A_1} \begin{pmatrix} S_H - \frac{\psi_1}{\mu_1} \\ R_H \\ S_R - \frac{\psi_3}{\mu_3} \\ S_F - \frac{\psi_{2s}}{\mu_2} \end{pmatrix} + \mathbf{A_2} \begin{pmatrix} E_H \\ I_{HA} \\ I_{HB} \\ E_R \\ I_{RA} \\ I_{RB} \\ I_F \\ A \end{pmatrix}$$

and

$$\begin{pmatrix} \alpha_1 k S_H - (\alpha_2 + \mu_1) E_H, \\ \tau_1 \alpha_2 E_H - \rho \alpha_3 I_{HA} - (1-\rho)\alpha_3 I_{HA} - (\mu_1 + \kappa_1) I_{HA}, \\ (1-\tau_1)\alpha_2 E_H + \rho \alpha_3 I_{HA} - \alpha_4 I_{HB} - (\mu_1 + \delta_1) I_{HB}, \\ \gamma_1 M S_R - (\gamma_2 + \mu_3) E_R, \\ \tau_2 \gamma_2 E_R - \gamma_3 I_{RA} - (\mu_3 + \kappa_2) I_{RA}, \\ (1-\tau_2)\gamma_2 E_R + \gamma_3 I_{RA} - (\mu_3 + \delta_3) I_{RB}, \\ \beta Y S_F - (\mu_2 + \delta_2) I_F, \\ \lambda_4 + \eta_1 \dfrac{I_{HB}}{N_1} + \eta_2 \dfrac{I_{RB}}{N_3} - \mu_4 A \end{pmatrix} = \mathbf{A_3} \begin{pmatrix} E_H \\ I_{HA} \\ I_{HB} \\ E_R \\ I_{RA} \\ I_{RB} \\ I_F \\ A \end{pmatrix}$$

For

$$
\begin{aligned}
k =&(\Gamma_{hh}\frac{I_{HB}}{N_1}+\Gamma_{fh}\frac{I_F}{N_2}+\Gamma_{rh}\frac{I_{RB}}{N_3}+\omega_1 A)\\
M =&(\Gamma_{rr}\frac{I_{RB}}{N_3}+\Gamma_{fr}\frac{I_F}{N_2}+\Gamma_{hr}\frac{I_{HB}}{N_1}+\omega_2 A)\\
Y =&(\Gamma_{hf}\frac{\rho_1 I_{HA}+\rho_2 I_{HB}}{N_1}+\Gamma_{rf}\frac{\rho_3 I_{RA}+\rho_4 I_{RB}}{N_3})
\end{aligned}
$$

Now using the transmitting and non-transmitting element, we will have the matrices A_1, A_2 and A_3 as below:

$$
\mathbf{A_1}=\begin{pmatrix}
-\mu_1 & \varpi & 0 & 0\\
0 & -(\varpi+\mu_1) & 0 & 0\\
0 & 0 & -\mu_3 & 0\\
0 & 0 & 0 & -\mu_2
\end{pmatrix} \tag{22}
$$

$$
\mathbf{A_2}=\begin{pmatrix}
0 & 0 & \frac{-\alpha_1\Gamma_{hh}S_H^0}{N_1} & 0 & 0 & \frac{-\alpha_1\Gamma_{rh}S_H^0}{N_3} & \frac{-\alpha_1\Gamma_{fh}S_H^0}{N_2} & -\alpha_1\omega_1 S_H^0\\
0 & (1-\rho)\alpha_3 & \alpha_4 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & \frac{-\gamma_1\Gamma_{hr}S_R^0}{N_1} & 0 & 0 & \frac{-\gamma_1\Gamma_{rr}S_R^0}{N_3} & \frac{-\gamma_1\Gamma_{fr}S_R^0}{N_2} & -\gamma_1\omega_2 S_R^0\\
0 & \frac{-\beta\rho_1\Gamma_{hf}S_F^0}{N_1} & \frac{-\beta\rho_2\Gamma_{hf}S_F^0}{N_1} & 0 & \frac{-\beta\rho_3\Gamma_{rf}S_F^0}{N_3} & \frac{-\beta\rho_4\Gamma_{rf}S_F^0}{N_3} & 0 & 0
\end{pmatrix} \tag{23}
$$

$$
\mathbf{A_3}=\begin{pmatrix}
-n_1 & 0 & \frac{\alpha_1\Gamma_{hh}S_H^0}{N_1} & 0 & 0 & \frac{\alpha_1\Gamma_{rh}S_H^0}{N_3} & \frac{\alpha_1\Gamma_{fh}S_H^0}{N_2} & \alpha_1\omega_1 S_H\\
\tau_1\alpha_2 & -n_2 & 0 & 0 & 0 & 0 & 0 & 0\\
n_8 & \rho\alpha_3 & -n_3 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & \frac{\gamma_1\Gamma_{hr}S_R^0}{N_1} & -n_4 & 0 & \frac{\gamma_1\Gamma_{rr}S_R^0}{N_3} & \frac{\gamma_1\Gamma_{fr}S_R^0}{N_2} & \gamma_1\omega_2 S_R^0\\
0 & 0 & 0 & \tau_2\gamma_2 & -n_5 & 0 & 0 & 0\\
0 & 0 & 0 & (1-\tau_2)\gamma_2 & \gamma_3 & -n_6 & 0 & 0\\
0 & n_9 & \frac{\beta\rho_2\Gamma_{hf}S_F^0}{N_1} & 0 & \frac{\beta\rho_3\Gamma_{rf}S_F^0}{N_3} & \frac{\beta\rho_4\Gamma_{rf}S_F^0}{N_3} & -n_7 & 0\\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu_4
\end{pmatrix} \tag{24}
$$

where

$$
\begin{array}{lll}
n_1=(\alpha_2+\mu_1) & n_2=(\alpha_3+\mu_1+\kappa_1) & n_3=(\alpha_4+\mu_1+\delta_1)\\
n_4=(\gamma_2+\mu_3) & n_5=(\gamma_3+\mu_3+\kappa_2) & n_6=(\mu_3+\delta_3)\\
n_7=(\mu_2+\delta_2) & n_8=(1-\tau_1)\alpha_2 & n_9=\frac{\beta\rho_1\Gamma_{hf}S_F^0}{N_1}\\
S_H^0=\frac{\psi_1}{\mu_1} & S_R^0=\frac{\psi_3}{\mu_3} & S_F^0=\frac{\psi_{2s}}{\mu_2}
\end{array}
$$

Computing the eigenvalues of matrix A_1, we find that the eigenvalues are $-\mu_1$, $-\mu_2$, $-\mu_3$ and $-(\varpi+\mu_1)$. The result now confirms that the system

$$
\frac{dY_n}{dt}=A_1(Y_n-Y_{E_0,n})+A_2Y_i
$$

is globally and asymptotically stable at Y_{E_0}. Also we find that all its off-diagonal elements of the matrix A_3 are non-negative and thus A_3 is a Metzler stable matrix. Therefore Disease Free Equilibrium point for pneumonic plague system is globally asymptotically stable and as a result we have the following theorem:

Theorem 4.9

The disease-free equilibrium point is globally asymptotically stable in E^0 if $R_0 < 1$and unstable if $R_0 > 1$.

4.4.5 Existence of Endemic Equilibrium

Now, we investigate conditions for existence of the endemic equilibrium points of pneumonic plague disease. The equilibrium point $E^*(S_H^*, E_H^*, I_{HA}^*, I_{HB}^*, R_H^*, S_R^*, E_R^*, I_{RA}^*, I_{RB}^*, S_F^*, I_F^*, A^*)$ is obtained by solving the equations obtained by setting the derivatives of (1)-(4) equal to zero.

If we let λ_H^*, λ_R^*, λ_F^* and λ_A^* be the force of infection for human beings, rodents, fleas and the environment respectively as given in (25) - (28).

$$\lambda_H^* = \Gamma_{hh}\frac{I_{HB}^*}{N_1^*} + \Gamma_{fh}\frac{I_F^*}{N_2^*} + \Gamma_{rh}\frac{I_{RB}^*}{N_3^*} + \omega_1 A^* \tag{25}$$

$$\lambda_R^* = \Gamma_{rr}\frac{I_{RB}^*}{N_3^*} + \Gamma_{fr}\frac{I_F^*}{N_2^*} + \Gamma_{hr}\frac{I_{HB}^*}{N_1^*} + \omega_2 A^* \tag{26}$$

$$\lambda_R^* = \Gamma_{hf}\rho\frac{I_{HA}^*}{N_1^*} + \Gamma_{rf}(1-\rho)\frac{I_{RA}^*}{N_3^*} \tag{27}$$

$$\lambda_A^* = \lambda_4 + \eta_1\frac{I_{HB}^*}{N_1^*} + \eta_2\frac{I_{RB}^*}{N_3^*} \tag{28}$$

It is clear that λ_H^* is an increasing function of I_{HB}, I_{RB}, I_F and A. When the the force of infection is high, the rate at which human beings progress from susceptible to exposed will increase, thus the number of human beings becoming exposed to the disease will as well increase. The increase of number of exposed human beings will lead to the increases of the number of human beings progressing and become bubonic or pneumonic plague infectives. However when the force of infection is low, the rate at which human beings progress from susceptible to exposed decreases and consequently it decreases the infection rate. That is to say if we assume that when the force of infection is high then $I_{HB} = I_{HB1}$, $I_{RB} = I_{RB1}$, $I_F = I_{F1}$ and $A = A1$ and when the force of infection is low then $I_{HB} = I_{HB2}$, $I_{RB} = I_{RB2}$, $I_F = I_{F2}$ and $A = A1$, since λ_H^* is an increasing function then $\lambda_H^*(I_{HB1}, I_{RB1}, I_{F1}, A1) > \lambda_H^*(I_{HB2}, I_{RB2}, I_{F2}, A2)$.

If the force of infection for human being is assumed to be very high, that is $\lambda_H^* \to \infty$, gradually the susceptible human will approach zero $S_H \approx 0$ and recovered human beings will approach a

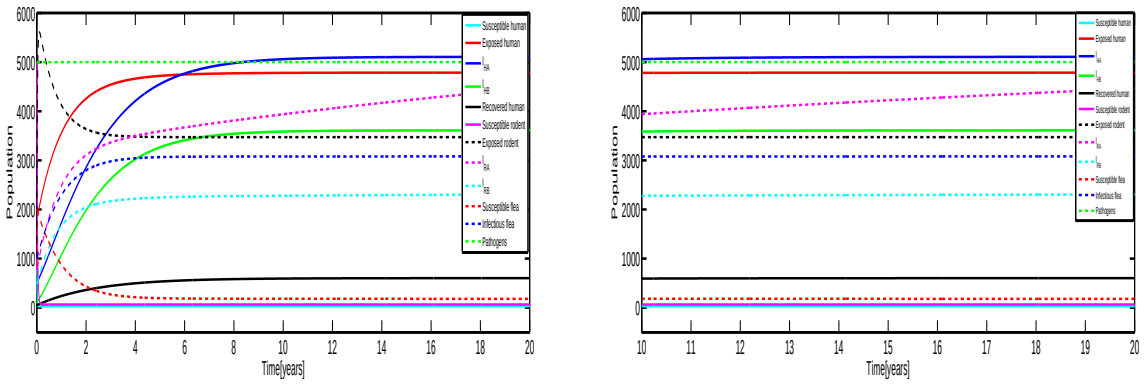
non-zero endemic point. Moreover the number of exposed human beings (E_H), human beings infected with bubonic plague (I_{HA}) and human beings infected with pneumonic plague (I_{HB}) will rise approaching a non-zero endemic point E_H^*, I_{HA}^* and I_{HB}^*.

The force of infection in rodent λ_R^* is an increasing function of I_{RB}, I_{HB}, I_F and A. As we increase the force of infection for rodent, that is $\lambda_R^* \to \infty$, gradually the number of susceptible rodents will approach zero $S_R \approx 0$. As the progression rate of the susceptible rodent to infected increases, the rodent exposed to the disease E_R, the number rodent infected with bubonic plague I_{RA} and the number of rodent infected with pneumonic plague I_{RB} will rise and approach a non-negative endemic point, E_R^*, I_{RA}^* and I_{RB}^*.

The force of infection in flea (λ_F^*) is an increasing function of I_{RA} and I_{HA}. Now assuming the enormous increasing force of infection for flea, that is as $\lambda_F^* \to \infty$, the number of susceptible fleas, S_F, will gradually approach zero. As the rate at which a flea gets infection increases, I_F will approach non-zero endemic level I_F^*.

Force of infection in the environment in our case is an overall rate at which pathogens are populated in the environment. λ_A^* is the increasing function of I_{HB} and I_{RB}. Now if we assume the mammoth increase of the force of infection to the environment, that is as $\lambda_A^* \to \infty$ will lead to the proportional increase the the number of pathogens shad in the environment.

Using the study by De La Sen *et al.* (2011), we study the existence of endemic equilibrium through numerical simulation. We choose the values of the parameter that constitute the basic reproduction number in such a way that $R_0 > 1$, in our case we have $R_0 = 76$.



(a) **(b)**

Figure 24: The solution trajectories showing the endemic equilibrium point.

In order to examine the existence of endemic equilibrium point we show that the exposed, infected and recovered classes in human beings, rodents and fleas and the number of pathogens in the environment are different from zero. Figure 24b is the zoomed view of Fig. 24a which

shows that; the susceptible population in human being, rodent and flea approaches zero while on the other hand the exposed, infected and the recovery classes in human being, rodent flea and the pathogens in environment reaches maximum and then converging to non-zero endemic equilibrium point.

We then derive the conditions under which the endemic equilibrium points are stable or unstable. That is, we show whether the solution starting sufficiently close to the equilibrium remains close to the equilibrium and approaches the equilibrium as $t \to \infty$, or if there are solutions starting arbitrary close to the equilibrium which do not approach it respectively.

4.4.6 Global stability of Endemic equilibrium point

Van den Driessche and Watmough (2002) postulate that the local stability of the Disease Free Equilibrium advocates for local stability of the Endemic Equilibrium for the reverse condition. We therefore focus on finding the global stability of Endemic equilibrium. We use Korobeinikov approach in which we formulate a suitable Lyapunov function for pneumonic plague model (Van den Driessche and Watmough, 2002; Korobeinikov, 2004, 2007).
The Lyapunov function is as given in the form below;

$$V = \sum a_i(y_i - y_i^* \ln y_i)$$

where a_i is defined as a properly selected positive constant, y_i defines the population of the i^{th} compartment, and y_i^* is the equilibrium point.
We will have the following Lyapunov function:

$$\begin{aligned} V = \; & W_1(S_H - S_H^* \ln S_H) + W_2(E_H - E_H^* \ln E_H) + W_3(I_{HA} - I_{HA}^* \ln I_{HA}) + W_4(I_{HB} \\ & - I_{HB}^* \ln I_{HB}) + W_5(R_H - R_H^* \ln R_H) + W_6(S_R - S_R^* \ln S_R) + W_7(E_R - E_R^* \ln E_R) \\ & + W_8(I_{RA} - I_{RA}^* \ln I_{RA}) + W_9(I_{RB} - I_{RB}^* \ln I_{RB}) + W_{10}(S_F - S_F^* \ln S_F) \\ & + W_{11}(I_F - I_F^* \ln I_F) + W_{12}(A - A^* \ln A) \end{aligned}$$

The constants W_i are non-negative in Φ for $i = 1, 2, 3...12$. The function V together with its constants $W_1, W_2...W_{12}$ are chosen such that V is continuous and differentiable in Φ.

We compute the time derivative of V to get;

$$\begin{aligned} \tfrac{dV}{dt} = \; & W_1(1 - \tfrac{S_H^*}{S_H})\tfrac{dS_H}{dt} + W_2(1 - \tfrac{E_H^*}{E_H})\tfrac{dE_H}{dt} + W_3(1 - \tfrac{I_{HA}^*}{I_{HA}})\tfrac{dI_{HA}}{dt} + W_4(1 - \tfrac{I_{HB}^*}{I_{HB}})\tfrac{dI_{HB}}{dt} \\ & + W_5(1 - \tfrac{R_H^*}{R_H})\tfrac{dR_H}{dt} + W_6(1 - \tfrac{S_R^*}{S_R})\tfrac{dS_R}{dt} + W_7(1 - \tfrac{E_R^*}{E_R})\tfrac{dE_R}{dt} + W_8(1 - \tfrac{I_{RA}^*}{I_{RA}})\tfrac{dI_{RA}}{dt} \\ & + W_9(1 - \tfrac{I_{RB}^*}{I_{RB}})\tfrac{dI_{RB}}{dt} + W_{10}(1 - \tfrac{S_F^*}{S_F})\tfrac{dS_F}{dt} + W_{11}(1 - \tfrac{I_F^*}{I_F})\tfrac{dI_F}{dt} \\ & + W_{12}(1 - \tfrac{A^*}{A})\tfrac{dA}{dt} \end{aligned}$$

Using system (1) - (4) we will have

$$\begin{aligned}
\frac{dV}{dt} = \; & W_1(1-\tfrac{S_H^*}{S_H})[\psi_1+\varpi R_H-\alpha_1(\Gamma_{hh}\tfrac{I_{HB}}{N_1}+\Gamma_{fh}\tfrac{I_F}{N_2}+\Gamma_{rh}\tfrac{I_{RB}}{N_3}+\omega_1 A)S_H-\mu_1 S_H,] \\
& +W_2(1-\tfrac{E_H^*}{E_H})[\alpha_1(\Gamma_{hh}\tfrac{I_{HB}}{N_1}+\Gamma_{fh}\tfrac{I_F}{N_2}+\Gamma_{rh}\tfrac{I_{RB}}{N_3}+\omega_1 A)S_H-(\alpha_2+\mu_1)E_H] \\
& +W_3(1-\tfrac{I_{HA}^*}{I_{HA}})[\tau_1\alpha_2 E_H-\rho\alpha_3 I_{HA}-(1-\rho)\alpha_3 I_{HA}-(\mu_1+\kappa_1)I_{HA}] \\
& +W_4(1-\tfrac{I_{HB}^*}{I_{HB}})[(1-\tau_1)\alpha_2 E_H+\rho\alpha_3 I_{HA}-\alpha_4 I_{HB}-(\mu_1+\delta_1)I_{HB}] \\
& +W_5(1-\tfrac{R_H^*}{R_H})[\alpha_4 I_{HB}+(1-\rho)\alpha_3 I_{HA}-\varpi R_H-\mu_1 R_H] \\
& +W_6(1-\tfrac{S_R^*}{S_R})[\psi_3-\gamma_1(\Gamma_{rr}\tfrac{I_{RB}}{N_3}+\Gamma_{fr}\tfrac{I_F}{N_2}+\Gamma_{hr}\tfrac{I_{HB}}{N_1}+\omega_2 A)S_R-\mu_3 S_R] \\
& +W_7(1-\tfrac{E_R^*}{E_R})[\gamma_1(\Gamma_{rr}\tfrac{I_{RB}}{N_3}+\Gamma_{fr}\tfrac{I_F}{N_2}+\Gamma_{hr}\tfrac{I_{HB}}{N_1}+\omega_2 A)S_R-(\gamma_2+\mu_3)E_R] \\
& +W_8(1-\tfrac{I_{RA}^*}{I_{RA}})[\tau_2\gamma_2 E_R-\gamma_3 I_{RA}-(\mu_3+\kappa_2)I_{RA}] \\
& +W_9(1-\tfrac{I_{RB}^*}{I_{RB}})[(1-\tau_2)\gamma_2 E_R+\gamma_3 I_{RA}-(\mu_3+\delta_3)I_{RB}] \\
& +W_{10}(1-\tfrac{S_F^*}{S_F})[\psi_{2s}-\beta(\Gamma_{hf}\tfrac{\rho_1 I_{HA}+\rho_2 I_{HB}}{N_1}+\Gamma_{rf}\tfrac{\rho_3 I_{RA}+\rho_4 I_{RB}}{N_3})S_F-\mu_2 S_F] \\
& +W_{11}(1-\tfrac{I_F^*}{I_F})[\beta(\Gamma_{hf}\tfrac{\rho_1 I_{HA}+\rho_2 I_{HB}}{N_1}+\Gamma_{rf}\tfrac{\rho_3 I_{RA}+\rho_4 I_{RB}}{N_3})S_F-(\mu_2+\delta_2)I_F] \\
& +W_{12}(1-\tfrac{A^*}{A})[\lambda_4+\eta_1\tfrac{I_{HB}}{N_1}+\eta_2\tfrac{I_{RB}}{N_3}-\mu_4 A]
\end{aligned}$$

Using system (1) - (4) at endemic equilibrium we derive the following;

$$\begin{aligned}
\frac{dV}{dt} = \; & -W_1(1-\tfrac{S_H^*}{S_H})^2-W_2(1-\tfrac{E_H^*}{E_H})^2-W_3(1-\tfrac{I_{HA}^*}{I_{HA}})^2-W_4(1-\tfrac{I_{HB}^*}{I_{HB}})^2 \\
& -W_5(1-\tfrac{R_H^*}{R_H})^2-W_6(1-\tfrac{S_R^*}{S_R})^2-W_7(1-\tfrac{E_R^*}{E_R})^2-W_8(1-\tfrac{I_{RA}^*}{I_{RA}})^2 \\
& -W_9(1-\tfrac{I_{RB}^*}{I_{RB}})^2-W_10(1-\tfrac{S_F^*}{S_F})^2-W_{11}(1-\tfrac{I_F^*}{I_F})^2 \\
& -W_{12}(1-\tfrac{A^*}{A})^2+F(S_H,E_H,I_{HA},I_{HB},R_H,S_R,E_R,I_{RA},I_{RB},S_F,I_F,A)
\end{aligned}$$

where the function $F(S_H,E_H,I_{HA},I_{HB},R_H,S_R,E_R,I_{RA},I_{RB},S_F,I_F,A)$ is non-positive, Now following the procedures by McCluskey (2006) and Korobeinikov and Wake (2002). We take that

$$F(S_H,E_H,I_{HA},I_{HB},R_H,S_R,E_R,I_{RA},I_{RB},S_F,I_F,A)\leq 0$$

for all values of

$$S_H,E_H,I_{HA},I_{HB},R_H,S_R,E_R,I_{RA},I_{RB},S_F,I_F,A.$$

Then $\frac{dV}{dt}\leq 0$ for all values of $S_H,E_H,I_{HA},I_{HB},R_H,S_R,E_R,I_{RA},I_{RB},S_F,I_F,A$ and it is zero when $S_H=S_H^*,E_H=E_H^*,I_{HA}=I_{HA}^*,I_{HB}=I_{HB}^*,R_H=R_H^*,S_R=S_R^*,E_R=E_R^*,I_{RA}=I_{RA}^*,I_{RB}=I_{RB}^*,S_F=S_F^*,I_F=I_F^*,A=A^*$. Hence the largest compact invariant set in $S_H,E_H,I_{HA},I_{HB},R_H,S_R,E_R,I_{RA},I_{RB},S_F,I_F,A$ such that $\frac{dV}{dt}=0$ is the singleton E^* which is the Endemic Equilibrium point of the pneumonic plague system (1) - (4). Now using LaSalles's invariant principle by La Salle (1976), it implies that E^* is globally asymptotically stable in the interior of the region of S_H, E_H, I_{HA}, I_{HB}, R_H, S_R, E_R, I_{RA}, I_{RB}, S_F, I_F, A and thus leads to the theorem below:

Theorem 4.10

If $R_0>1$ then the model system (1) - (4) of pneumonic plague has a unique endemic equilib-

rium point E^* which is globally asymptotically stable in S_H, E_H, I_{HA}, I_{HB}, R_H, S_R, E_R, I_{RA}, I_{RB}, S_F, I_F, A.

4.5 Sensitivity and Elasticity analysis and Numerical Simulation

In this section, we determine the behavior and strength of model predictions with respect to parameter values. We use sensitivity and elasticity analysis to determine the impact of k_{ij} on the basic reproduction number R_0 in order to set the required control strategies for pneumonic plague.

4.5.1 Parameter Estimation

The parameters are taken from the literature that relate to this study, the present information on pneumonic plague and through estimation using sensitivity analysis and simulations. Table 9 shows the values of the parameters as used in the model.

Table 9: Parameter values for pneumonic plague disease

Parameters	**Value/Range**	**Reference/Source**
Γ_{rf}	0.6	Ngeleja *et al.* (2016)
Γ_{fh}	0.09	Benkirane *et al.* (2009)
Γ_{fr}	4.7	Li (1993)
ρ	0.7	Estimated
α_1	0.9	Ngeleja *et al.* (2016)
α_4	0.006	Estimated
γ_1	0.9	Ngeleja *et al.* (2016)
Γ_{hf}	0.28	Benkirane *et al.* (2009)
λ_4	0.89	Ngeleja *et al.* (2016)
α_2	0.95	Estimated
γ_2	0.91	Estimated
α_3	0.6	estimated
ϖ	0.1	Keeling and Gilligan (2000*a*)
μ_1	0.04	Keeling and Gilligan (2000*a*)
η_1	0.37	Estimated
δ_1	0.04	Keeling and Gilligan (2000*a*)
η_2	0.89	Estimated

Continued on next page

Table 9 – *Continued from previous page*

Parameters	**Value/Range**	**Reference/Source**
δ_3	0.05	Keeling and Gilligan (2000*b*)
μ_3	0.2	Galtier and Mouchiroud (1998)
ω_1	0.8	Estimated
ω_2	0.04	Estimated
μ_4	0.1	Ngeleja *et al.* (2016)
μ_2	0.07	Benkirane *et al.* (2009)
τ_1	0.6	Estimated
τ_2	0.4	Estimated
δ_2	0.03	Benkirane *et al.* (2009)
γ_3	0.015	Estimated
ψ_1	0.09	Ngeleja *et al.* (2016)
ψ_{2S}	0.008	Keeling and Gilligan (2000*b*)
ψ_3	0.03	Keeling and Gilligan (2000*a*)
β	0.99	Ngeleja *et al.* (2016)
Γ_{hh}	0.019	Estimated
Γ_{rr}	0.029	Estimated
Γ_{hr}	0.005	Estimated
Γ_{rh}	0.09	Estimated

Figure 25a, Fig. 25b, Fig. 25c and Fig. 25d show the dynamics of the disease in human beings, rodents, fleas and pathogens in the environment respectively. In human beings, we see that the the exposed E_H, bubonic and pneumonic plague infectious I_{HA} and I_{HB}, and recovery R_H classes slightly increase before it settle at its equilibrium points. The susceptible class S_H experience a fast decrease within the first year and then it gradually decrease to its endemic point. In rodent population, all compartments S_R, E_R , I_{RA} and I_{RB} show a marginal increase before they all attain the endemic equilibrium point. The compartment in fleas and pathogens in the environment also experience the marginal increase before they reach the endemic point.

Bubonic plague serves as the primary stage of pneumonic plague in this study, it is mainly transferred when the infected flea bites the susceptible human being or rodent. The fraction of human being and rodent infected with bubonic plague if not treated may progress and become the pneumonic plague infectives. This means that the increase of the number of human beings

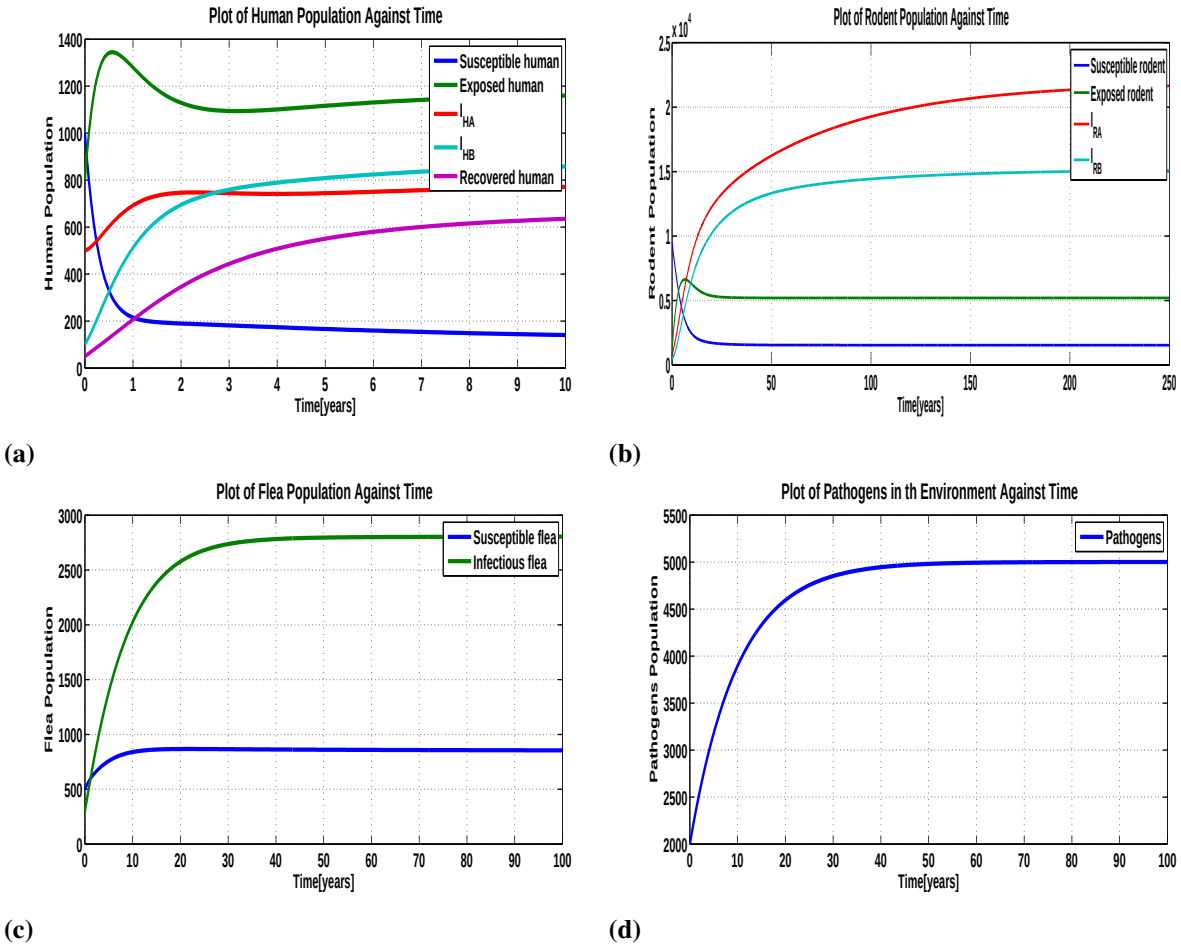
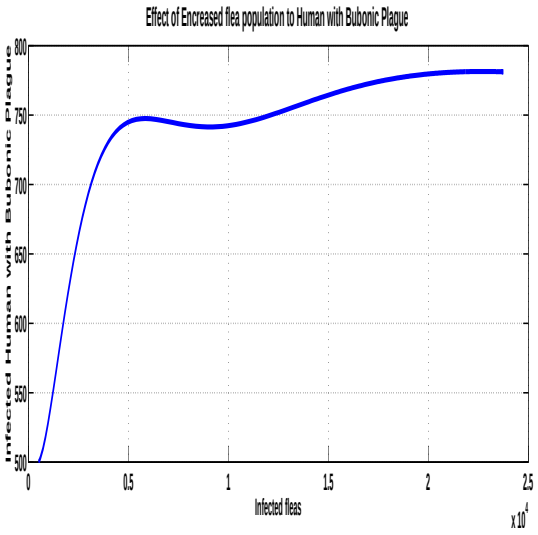


Figure 25: The dynamics of human beings, rodents, fleas and pathogens in the environment with baseline parameter values given in Table 9.

and rodents with bubonic plague will also increase the number of human beings and rodents with pneumonic plague (Felek *et al.*, 2010). Figure 26 shows the influence of number of infectious individuals due to the increased number of infected flea to the human beings and rodents infected with bubonic plague. Figure 27 shows the influence of number of infectious individuals due to human beings and rodents infected with bubonic plague to the human beings and rodents with pneumonic plague. This output is because the increase of the number of individual with bubonic plague consequently increases the progression rate of individuals (human being and rodent) with Bubonic Plague to individuals with Pneumonic Plague.

Figure 26 shows that when the number of infected flea increases the number of human beings and rodents infected with Bubonic plague also increase. It implies that the increased number of infected fleas will increase the probability of a human being or a rodent to be bitten by the infected flea. As a result it increases the number of human beings and rodents infected with Bubonic plague.



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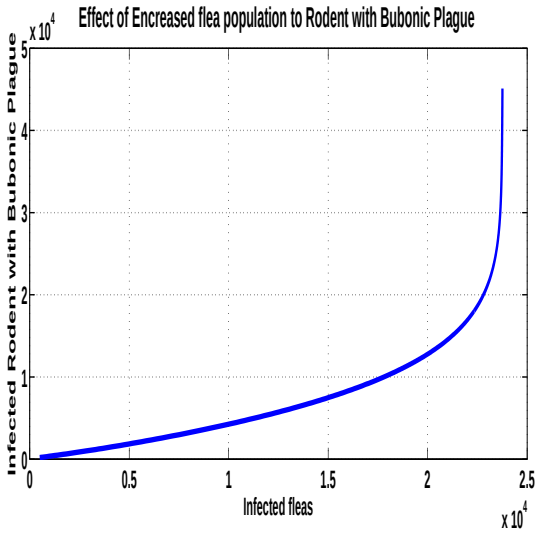

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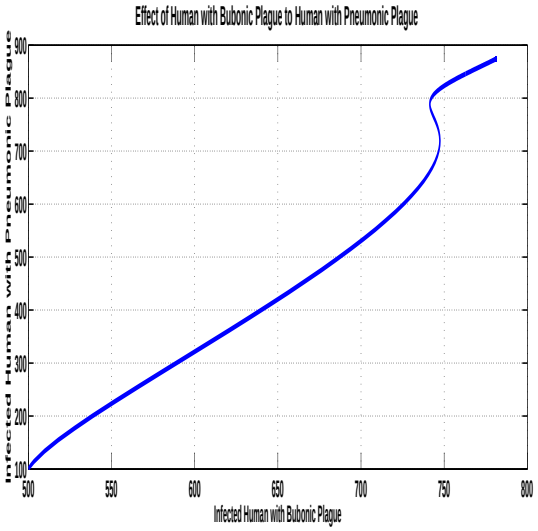
Figure 26: The effect of increased infected fleas on the number of human beings and rodents with Bubonic Plague



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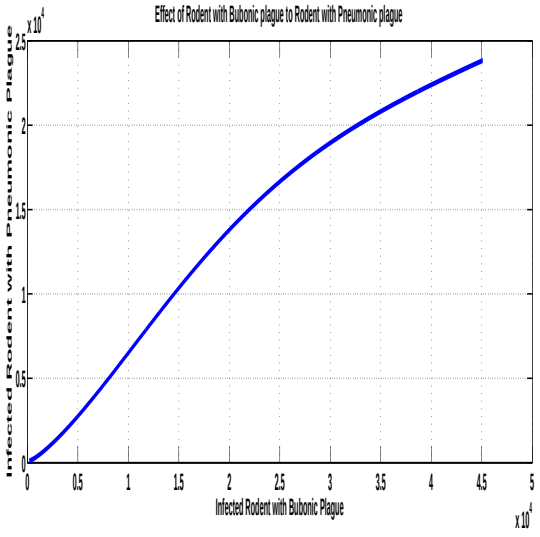

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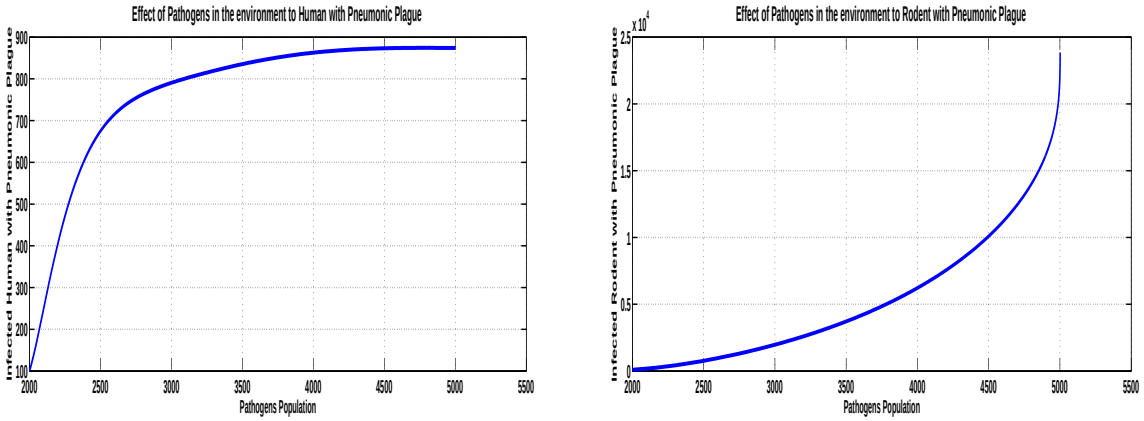
Figure 27: The effect of increased number of human beings and rodents with Bubonic Plague on the number of human beings and rodents with Pneumonic Plague



(a) **(b)**

Figure 28: The effect of increased number pathogens in the environment on the number of human beings and rodents with Pneumonic Plague

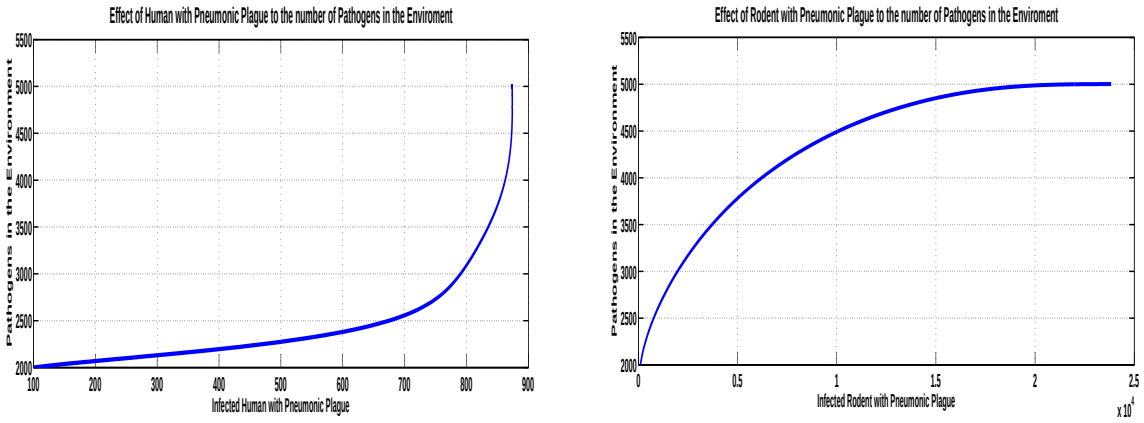
The environment infested with pathogens also plays a great role in transmitting the pneumonic plague bacteria to the human being or rodent populations. The bacteria may be transmitted through airborne transmission (droplet contact). When a human being or rodent with pneumonic plague coughs or sneezes the bacteria are moved to the environment and upon adequate contact it may lead to infection to human beings or rodents (Prentice and Rahalison, 2007).

Figure 28 shows the influence of pathogens in the environment to the number of human beings and rodents with pneumonic plague. The figure portrays that the increase in the number of pathogens in the environment proportionally increases the number of human beings and rodents with Pneumonic Plague, this is due to the fact that the increase the pathogens in the environment will also increase the rate/probability that air that one (human being or rodents) breathes in contain *yersinia pestis* which may leads to infection.

Environment also is greatly affected when the number of human and rodent with Pneumonic Plague is increased (Himsworth *et al.*, 2013). In Fig 29, we see that as the number of human and rodent with pneumonic plague increases the pathogens in the environment increase as well. This result is realistic due to the fact that human and rodent infected with Pneumonic Plague do release yersinia pestis bacteria into the environment through coughing or sneezing (Orloski and Lathrop, 2003).

4.5.2 Sensitivity and Elasticity analysis of R_0

In this section, we determine the effect of parameters in the variation of the basic reproduction number using sensitivity analysis. We also perform the elasticity analysis to quantify the relative



(a) **(b)**

Figure 29: The effect of increased number of human beings and rodents with Pneumonic Plague on the number of pathogens in the environment

change in R_0 in response to the change in a parameter. Hartemink (2009) analyzed the steps to study the sensitivity and elasticity of the basic reproduction number R_0 to the changes in elements k_{ij} or to the parameters that describe them. We employ the steps in our model as given below.

Sensitivity

The sensitivity s_{ij} of a matrix K is defined as the change in the basic reproduction number (R_0) which is the the maximum modulus of the eigenvalues of the matrix K due to change in elements k_{ij} given by

$$s_{ij} = \frac{\partial R_0}{\partial k_{ij}}. \tag{29}$$

The values s_{ij} form a sensitivity matrix S_{ij} which is computed from the left and right eigenvectors of the next generation matrix corresponding to its dominant eigenvalue (Caswell, 2001).

For individual parameters the sensitivity $s(\lambda)$ is given by

$$s(\lambda) = \sum_{ij} \frac{\partial R_0}{\partial k_{ij}} \frac{\partial k_{ij}}{\partial \lambda}. \tag{30}$$

Elasticity

Elasticity is defined as the proportional change in R_0 due to a proportional change in the matrix element. Now the elasticity e_{ij} of a matrix element k_{ij} is defined as

$$e_{ij} = \frac{k_{ij}}{R_0}\frac{\partial R_0}{\partial k_{ij}}. \tag{31}$$

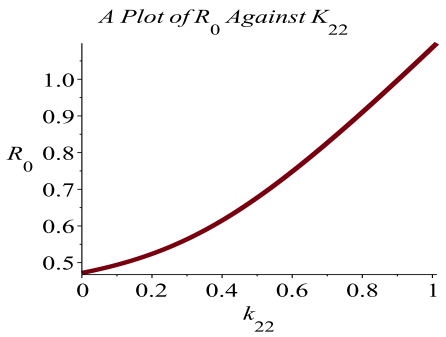
For individual parameters the elasticity $e(\lambda)$ is given by

$$e(\lambda) = \frac{\lambda}{R_0}\sum_{ij}\frac{\partial R_0}{\partial k_{ij}}\frac{\partial k_{ij}}{\partial \lambda}. \tag{32}$$

Table 10 shows the sensitivity and elasticity of the basic reproduction number R_0 for the given parameter values. From the table we see that R_0 is most sensitive to expected number of new cases of the contaminated environment caused by one rodent infected with pneumonic plague k_{64}. R_0 is also sensitive to other k_{ij}^s like the the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with pneumonic plague (k_{44}), the expected number of new cases of contaminated environment caused by one infected human beings with pneumonic plague (k_{62}), the expected number of new cases of human beings infected with pneumonic plague caused by one infected rodent with pneumonic plague (k_{24}), the expected number of new cases of rodent infected with pneumonic plague caused by one infected human beings with pneumonic plague (k_{42}) and the expected number of new cases of rodent infected with pneumonic plague caused by contaminated environment (k_{46}). The basic reproduction number (R_0) is least sensitive to (k_{26}) which is the expected number of new cases of human beings infected with pneumonic plague caused by infected environment. From Table 10, we also see that R_0 is more elastic to the expected number of new cases of infected environment caused by one infected rodent with pneumonic plague (k_{64}). It is also least elastic to the expected number of new cases of human beings infected with pneumonic plague caused by one infected human beings with pneumonic plague (k_{22}).

From the Table 10 it can be seen that the sensitivity of all $k_{ij}s$ are positive. The positive sign implies that increasing (decreasing) any k_{ij} will consequently increase (decrease) the basic reproduction number. For example, the sensitivity of $k_{64} = 0.408$ implies that increasing the expected number of new cases of infected environment caused by one infected rodent with pneumonic plague by 10% will increase the value of the basic reproduction number by 4%. Figure 30, shows the effect of k_{22}, k_{24}, k_{26}, k_{42}, k_{44}, k_{46}, k_{62} and k_{64} on the basic reproduction number .

The marginal increase of each k_{ij} brings about a significant increase in the basic reproduction number, which means that to effectively control the disease an effort should be made to reduce



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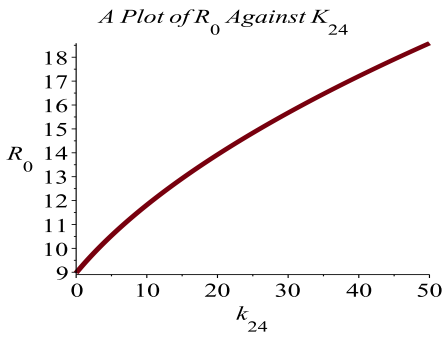

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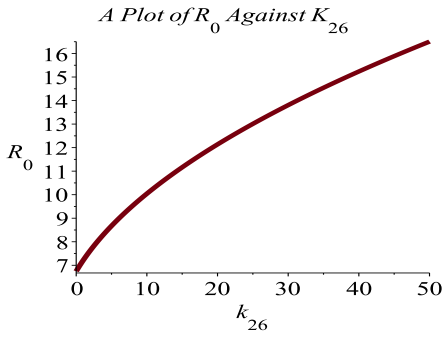

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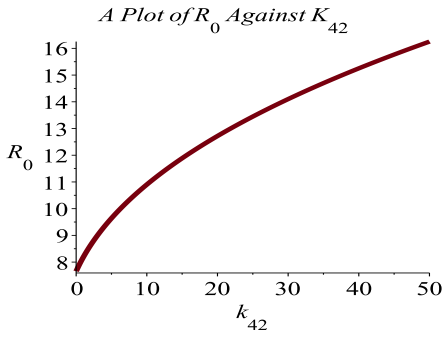

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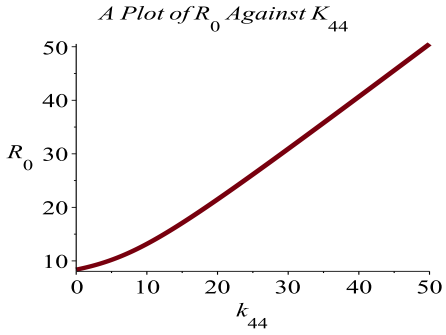

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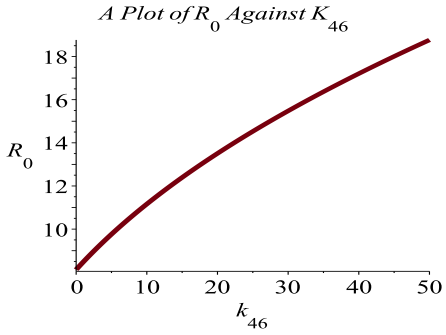

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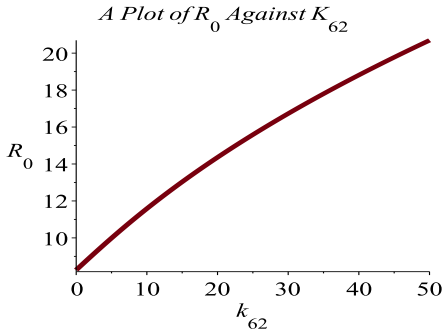

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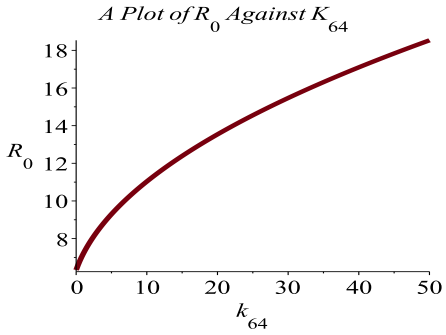


(h)

Figure 30: The Effect of k_{ij} on the Basic Reproduction Number

Table 10: Sensitivity and elasticity of R_0 for pneumonic plague.

Variable	Sensitivity Index	Elasticity
k_{22}	0.2818959031	0.031
k_{24}	0.3345433940	0.038
k_{26}	0.2748857038	0.214
k_{42}	0.3226507761	0.138
k_{44}	0.3829097350	0.123
k_{46}	0.3146270825	0.121
k_{62}	0.3437425664	0.113
k_{64}	0.4079406747	0.222

the magnitude of each k_{ij}. We then need to reduce expected number of new cases of human beings infected with pneumonic plague caused by one infected human beings with pneumonic plague k_{22}.

This may be done through reducing the probability that human being survive the incubation period, human's incubation period, and adequate contact rate between people infected with pneumonic plague. k_{24} may be reduced through reducing adequate contact rate between rodent infected with Pneumonic Plague to human being, The probability that a rodent infected with pneumonic plague survives the incubation period and the infectious period of rodent with pneumonic plague, k_{26} may be reduced by reducing the period that the environment remains contaminated with pathogens causing the disease, The probability that the environment survive the period taken by pathogens to reach the threshold necessary to infect the environment and thus transmit pneumonic plague disease to human beings and Adequate contact rate: Pathogens in the environment to human beings. We can reduce the value of k_{42} by reducing the probability that human beings with Pneumonic Plague survive the incubation period, Infectious period of human beings with pneumonic plague and the adequate contact rate between the human beings infected with Pneumonic Plague and rodent. Reducing k_{44} may be by reducing the infectious period of rodent infected with pneumonic plague, the adequate contact rate between the rodent with pnemonic plague and a susceptible rodent and the probability that a rodent survives the period between exposure and onset of symptoms of pneumonic plague. k_{46} can be controlled by reducing the adequate contact rate from pathogens in the environment to rodent, the period that the environment remain contaminated with pathogens causing the disease and the probability that pathogens survive the period to reach the threshold necessary to contaminate the environment and thus transmit pneumonic plague disease to rodent. k_{62} may be reduced by reducing the probability that a human beings with pneumonic plague and capable of transmitting the pathogens to the environment survive the incubation period, the infectious period of a

human being infected with pneumonic plague, and the shading rate of pathogens in the soil/environment from a human being infected with pneumonic plague and we can as well reduce k_{64} by reducing the probability that a rodent with pneumonic plague and capable of transmitting the pathogens to the environment survive the incubation period, the infective period of a rodent infected with pneumonic plague, and the shading rate of pathogens in the soil/environment from a rodent infected with pneumonic plague.

4.6 Discussion

The magnificent transmission capacity displayed in the numerical results, show that, Pneumonic plague is very fatal and threaten the life of human beings, rodents (including the domestic animals) and the fleas. The results demonstrate the vital role played by human beings and rodents with bubonic plague as agents in the transmission and spread of the pneumonic plague disease. It is a fact that if an individual (human being or rodent) with bubonic plague is not treated, the probability of progressing and becoming the pneumonic plague infective is very high (Lathem *et al.*, 2007). Thus the result justifies the reason why an infected flea plays the vital role in the transmission of pneumonic plague, for it is the main agent for bubonic plague transmission to both human beings and rodents.

Pneumonic plague is on top of list of diseases that could be used as a bio-weapon (Oren, 2009). The results in this study show a significant relationship between the increase of the number of human beings and rodents with pneumonic plague and the pathogens in the environment. This implies that when the environment is favorable for the pathogens to spread the disease becoming extremely dangerous with increased prevalence and deaths.

Results in Fig 30 show a positive relationship between the basic reproduction number and the expected number of new cases of each pair k_{ij}. This means that as the number of new cases of i caused by one infected individual j increases. It consequently increases the basic reproduction number. Now since all individuals act as the potential agents for transmission of the disease, this indicates to us that when the disease occur it will spread to a large community very fast.

The strategy that may have a great and positive impact on the control of pneumonic plague, is the one that will reduce the effect of k_{ij} on the basic reproduction number. This may generally be done through the following strategies: one is reducing the individual's infective period; two is reducing the probability that the individual survives the incubation period, and three is reducing the adequate contact rate between one infective agent and the other susceptible individuals. These three strategies will reduce the number of infections an individual can produce

by reducing the values of k_{ij} and as a result reduce the value of the basic reproduction number.

4.7 Conclusion

A deterministic SEIR model with modification was developed and analysed to study the dynamics of pneumonic plague. The analytical results show that the disease free equilibrium point (DFE) and the endemic equilibrium point (EE) exist and were found to be locally and globally asymptotically stable whenever they exist. In order to determine the number of infections an individual can produce we computed the basic reproduction number using the next generation Matrix method.

From this study it is clear, from the analytical results and simulations, that pneumonic plague can be very dangerous to a point of being fatal. There must be plans that will effectively analyze the control strategies of the disease when it occurs. With the support of the numerical analyses in this study we recommend that any control strategy for pneumonic plague should concentrate on reducing the effect of the expected number of new cases of each pair k_{ij} has to the basic reproduction number.

CHAPTER FIVE

Mathematical model for plague disease dynamics with *Yersinia pestis* in the environment [4]

Abstract: In this chapter, we develop a deterministic model to study the dynamics of plague disease. The model considers three forms of plague disease which are bubonic plague, septicemic plague and pneumonic plague. In the model we consider four populations: human beings, rodents, fleas and pathogens in the environment. We determine conditions for extinction and persistence of the disease using the basic reproduction number. We establish the conditions for local and global stability of disease free and endemic equilibrium points. Sensitivity analysis of the basic reproduction number is computed to determine the parameters to which the basic reproduction number is most and least sensitive. We use numerical simulations to show the dynamical behaviour of the model that brings out factors that influence the spread and transmission of plague disease. According to the results we point out the necessity of early treatment in order to reduce the number of individuals that progress from one primary form of plague disease to secondary forms. It is also recommended that proper measure be taken to reduce the force of infection to human beings, rodent, flea and to the environment

Keywords: Plague disease; sensitivity analysis; Yersinia pestis; endemic equilibrium; disease free equilibrium; environmental transmission.

5.1 Introduction

Plague holds an extraordinary record in history and has brought about massive effects on the development of modern civilization. It has affected different countries around the world on continents such as Asia, Africa and Europe. At its early days the root of plague was unknown so it led to massive deaths and panic of the people all around the world (Fraser *et al.*, 2007). Plague is very severe, frequently lethal and potentially epidemic re-imaging disease caused by infection with the Gram negative bacterium called Yersinia pestis. It is primarily carried by wild rodents (most notably rats) and spread to humans via flea bites. It remains to be notorious and a threat to human societies throughout history, due to the unrivaled scale of death and devastation it brought over the history (Wagner *et al.*, 2014).

Plague disease mainly occurs in three forms which are bubonic, septicemic and pneumonic plague (Kugeler *et al.*, 2015). The adequate contact between the flea infested with pathogens

[4]This chapter is based on the manuscript: Mathematical model for plague disease dynamics with *Yersinia pestis* in the environment.

and the susceptible individual (through bite) results in primary bubonic plague or septicemic plague. In very rare cases one may get bubonic plague infection through contact with contaminated fluid or tissue. Septicemic plague occurs when the bacteria infect blood streams. One may be exposed to septicemic plague through physical contact (including sexual contact). An example is when humans being without using proper precautions, handles tissue or body fluids of an animal that is infected by plague during skinning infected animal. Animals like cats may be infected by eating infected rats. The other and most severe form of plague is pneumonic Plague which is transmitted through infectious droplets. When a person with plague pneumonia coughs, droplets containing the plague bacteria are deposited into air, and if these bacteria-containing droplets are breathed in by another person they can cause pneumonic plague infection (Butler, 2013; Prentice and Rahalison, 2007; Butler, 2012).

When the environmental conditions are favorable, Yersinia pestis may survive outside the host and remain infectious for a over 24 hours as an aerosol. But when it is exposed to the sunlight and heat outside of the living host it will quickly die after an hour (Eisen *et al.*, 2008; Gengler *et al.*, 2015). In addition the study by Chenau *et al.* (2014) and McCauley *et al.* (2015) also postulate that plague bacterium can survive for at least 24 days in contaminated soil under natural conditions. This indicates that soil/environment may be used as an important agent in the transmission and spread of plague disease especially in pneumonic form.

Plague disease does not only occur naturally, numerous countries have found ways to use plague bacteria as a biological weapon. Substantial researches on the same have been conducted by many countries mostly developed countries. Some countries were able to make an actual weapon system that spread the plague bacteria (Yersinia pestis) directly, without the need of a vector (e.g fleas). An example is that of the Japanese army who used plague as a weapon against the Chinese in which the attacker dropped plague-infected fleas from an airplane (Szinicz, 2005). Due to its enormous potential of being used as a bio-weapon plague is raising concern at the level of individual, community and national security as it can be used by terrorists.

Yersinia pestis, can sustain their survival in a cycle that involve rodents (mostly wild rats) and fleas. Other domestic animals like cat, dogs and goats may also support the survival of yersinia pestis bacteria (Laudisoit *et al.*, 2012). Plague may persist in a community for a very long time through the enzootic cycle, in which plague bacteria circulate within some rodent and other few domestic animals population at very low rate. The low circulation rate within these populations makes them save as a long time reservoirs for bacteria. But in other cases plague disease is epizootic, in which some animal species including human become infected, causing an outbreak (Burt, 2006).

Africa is among the continents that have been greatly affected by plague. The study by Neerinckx *et al.* (2010) narrates that most plague cases in human since the 1990s have occurred in Africa. Almost all of the reported cases in the last 20 years have occurred among people and communities in small towns and villages or agricultural areas. The number of plague cases reported each year is still significant although the true number may be higher as reported by Neerinckx *et al.* (2010). Plague remains to be a public-health concern in the world but most particularly in African countries where there is low economy and poor living conditions and sanitation. Due to the seasonal distribution of yersinia pestis reservoirs which are mainly rats and the vector flea the occurrence of plague disease is also seasonal (Elschner *et al.*, 2012).

Studies of plague disease particularly with mathematical approach have generally focused on specific form of plague predominantly bubonic plague and very few of pneumonic and septicemic plague. But in order to understand the clear dynamics of plague disease there is a need to assume the possibility of all the three forms of plague in the community at the same time for adequate control strategy (Pechous *et al.*, 2015). As postulated by Mead (2013), the three main forms of plague have very stable mutual occurrences. When an infected individual with one primary form of plague disease for example bubonic plague is not treated may progress to the another secondary stage of the disease like Septicemic or pneumonic. This justifies the possibility of the occurrence of all three forms of plague in the community. This study focuses in developing the mathematical model that includes all three major forms of plague with the full coverage of their modes of transmissions in order to study its dynamics and spreading capacity.

5.2 Mathematical formulation

In this section, we formulate a model using the standard SEIR (Susceptible, Exposed, Infectious, Recoveries) models in order to study the dynamics of the plague disease and ultimately analyze the best way to combat the disease when it occurs in a community .

5.2.1 Variables and Parameters used in the model and their description

In this section we present variable and parameter and their description used in the model

Table 11: Variables and their description for plague disease.

Variable	Description
S_H	Susceptible Human population
E_H	Exposed human population
I_{HB}	Infectious human population with bubonic plague
I_{HS}	Infectious human population with septicemic plague
I_{HP}	Infectious human population with Pneumonic plague
R_H	Recovered Human population
S_R	Susceptible rodents
E_R	Exposed rodents
I_{RB}	Infectious rodents with bubonic plague
I_{RS}	Infectious rodents with septicemic plague
I_{RP}	Infectious rodents with pneumonic plague
S_F	Susceptible fleas
I_F	Infected fleas
A	Pathogens in the soil/environment

Table 12: Parameters and their description for plague disease.

Parameters	Description
Γ_{rbf}	Adequate contact rate: between I_{RB} and flea
Γ_{rsf}	Adequate contact rate: between I_{RS} and flea
Γ_{fh}	Adequate contact rate: between infectious flea and human
Γ_{fr}	Adequate contact rate: between infectious flea and rodent
Γ_{hph}	Adequate contact rate: between I_{HP} and S_H
Γ_{hsh}	Adequate contact rate: between I_{HS} and S_H
Γ_{rbh}	Adequate contact rate: between I_{RB} and S_H
Γ_{rph}	Adequate contact rate:between I_{RP} and S_H
Γ_{rsh}	Adequate contact rate: between I_{RS} and S_H
α_1	Probability that human progress from susceptible to exposed
α_2	Progression rate out of exposed human to infectious state
$\rho_1\alpha_3$	Progression rate out of I_{HB} to I_{HP}
$\rho_2\alpha_3$	Progression rate out of I_{HB} to R_H

Continued on next page

Table 12 – *Continued from previous page*

Parameters	**Description**
$\rho_3\alpha_3$	Progression rate out of I_{HB} to I_{HS}
δ_{1b}	Disease induced death rate of I_{HB}
α_4	Progression rate out of I_{HS} to I_{HP} and R_H
δ_{1s}	Disease induced death rate of I_{HS}
α_5	Progression rate out of I_{HP} to R_H
δ_{1p}	Disease induced death rate of I_{HP}
γ_1	Probability that rodent progress from susceptible to exposed state
Γ_{hbf}	Adequate contact rate: between I_{HB} and flea
Γ_{hsf}	Adequate contact rate: between I_{HS} and flea
Γ_{rpr}	Adequate contact rate: between I_{RP} and S_R
Γ_{rsr}	Adequate contact rate: between I_{RS} and S_R
Γ_{hpr}	Adequate contact rate: between I_{HP} and S_R
Γ_{hsr}	Adequate contact rate: between I_{HS} and S_R
γ_2	The rate at which rodent become infectious .
γ_3	Progression rate out of I_{RB} to I_{RS} and I_{RP}
δ_{3b}	Disease induced death rate of I_{RB}
γ_4	Progression rate out of I_{RS} to I_{RP}
δ_{3s}	Disease induced death rate of I_{RS}
δ_{3p}	Disease induced death rate of I_{RP}
ϖ	Progression rate of recovered human being to susceptible state
μ_1	Natural death rate for Human being
μ_2	Natural death rate for Flea
μ_3	Natural death rate for rodent
ω_1	Adequate contact rate: between Pathogens and Human being
ω_2	Adequate contact rate: between Pathogens and rodent
η_1	Recruitment rate of pathogens to the environment by I_{HP}
η_2	Recruitment rate of pathogens to the environment by I_{RP}
μ_4	Natural death rate for Pathogens
ψ_1	Recruitment rate of human beings
ψ_2	Recruitment rate of fleas
ψ_3	Recruitment rate of rodents

5.2.2 Model description

In the Model, we have four populations which are the Human population, Fleas, Rodents and the Pathogens in the environment. The Human population is divided into six subgroups: the subgroup of people who have not contracted the disease but may get it if they get to contact I_{HS}, I_{HP}, I_{RS}, I_{HP}, I_F or A to be referred to as susceptible and denoted by S_H, People who have the disease but haven't shown any symptom and incapable of transmitting the disease to be referred to as Exposed and denoted by E_H; those who are infected and capable of transmitting the disease are divided into three subgroups: there are those who have bubonic plague denoted by I_{HB}, those with septicemic plague denoted by I_{HS} and those who have Pneumonic plague disease denoted by I_{HP}. The fraction of population in I_{HB} if treated may recover and move to subgroup R_H otherwise they progress either to a septicemic disease infectives I_{HS}, or to pneumonic plague disease infective I_{HP} or else they die. The population in the subgroup I_{HS} if treated they recover and progress to the subgroup R_H and if not treated they progress and join subgroup I_{HP} otherwise they die. The population of the subgroup I_{HP} is considered as a very dangerous stage of plague disease, it is very fatal stage of plague disease with the fatality rate of about 100%, however if treated they recover and join subgroup R_H otherwise they die. So the total human population N_1 is as given by (1):

$$N_1 = S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H. \tag{1}$$

Fleas are divided into two sub-groups, those who have not contracted the disease but may get it if they get in contact with infectious agent (rodent or human) referred to as susceptible flea and denoted by S_F and those who are infected and are capable of transmitting the disease referred to as infectives and denoted by I_F. The total flea population N_2 is as given by (2)

$$N_2 = S_F + I_F. \tag{2}$$

The rodents are divided into five sub-groups; those who have not contracted the disease but may get it if they get in contact with I_{HS}, I_{HP}, I_{RS}, I_{HP}, I_F or A, referred to as susceptible rodents and denoted by S_R; those who have the disease but haven't shown any symptom and incapable of transmitting the disease referred to as Exposed and denoted by E_R, those who are infected and capable of transmitting the disease are divided into three subgroups, there are those who have bubonic plague denoted by I_{RB}, those with septicemic plague denoted by I_{RS} and those who have Pneumonic plague I_{RP}. The fraction of population in I_{RB} may progress to either a septicemic plague disease infectives I_{RS}, or to preneumonic plague disease infectives I_{RP}. The rodent population in the subgroup I_{RS} may either progress to preneumonic plague disease infectives I_{RP} otherwise they die. The population in the subgroup I_RP is considered as a very dangerous stage of plague disease and very fatal so the mortality due to disease in this subgroup

is approximated to be 100% . Then the total rodent population N_3 is as given by (3)

$$N_3 = S_R + E_R + I_{RB} + I_{RS} + I_{RP}. \tag{3}$$

The individuals with pneumonic plague may release pathogens causing plague disease to the environment denoted by A through coughing or sneezing. When the condition in soil/environment is favorable, pathogens may remain infectious in the environment for long time. When a susceptible individual adequately interact with the environment infested with yersinia pestis gets the disease even in the absence of any vector.

Now, based on the description of interaction stated, we develop the a compartmental diagram that describe dynamics of the plague disease in Human, Rodent, Flea and Pathogens in the environment as given in Fig 31

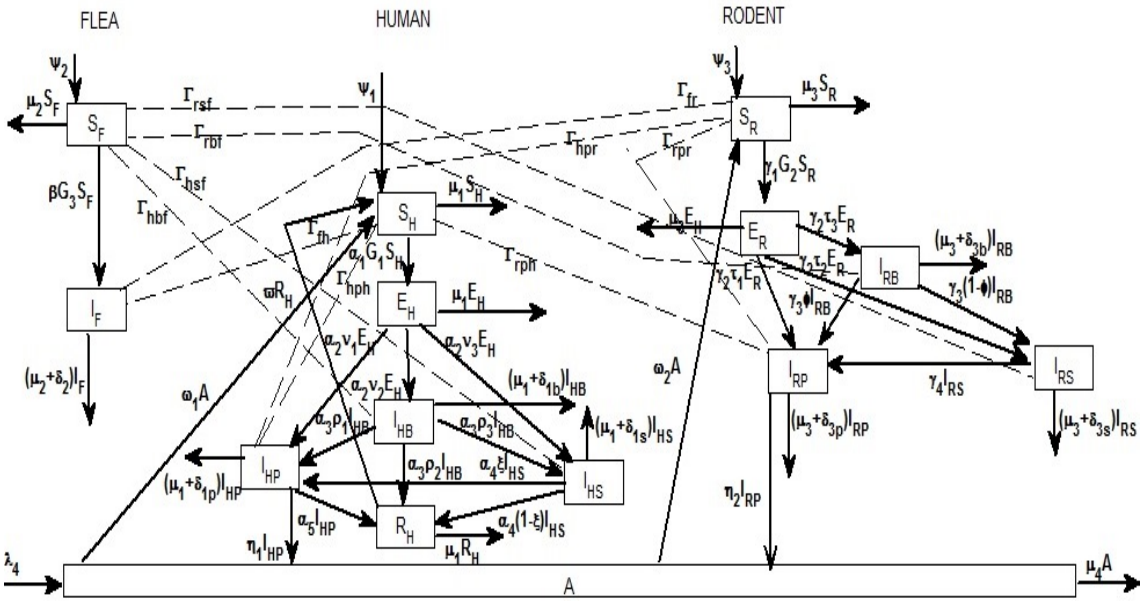


Figure 31: Compartment Model for Plague Disease

5.2.3 Description of interactions

The susceptible fleas in sub-group S_F get *Yersinia pestis* bacteria through biting the infected rodent I_{RB} or I_{RS} who are the primary reservoir for the bacteria and become infected at the rates Γ_{rbf} and Γ_{rsf} respectively. Flea may also get the disease when they bite the infected human being with bubonic plague I_{HB} or septicemic plague I_{HS} at the rates Γ_{hbf} and Γ_{hsf} respectively. Thus the flea population gets plague infection with the force of infection given in (4)

$$G_3 = \frac{\Gamma_{hbf} I_{HB} + \Gamma_{hsf} I_{HS}}{N_1} + \frac{\Gamma_{rbf} I_{RB} + \Gamma_{rsf} I_{RS}}{N_3}. \tag{4}$$

The human population may get the disease in one of the following ways: when the infected flea I_F bites and infect the susceptible human being S_H at a rate Γ_{fh}, when they interact with one another; this can be with either a person with pneumonic plague I_{HP} through airborne transmission or septicemic plague I_{HS} through physical or sexual contact at the rates Γ_{hph} and Γ_{hsh}, respectively. Other infection is through airborne transmission through interaction with rodent infected with pneumonic plague I_{RP} or through touching or eating the infected rodent with septicemic plague I_{RS} at rates of Γ_{rph} and Γ_{rsh}, respectively. Human beings may also get the infection from the environment when they breath in the bacteria or physically contact the infected material at the rate of ω_1. This is to say human population acquire plague disease following effective contact with infected human, rodent, flea and the environment with force of infection G_1 given by (5)

$$G_1 = \frac{\Gamma_{hph} I_{HP} + \Gamma_{hsh} I_{HS}}{N_1} + \Gamma_{fh} \frac{I_F}{N_2} + \frac{\Gamma_{rph} I_{RP} + \Gamma_{rsh} I_{RS}}{N_3} + \omega_1 A. \tag{5}$$

The subgroup S_H, after the infection, progress and become latent to the disease at a probability α_1. After 2 to 7 days the sub-groups E_H become infected into one of the three infectious classes I_{HB}, I_{HS} or I_{HP} (depending on the mode of transmission an individual is exposed to) and capable of transmitting the disease. The proportional of E_H progress and become infected by bubonic plague I_{HB}, septicemic plague I_{HS} or Pneumonic plague I_{HP} at the rate α_2 and proportional to ν_1, ν_2 or ν_3 respectively. The compartment I_{HB} if gets treatment they recover and move to sub group R_H at a rate α_3 otherwise they either progress to subgroups I_{HP} or I_{HS} at a rate α_3 or die either naturally at a rate μ_1 or due to the disease at a rate δ_{1b}. The fraction of human with septicemic plague I_{HS} if treated they recover at a rate α_4 and join R_H otherwise they either progress to subgroup I_{HP} at a rate α_4 or die due to a disease at a rate δ_{1s} or naturally at a rate μ_1. The compartments I_{HP} if treated they recover at a rate α_5 otherwise they die either naturally at a rate μ_1 or due to the disease at a rate δ_{1p}. The subgroup R_H attain temporally immunity then return and become susceptible S_H at a rate ϖ.

The rodent population may get a disease in one of the following ways: when the infected flea I_F bites and infect the susceptible rodent S_R at a rate Γ_{fr}, through interaction between rodent themselves, which may be with rodent infected by pneumonic plague I_{RP} or septicemic plague I_{RS} at the rates Γ_{rpr} and Γ_{rsr}, respectively. The other infection may be through interaction with human infected with either pneumonic plague I_{HP}, or septicemic plague I_{HS} at a rates of Γ_{hpr} and Γ_{hsr}, respectively. When the susceptible rodent sufficiently interact with the pathogens in environment through breathing in the bacteria or physically touch the infected material gets the infections at the rate of ω_2. Rodent also gets the disease through adequate interaction with Rodent, Human, Flea and Pathogens in the environment with force of infection G_2 given by (6)

$$G_2 = \frac{\Gamma_{hpr} I_{HP} + \Gamma_{hsr} I_{HS}}{N_1} + \Gamma_{fr} \frac{I_F}{N_2} + \frac{\Gamma_{rpr} I_{RP} + \Gamma_{rsr} I_{RS}}{N_3} + \omega_2 A. \tag{6}$$

The subgroup S_R, after the infection, they progress and become latent to the disease at a probability γ_1. After 2 to 7 days the sub-groups E_R become infected and capable of transmitting the disease, the fraction of it progress and become infected by bubonic plague I_{RB}, septicemic plague I_{RS} or Pneumonic plague I_{RP} at the rate γ_2 and proportional to τ_1,τ_2 or τ_3 respectively. The rodent in subgroup I_{RB} may either progress to subgroups I_{RP} or I_{RS} at a rate γ_3 or die either naturally at a rate μ_3 or due to the disease at a rate δ_{3b}. The compartment I_{RS} may either progress to I_{RP} at a rate γ_4 or die due to a disease at a rate δ_{3s} or naturally at a rate μ_3 and the compartments I_{RP} die either naturally at a rate μ_3 or due to the disease at a rate δ_{3p}.

With regard to the pathogens in the environment, we assume that the adequate interaction with S_H and S_R has a negligible effect on the dynamics of pathogens population size in the environment. The pathogens in the environment are populated at a constant rate λ_4. The infected human with pneumonic plague I_{HP} and Rodent with pneumonic plague I_{RP} also populate the environment A with the bacteria at the rate η_1 and η_2 respectively. Thus the environment is populated with pathogens causing plague disease with the force of infection G_4 given by (7)

$$G_4 = \lambda_4 + \eta_1 \frac{I_{HP}}{N_1} + \eta_2 \frac{I_{RP}}{N_3}. \tag{7}$$

The pathogens within the environment suffer natural mortality at a rate μ_4. Human population in sub-groups S_H and E_H, flea population in sub-group S_F and rodent population in sub-groups S_R and E_R suffer natural mortality at a rate μ_1, μ_2 and μ_3 respectively. The compartments I_{HB}, I_{HS}, I_{HP} , I_F, I_{RB}, I_{RS} and I_{RP} suffer both natural death at the rate μ_1, μ_2 and μ_3 and disease induced mortality at rates δ_{1b}, δ_{1s}, δ_{1p}, δ_2, δ_{3b}, δ_{3s} and δ_{3p} respectively. Human, Flea and rodent are recruited at the rate ψ_1, ψ_2 and ψ_3 respectively.

5.2.4 Model Equations for Plague Disease

We now use the variables and parameters and their descriptions given in Table 11 and Table 12, description of interactions and compartmental diagram which describe what is happening in human, rodent, flea and pathogens in the environment given in Fig 31 we derive the following set of differential equations:

Human Population

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1 G_1 S_H - \mu_1 S_H, \tag{8a}$$
$$\frac{dE_H}{dt} = \alpha_1 G_1 S_H - \alpha_2 E_H - \mu_1 E_H, \tag{8b}$$
$$\frac{dI_{HB}}{dt} = \alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB}, \tag{8c}$$
$$\frac{dI_{HS}}{dt} = \alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS}, \tag{8d}$$
$$\frac{dI_{HP}}{dt} = \alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP}, \tag{8e}$$
$$\frac{dR_H}{dt} = \alpha_3 \rho_2 I_{HB} + \alpha_4 (1 - \xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H. \tag{8f}$$

Rodent population

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1 G_2 S_R - \mu_3 S_R, \tag{9a}$$
$$\frac{dE_R}{dt} = \gamma_1 G_2 S_R - \gamma_2 E_R - \mu_3 E_R, \tag{9b}$$
$$\frac{dI_{RB}}{dt} = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \tag{9c}$$
$$\frac{dI_{RS}}{dt} = \gamma_2 \tau_2 E_R + \gamma_3 (1 - \phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}, \tag{9d}$$
$$\frac{dI_{RP}}{dt} = \gamma_2 \tau_1 E_R + \gamma_3 \phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \tag{9e}$$

Fleas

$$\frac{dS_F}{dt} = \psi_{2s} - \beta G_3 S_F - \mu_2 S_F, \tag{10a}$$
$$\frac{dI_F}{dt} = \beta G_3 S_F - (\mu_2 + \delta_2) I_F \tag{10b}$$

Pathogens in the environment

$$\frac{dA}{dt} = \lambda_4 + \frac{\eta_1 I_{HP}}{N_1} + \frac{\eta_3 I_{RP}}{N_3} - \mu_4 A. \tag{11}$$

5.3 Basic properties of the model

5.3.1 Invariant region

Plague disease affects Human population, Rodents, Fleas and pathogens in the environment. For the possible modeling process we assume that all state variables and parameters of the model are non-negative for $\forall t \geq 0$. The model system is analyzed in suitable feasible region where all state variables are positive. We obtain the region under the Theorem 5.11.

Theorem 5.11

All forward solutions in R_+^{14} of the system are feasible $\forall t \geq 0$ if they enter the invariant region Φ for $\Phi = \Omega_H \times \Omega_R \times \Omega_F \times \Omega_A$

where

$$\Omega_H = (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H) \in R_+^6 : S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H < N_1$$

$$\Omega_R = (S_R, E_R, I_{RB}, I_{RS}, I_{RP}) \in R_+^5 : S_R + E_R + I_{RB} + I_{RS} + I_{RP} < N_3$$

$$\Omega_F = (S_F, I_F) \in R_+^2 : S_F + I_F < N_2$$

$$\Omega_A = A \in R_+^1$$

And Φ is the positive invariant region of plague disease system.

Proof. We prove the theorem by taking into consideration one subgroup at a time.

For Human population:

We need to prove that the solution of the system 8 are feasible $\forall t > 0$ as they enter invariant region Ω_H

we now let $\Omega_H = (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H) \in R^6$ be any solution of the system with non-negative initial conditions

Using the total human population given in (1), we will have

$$\frac{dN_1}{dt} = \frac{dS_H}{dt} + \frac{dE_H}{dt} + \frac{dI_{HB}}{dt} + \frac{dI_{HS}}{dt} + \frac{dI_{HP}}{dt} + \frac{dR_H}{dt}. \tag{12}$$

Adding up the system (8) we get,

$$\frac{dN_1}{dt} = \psi_1 - \mu_1 N_1 - \delta_{1b} I_{HB} - \delta_{1s} I_{HS} - \delta_{1p} I_{HP}$$

$$\frac{dN_1}{dt} \leq \psi_1 - \mu_1 N_1.$$

We then get

$$\frac{dN_1}{dt} + \mu_1 N_1 \leq \psi_1.$$

Finding the integrating factor $IF = e^{\mu_1 t}$ and multiplying it through out we get

$$e^{\mu_1 t}\frac{dN_1}{dt} + e^{\mu_1 t} N_1 \mu_1 \leq \psi_1 e^{\mu_1 t},$$

which gives

$$\frac{d(N_1 e^{\mu_1 t})}{dt} \leq \psi_1 e^{\mu_1 t}.$$

Integrating on both sides yields

$$N_1 e^{\mu_1 t} \leq \frac{\psi_1}{\mu_1} e^{\mu_1 t} + C,$$

multiplying the equation by $e^{-\mu_1 t}$ we get

$$N_1 \leq \frac{\psi_1}{\mu_1} + Ce^{-\mu_1 t}.$$

Using the initial condition $t = 0, N_1(t = 0) = N_{10}$
then we will get

$$N_{10} - \frac{\psi_1}{\mu_1} \leq C,$$

substituting the constant we get

$$N_1 \leq \frac{\psi_1}{\mu_1} + (N_{10} - \frac{\psi_1}{\mu_1})e^{-\mu_1 t}.$$

When $N_{10} > \frac{\psi_1}{\mu_1}$ the population decreases asymptotically to $\frac{\psi_1}{\mu_1}$ and when $N_{10} < \frac{\psi_1}{\mu_1}$ the human population increases asymptotically to $\frac{\psi_1}{\mu_1}$ as in Fig 32

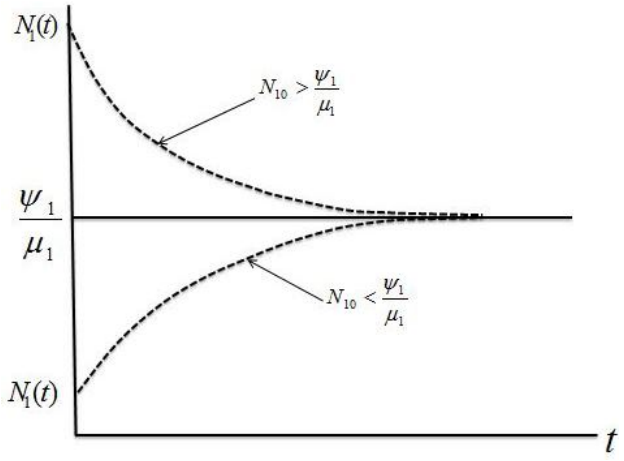


Figure 32: Feasible region for human system (Plague disease)

Hence all the feasible solution of the system (8) enter the region

$$\Omega_H = \left\{ (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H) : N_1 \leq Max \left\{ N_{10}, \frac{\psi_1}{\mu_1} \right\} \right\}.$$

For Rodent population

We need to prove that the solution of the subsystem 9 are feasible $\forall t > 0$ as they enter invariant region Ω_R

we now let $\Omega_R = (S_R, E_R, I_{RB}, I_{RS}, I_{RP}) \in R^5$ be any solution of the system with non-negative

initial conditions

Using the total rodent population given in (3) we have;

$$\frac{dN_3}{dt} = \frac{dS_R}{dt} + \frac{dE_R}{dt} + \frac{dI_{RB}}{dt} + \frac{dI_{RS}}{dt} + \frac{dI_{RP}}{dt}. \tag{13}$$

Adding up the subsystem (9)we get,

$$\frac{dN_3}{dt} = \psi_3 - \mu_3 N_3 - \delta_{3b} I_{RB} - \delta_{3s} I_{RS} - \delta_{3p} I_{RP},$$

we will then have

$$\frac{dN_3}{dt} \leq \psi_3 - \mu_3 N_3,$$

we then get

$$\frac{dN_3}{dt} + \mu_3 N_3 \leq \psi_3.$$

Finding the integrating factor $IF = e^{\mu_3 t}$ and multiplying it through out we get

$$e^{\mu_3 t}\frac{dN_3}{dt} + e^{\mu_3 t} N_3 \mu_3 \leq \psi_3 e^{\mu_3 t},$$

which gives

$$\frac{d(N_3 e^{\mu_3 t})}{dt} \leq \psi_3 e^{\mu_3 t}.$$

Integrating on both sides yields

$$N_3 e^{\mu_3 t} \leq \frac{\psi_3}{\mu_3} e^{\mu_3 t} + D,$$

multiplying the equation by $e^{-\mu_3 t}$ we get

$$N_3 \leq \frac{\psi_3}{\mu_3} + D e^{-\mu_3 t}.$$

Using the initial condition $t = 0, N_3(t = 0) = N_{30}$ then we will get

$$N_{30} - \frac{\psi_3}{\mu_3} \leq D,$$

substituting the constant we get

$$N_3 \leq \frac{\psi_3}{\mu_3} + (N_{30} - \frac{\psi_3}{\mu_3}) e^{-\mu_3 t}.$$

When $N_{30} > \frac{\psi_3}{\mu_3}$ the population decreases asymptotically to $\frac{\psi_3}{\mu_3}$ and when $N_{30} < \frac{\psi_3}{\mu_3}$ the rodent population increases asymptotically to $\frac{\psi_3}{\mu_3}$ as in Fig 33.

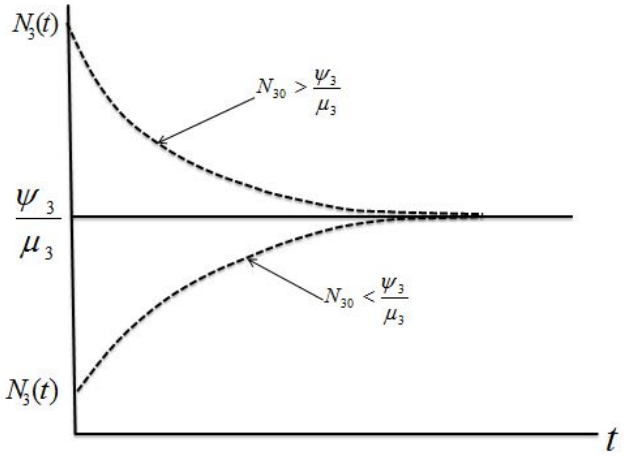


Figure 33: Feasible region for rodent system (Plague disease)

Hence all the feasible solution of the system (9) enter the region.

$$\Omega_R = \left\{ (S_R, E_R, I_{RB}, I_{RS}, I_{RP}) : N_3 \leq Max \left\{ N_{30}, \frac{\psi_3}{\mu_3} \right\} \right\}.$$

For Flea population We need to prove that the solution of the subsystem 10 are feasible $\forall t > 0$ as they enter invariant region Ω_F

we now let $\Omega_F = (S_F, I_F) \in R^2$ be any solution of the system with non-negative initial conditions

Using the total Flea population given in (2) we have:

$$\frac{dN_2}{dt} = \frac{dS_F}{dt} + \frac{dI_F}{dt}. \tag{14}$$

Adding up the system (10) we get,

$$\frac{dN_2}{dt} = \psi_{2s} - \mu_2 N_2 - \delta_2 I_F,$$

which can be written as

$$\frac{dN_2}{dt} \leq \psi_{2s} - \mu_2 N_2,$$

We then get

$$\frac{dN_2}{dt} + N_2\mu_2 \leq \psi_{2s}.$$

Finding the integrating factor $IF = e^{\mu_2 t}$ and multiplying it through out we get

$$e^{\mu_2 t}\frac{dN_2}{dt} + e^{\mu_2 t} N_2\mu_2 \leq (\psi_{2s})e^{\mu_2 t},$$

which gives

$$\frac{d(N_2 e^{\mu_2 t})}{dt} \leq (\psi_{2s})e^{\mu_2 t}.$$

Integrating on both sides yields

$$N_2 e^{\mu_2 t} \leq \frac{\psi_{2s}}{\mu_2} e^{\mu_2 t} + E,$$

multiplying the equation by $e^{-\mu_2 t}$ we get

$$N_2 \leq \frac{\psi_{2s}}{\mu_2} + Ee^{-\mu_2 t}.$$

Using the initial condition $t = 0, N_2(t = 0) = N_{20}$
then we will get

$$N_{20} - \frac{\psi_{2s}}{\mu_2} \leq E,$$

substituting the constant we get

$$N_2 \leq \frac{\psi_{2s}}{\mu_2} + (N_{20} - \frac{\psi_{2s}}{\mu_2})e^{-\mu_2 t}.$$

When $N_{20} > \frac{\psi_{2s}}{\mu_2}$ the population decreases asymptotically to $\frac{\psi_{2s}}{\mu_2}$ and when $N_{20} < \frac{\psi_{2s}}{\mu_2}$ the flea population increases asymptotically to $\frac{\psi_{2s}}{\mu_2}$ as in Fig 34.

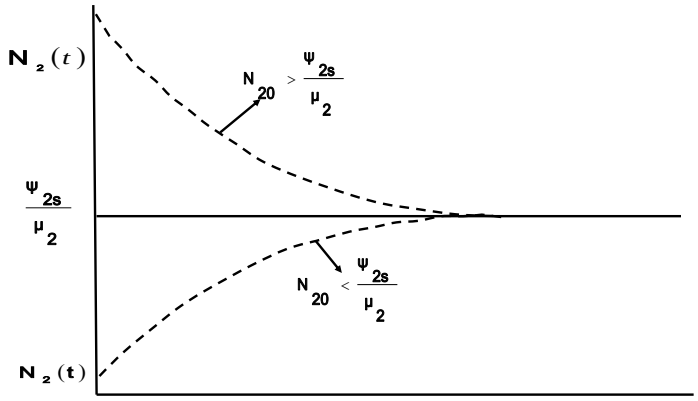


Figure 34: Feasible region for flea system (Plague disease)

Hence all the feasible solution of the system (10) enter the region

$$\Omega_F = \left\{ (S_F, I_F) : N_2 \leq Max \left\{ N_{20}, \frac{\psi_{2s}}{\mu_2} \right\} \right\}.$$

For Pathogens population

We need to prove that the solution of the system (Pathogens) are feasible $\forall t > 0$ as they enter invariant region Ω_A
we now let $\Omega_A = A \in R^1_+$ be any solution of the system with non-negative initial conditions
Then from the equation (11)

$$\frac{dA}{dt} = \lambda_4 + \eta_1 \frac{I_{HP}}{N_1} + \eta_2 \frac{I_{RP}}{N_3} - \omega_1 A - \omega_2 A - \mu_4 A. \tag{15}$$

But

$$I_{HP} \leq N_1, I_{RP} \leq N_3$$

Then this implies that

$$\frac{I_{HP}}{N_1} \leq 1, \frac{I_{RP}}{N_3} \leq 1.$$

Then the equation (15) becomes

$$\frac{dA}{dt} \leq \lambda_4 + \eta_1 + \eta_2 - \omega_1 A - \omega_2 A - \mu_4 A.$$

Then we will have

$$\frac{dA}{dt} + (\omega_1 + \omega_2 + \mu_4)A \leq \eta_1 + \eta_2 + \lambda_4.$$

Finding the integrating factor $IF = e^{(\omega_1+\omega_2+\mu_4)t}$ and multiplying it through out we get

$$e^{(\omega_1+\omega_2+\mu_4)t}\frac{dA}{dt} + e^{(\omega_1+\omega_2+\mu_4)t}(\omega_1 + \omega_2 + \mu_4)A \leq e^{(\omega_1+\omega_2+\mu_4)t}(\eta_1 + \eta_2 + \lambda_4),$$

which gives

$$\frac{d(Ae^{(\omega_1+\omega_2+\mu_4)t})}{dt} \leq (\eta_1 + \eta_2 + \lambda_4)e^{(\omega_1+\omega_2+\mu_4)t}.$$

Integrating on both sides yields

$$Ae^{(\omega_1+\omega_2+\mu_4)t} \leq \frac{\eta_1 + \eta_2 + \lambda_4}{\omega_1 + \omega_2 + \mu_4}e^{(\omega_1+\omega_2+\mu_4)t} + B.$$

Multiplying the equation by $e^{-(\omega_1+\omega_2+\mu_4)t}$ we get

$$A(t) \leq \frac{\eta_1 + \eta_2 + \lambda_4}{\omega_1 + \omega_2 + \mu_4} + Be^{-(\omega_1+\omega_2+\mu_4)t}.$$

Using the initial condition $t = 0, A(t = 0) = A_0$

then we will get

$$A_0 - \frac{\eta_1 + \eta_2 + \lambda_4}{\omega_1 + \omega_2 + \mu_4} \leq B,$$

substituting the constant we get

$$A(t) \leq \frac{\eta_1 + \eta_2 + \lambda_4}{\omega_1 + \omega_2 + \mu_4} + (A_0 - \frac{\eta_1 + \eta_2 + \lambda_4}{\omega_1 + \omega_2 + \mu_4})e^{-(\omega_1+\omega_2+\mu_4)t}.$$

When $A_0 > \frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ pathogens decreases asymptotically to $\frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ and when $N_{30} < \frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ pathogens increases asymptotically to $\frac{\eta_1+\eta_2+\lambda_4}{\mu_4}$ as in Fig 35.

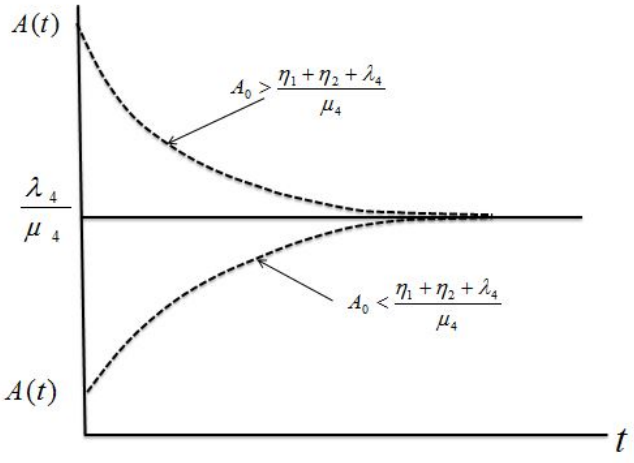


Figure 35: Feasible region for pathogens (Plague disease)

Hence the feasible solution of the system (11) enter the region

$$\Omega_A = \left\{ A : A \leq Max \left\{ A_0, \frac{\eta_1 + \eta_2 + \lambda_4}{\mu_4} \right\} \right\}$$

□

5.3.2 Positivity of the solution

We need to show that all variables and parameters of the model must be non negative $\forall t \geq 0$. We now solve the equations of the system in their patches for testing the positivity.

Theorem 5.12
Let the initial values of the system (8), (9), (10) and (11) be: ($S_H(0)$, $S_R(0)$,$S_F(0)$, A_0) > 0 and ($E_H(0)$, $I_{HB}(0)$, $I_{HS}(0)$, $I_{HP}(0)$, $R_H(0)$, $E_R(0)$, $I_{RB}(0)$, $I_{RS}(0)$, $I_{RP}(0)$, $I_F(0)$) ≥ 0. Then the solution set $S_H(t)$, $S_R(t)$, $S_F(t)$, $A(t)$, $E_H(t)$, $I_{HB}(t)$, $I_{HS}(t)$, $I_{HP}(t)$, $R_H(t)$, $E_R(t)$, $I_{RB}(t)$, $I_{RS}(t)$, $I_{RP}(t)$ and $I_F(t)$ are positive $\forall t \geq 0$.

Proof. **For Human System**
Using the first equation in system (8) we have

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1 G_1 S_H - \mu_1 S_H,$$

$$\frac{dS_H}{dt} \geq -(\alpha_1 G_1 + \mu_1) S_H.$$

Integration yields

$$S_H \geq S_{H0} e^{-\int_0^t (\alpha_1 G_1(x) + \mu_1) dx} > 0,$$

since

$$e^{-\left(\int_0^t (\alpha_1 G_1(x) + \mu_1) dx\right)} > 0.$$

From the second equation we have

$$\frac{dE_H}{dt} = \alpha_1 G_1 S_H - \alpha_2 E_H - \mu_1 E_H,$$

$$\frac{dE_H}{dt} \geq -(\alpha_2 + \mu_1) E_H.$$

Integration yields

$$E_H \geq E_{H0} e^{-(\alpha_2 + \mu_1)t} > 0,$$

since

$$e^{-(\alpha_2+\mu_1)t} > 0.$$

From the third equation of system (8) we have

$$\frac{dI_{HB}}{dt} = \alpha_2\nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b})I_{HB}$$

$$\frac{dI_{HB}}{dt} \geq -(\alpha_3 + \mu_1 + \delta_{1b})I_{HB}.$$

Integrating we get

$$I_{HB} \geq I_{HB0}e^{-(\alpha_3+\mu_1+\delta_{1b})t} > 0,$$

since

$$e^{-(\alpha_3+\mu_1+\delta_{1b})t} > 0.$$

Fourth equation of the system we will have

$$\frac{dI_{HS}}{dt} = \alpha_3\rho_3 I_{HB} + \alpha_2\nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s})I_{HS}$$

$$\frac{dI_{HS}}{dt} \geq -(\alpha_4 + \mu_1 + \delta_{1s})I_{HS}.$$

Integrating we get

$$I_{HS} \geq I_{HS0}e^{-(\alpha_4+\mu_1+\delta_{1s})t} > 0,$$

since

$$e^{-(\alpha_4+\mu_1+\delta_{1s})t} > 0.$$

The fifth equation will be

$$\frac{dI_{HP}}{dt} = \alpha_2\nu_1 E_H + \alpha_3\rho_1 I_{HB} + \alpha_4\xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p})I_{HP}.$$

$$\frac{dI_{HP}}{dt} \geq -(\alpha_5 + \mu_1 + \delta_{1p})I_{HP}.$$

Integrating we get

$$I_{HP} \geq I_{HP0}e^{-(\alpha_5+\mu_1+\delta_{1p})t} > 0.$$

since

$$e^{-(\alpha_5+\mu_1+\delta_{1p})t} > 0.$$

And the last equation in system (8) we have

$$\frac{dR_H}{dt} = \alpha_3\rho_2 I_{HB} + \alpha_4(1-\xi)I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H..$$

$$\frac{dR_H}{dt} \geq -(\varpi + \mu_1)R_H.$$

Integrating we get

$$R_H \geq R_{H0}e^{-(\varpi+\mu_1)t} > 0,$$

since

$$e^{-(\varpi+\mu_1)t} > 0.$$

For Rodent System

Using equation one from system (9) we have

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1 G_2 S_R - \mu_3 S_R,.$$

$$\frac{dS_R}{dt} \geq -(\gamma_1 G_2 + \mu_3) S_R.$$

Integrating we get

$$S_R \geq S_{R0} e^{-\int_0^t (\gamma_1 G_2(x) + \mu_3) dx} > 0,$$

since

$$e^{-\left(\int_0^t (\gamma_1 G_2(x) + \mu_3) dx\right)} > 0.$$

From the second equation of the system (9) we have

$$\frac{dE_R}{dt} = \gamma_1 G_2 S_R - \gamma_2 E_R - \mu_3 E_R,$$

from here we get

$$\frac{dE_R}{dt} \geq -(\gamma_2 + \mu_3) E_R.$$

Integrating we get

$$E_R \geq E_{R0} e^{-(\gamma_2+\mu_3)t} > 0,$$

since

$$e^{-(\gamma_2+\mu_3)t} > 0.$$

And the from the third equation of system (9) we have

$$\frac{dI_{RB}}{dt} = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}.$$

We will then have

$$\frac{dI_{RB}}{dt} \geq -(\gamma_3 + \mu_3 + \delta_{3b}) I_{RB}.$$

Integrating we get

$$I_{RB} \geq I_{RB0} e^{-(\gamma_3+\mu_3+\delta_{3b})t} > 0,$$

since

$$e^{-(\gamma_3+\mu_3+\delta_{3b})t} > 0.$$

The fourth equation will be

$$\frac{dI_{RS}}{dt} = \gamma_2 \tau_2 E_R + \gamma_3 (1-\phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}.$$

We will then have

$$\frac{dI_{RS}}{dt} \geq -(\gamma_4 + \mu_3 + \delta_{3s})I_{RS}.$$

Integrating we get

$$I_{RS} \geq I_{RS0}e^{-(\gamma_4+\mu_3+\delta_{3s})t} > 0,$$

since

$$e^{-(\gamma_4+\mu_3+\delta_{3s})t} > 0.$$

And the from the last equation of system (9) we have

$$\frac{dI_{RP}}{dt} = \gamma_2\tau_1 E_R + \gamma_3\phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p})I_{RP}.$$

We will then have

$$\frac{dI_{RP}}{dt} \geq -(\mu_3 + \delta_{3p})I_{RP}.$$

Integrating we get

$$I_{RP} \geq I_{RP0}e^{-(\mu_3+\delta_{3p})t} > 0,$$

since

$$e^{-(\mu_3+\delta_{3p})t} > 0.$$

For Flea System

Now from the first equation of system (10) we will have

$$\frac{dS_F}{dt} = \psi_{2s} - \beta G_3 S_F - \mu_2 S_F.$$

$$\frac{dS_F}{dt} \geq -(\beta G_3 + \mu_2)S_F.$$

Integrating we get

$$S_F \geq S_{F0}e^{-\int_0^t(\beta G_3(x)+\mu_2)dx} > 0,$$

since

$$e^{-\left(\int_0^t(\beta G_3(x)+\mu_2)dx\right)} > 0.$$

Taking the second equation we have

$$\frac{dI_F}{dt} = \beta G_3 S_F - (\mu_2 + \delta_2)I_F.$$

Then we have

$$\frac{dI_F}{dt} \geq -(\mu_2 + \delta_2)I_F.$$

Integrating we have

$$I_F \geq I_{F0}e^{-(\mu_2+\delta_2)t} > 0,$$

since

$$e^{-(\mu_2+\delta_2)t} > 0.$$

For Pathogens in the Environment

The subgroup has only one equation so using equation (11) we will have

$$\frac{dA}{dt} = \lambda_4 + \eta_1 \frac{I_{HP}}{N_1} + \eta_2 \frac{I_{RP}}{N_3} - \omega_1 A - \omega_2 A - \mu_4 A.$$

If we take $\omega_1 + \omega_2 = \omega$

Then we will have

$$\frac{dA}{dt} \geq -(\omega + \mu_4)A.$$

Integrating we get

$$A \geq A_0 e^{-(\omega+\mu_4)t} > 0,$$

Since

$$e^{-(\omega+\mu_4)t} > 0.$$

□

Therefore the proof conclude that all variable in the plague disease model are positive.

5.4 Model analysis

In this section we consider existence of equilibrium states, reproduction number and stability of the equilibrium points.

5.4.1 Disease Free Equilibrium

The model has disease free equilibrium which is obtained by setting $I_{HB} = I_{HS} = I_{HP} = E_H = R_H = 0$, $I_{RB} = I_{RS} = I_{RP} = E_R = 0$, $I_F = 0$ and $A = 0$ for Human beings, Rodents, Fleas and pathogens in the environment systems respectively. We then substitute the above into the system (8),(9),(10) and (11) which are the systems for Human being, Rodents, Fleas and Pathogens respectively. Then we have the disease free-equilibrium point given as: $E_H^0 = \left(\frac{\psi_1}{\mu_1}, 0, 0, 0, 0, 0\right)$, $E_R^0 = \left(\frac{\psi_3}{\mu_3}, 0, 0, 0, 0\right)$, $E_F^0 = \left(\frac{\psi_{2s}}{\mu_2}, 0\right)$ and $E_A^0 = 0$ for human, Rodent, Flea and pathogen respectively.

Then the disease free equilibrium of the entire system

$$E^0(S_H^0, E_H^0, I_{HB}^0, I_{HS}^0, I_{HP}^0, R_H^0, S_R^0, E_R^0, I_{RB}^0, I_{RS}^0, I_{RP}^0, S_F^0, I_F^0, A^0)$$
$$= (\frac{\psi_1}{\mu_1}, 0, 0, 0, 0, 0, \frac{\psi_3}{\mu_3}, 0, 0, 0, 0, \frac{\psi_{2s}}{\mu_2}, 0, 0)$$

5.4.2 Basic Reproduction Number R_0

We define the basic reproduction number as the expected number of secondary cases produced by a single infected individual during the entire infectious period of that particular individual into a completely susceptible population. The epidemiological criterion of R_0 is that; if $R_0 < 1$ then the single infected individual in entirely susceptible population infects less than one individual and hence the disease may be eradicated in the population and thus the disease-free equilibrium point is asymptotically stable and cannot invade the population and if $R_0 > 1$ it means that a single infected individual in entirely susceptible population infects more than one individuals and hence the disease may persist in the population, then, the disease free equilibrium point is unstable and can invade the population and persist for a long time (Allen *et al.*, 2008). There are several methods on how to find the the basic reproductive number but this study is will be computed by using next generation method as described by Van den Driessche and Watmough (2002).

We compute the basic reproduction number R_0 using the next generation matrix as outlined by Heesterbeek (2000) and Diekmann *et al.* (1990). The method has the advantage over the usual next generation method that; the steps to reach an estimate of R_0 and the matrix elements of the next-generation matrix have a clear biological basis. It is easy to handle complex diseases like plague disease which has multiple transmission roots from different infection agents.

The peculiarity of plague disease is influenced by three main factors: One is the fact that Plague infection occurs in three main forms which are bubonic which is transmitted through flea bite. Septcemic plague which is mainly transmitted through indirect contact example touching or eating the infected animals, flea bite and Physical contact including sexual contact. And pneumonic plague which is mainly transmitted through airborne transmission. Two is the involvement of two hosts (Human and rodent) and one vector (flea). And three is the possibility of the plague bacteria to remain infectious for a long time in a soil/environment and capable of transmitting the disease to the susceptible individuals without the need of a vector flea.

Now, each transmission agent in different plague infectious form differ in the way it transmit the bacterial within or outside the individual's population. It is therefore important to analyze and compute the role of each infectious agent in determining the threshold quantity that will tell whether the disease will occur or die out. The risk that an outbreak will actually occur, determine the initial exponential increase in the number of infected individuals and determine the fraction of population that would be used for control purposes.

To do this we first categorize individuals by their state at the moment they become infected

(type at infection). These types-at-infection refers specifically to the birth of the infection in the individual. These categories (type at infection) differs in the way they transmit plague disease which in-turn differentiate their ability to produce secondary cases.

In our case we categories the individuals into eight states and label them as follows: Human infected with bubonic plague (type 1), Human infected with septsemic plague (type 2), Human infected with pneumonic plague (type 3), Rodent infected with bubonic plague (type 4), Rodent infected with septcemic plague (type 5), Rodent infected with pneumonic plague (type 6) Flea infested with pathogens (type 7) and the Pathogens in the environment (type 8).

We assume and label individual with bubonic plague as stage one of the disease, septsemic plague as stage two and pneumonic plague as stage three. We also assume that each stage is the secondary stage of the later. When an individual in stage one graduate to stage two we only consider the current stage and ignore the later. We assume that the infection only goes in ascending direction that is from stage one to two or two to three not the reverse of it.

Since the system has eight types-at-infection, the next-generation matrix, K, will be a 8×8 matrix with elements k_{ij} s . Each of the elements k_{ij} stands for expected number of new cases of i caused by one infected individual of j. We now define a matrix K whose entries are k_{ij}. The resulting next generation matrix is as given in (16).

$$\mathbf{K} = \begin{pmatrix} k_{11} & k_{12} & k_{13} & k_{14} & k_{15} & k_{16} & k_{17} & k_{18} \\ k_{21} & k_{22} & k_{23} & k_{24} & k_{25} & k_{26} & k_{27} & k_{28} \\ k_{31} & k_{32} & k_{33} & k_{34} & k_{35} & k_{36} & k_{37} & k_{38} \\ k_{41} & k_{42} & k_{43} & k_{44} & k_{45} & k_{46} & k_{47} & k_{48} \\ k_{51} & k_{52} & k_{53} & k_{54} & k_{55} & k_{56} & k_{57} & k_{58} \\ k_{61} & k_{62} & k_{63} & k_{64} & k_{65} & k_{66} & k_{67} & k_{68} \\ k_{71} & k_{72} & k_{73} & k_{74} & k_{75} & k_{76} & k_{77} & k_{78} \\ k_{81} & k_{82} & k_{83} & k_{84} & k_{85} & k_{86} & k_{87} & k_{88} \end{pmatrix} \tag{16}$$

Then, $R_0 = \rho(K)$ where $\rho(K)$ is spectral radius of K.

The k_{11} is the expected number of new cases of human infected with bubonic plague caused by one infected human with bubonic plague, k_{12} is the expected number of new cases of human infected with bubonic plague caused by one infected human with septicemic plague, k_{13} is the expected number of new cases of human infected with bubonic plague caused by one infected human with pneumonic plague, k_{14} is the expected number of new cases of human infected with bubonic plague caused by one infected rodent with bubonic plague, k_{15} is the expected number of new cases of human infected with bubonic plague caused by one infected rodent

with septicemic plague, k_{16} is the expected number of new cases of human infected with bubonic plague caused by one infected rodent with pneumonic plague, k_{17} is the expected number of new cases of human infected with bubonic plague caused by one infected flea, k_{18} is the expected number of new cases of human infected with bubonic plague caused by infected environment.

The k_{21} is the expected number of new cases of human infected with septicemic plague caused by one infected human with bubonic plague, k_{22} is the expected number of new cases of human infected with septicemic plague caused by one infected human with septicemic plague, k_{23} is the expected number of new cases of human infected with septicemic plague caused by one infected human with pneumonic plague, k_{24} is the expected number of new cases of human infected with septicemic plague caused by one infected rodent with bubonic plague, k_{25} is the expected number of new cases of human infected with septicemic plague caused by one infected rodent with septicemic plague, k_{26} is the expected number of new cases of human infected with septicemic plague caused by one infected rodent with pneumonic plague, k_{27} is the expected number of new cases of human infected with septicemic plague caused by one infected flea, k_{28} is the expected number of new cases of human infected with septicemic plague caused by infected environment.

The k_{31} is the expected number of new cases of human infected with pneumonic plague caused by one infected human with bubonic plague, k_{32} is the expected number of new cases of human infected with pneumonic plague caused by one infected human with septicemic plague, k_{33} is the expected number of new cases of human infected with pneumonic plague caused by one infected human with pneumonic plague, k_{34} is the expected number of new cases of human infected with pneumonic plague caused by one infected rodent with bubonic plague, k_{35} is the expected number of new cases of human infected with pneumonic plague caused by one infected rodent with septicemic plague, k_{36} is the expected number of new cases of human infected with pneumonic plague caused by one infected rodent with pneumonic plague, k_{37} is the expected number of new cases of human infected with pneumonic plague caused by one infected flea, k_{38} is the expected number of new cases of human infected with pneumonic plague caused by infected environment.

The k_{41} is the expected number of new cases of rodent infected with bubonic plague caused by one infected human with bubonic plague, k_{42} is the expected number of new cases of rodent infected with bubonic plague caused by one infected human with septicemic plague, k_{43} is the expected number of new cases of rodent infected with bubonic plague caused by one infected human with pneumonic plague, k_{44} is the expected number of new cases of rodent infected with bubonic plague caused by one infected rodent with bubonic plague, k_{45} is the expected number of new cases of rodent infected with bubonic plague caused by one infected rodent with

septicemic plague, k_{46} is the expected number of new cases of rodent infected with bubonic plague caused by one infected rodent with pneumonic plague, k_{47} is the expected number of new cases of rodent infected with bubonic plague caused by one infected flea, k_{48} is the expected number of new cases of rodent infected with bubonic plague caused by infected environment.

The k_{51} is the expected number of new cases of rodent infected with septicemic plague caused by one infected human with bubonic plague, k_{52} is the expected number of new cases of rodent infected with septicemic plague caused by one infected human with septicemic plague, k_{53} is the expected number of new cases of rodent infected with septicemic plague caused by one infected human with pneumonic plague, k_{54} is the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with bubonic plague, k_{55} is the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with septicemic plague, k_{56} is the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with pneumonic plague, k_{57} is the expected number of new cases of rodent infected with septicemic plague caused by one infected flea, k_{58} is the expected number of new cases of rodent infected with septicemic plague caused by infected environment.

The k_{61} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected human with bubonic plague, k_{62} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected human with septicemic plague, k_{63} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected human with pneumonic plague, k_{64} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with bubonic plague, k_{65} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with septicemic plague, k_{66} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected rodent with pneumonic plague, k_{67} is the expected number of new cases of rodent infected with pneumonic plague caused by one infected flea, k_{68} is the expected number of new cases of rodent infected with pneumonic plague caused by infected environment.

The k_{71} is the expected number of new cases of of new cases of flea infested with *Yersinia pestis* caused by one infected human with bubonic plague, k_{72} is the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected human with septicemic plague, k_{73} is the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected human with pneumonic plague, k_{74} is the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with bubonic plague, k_{75} is the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with septicemic

plague, k_{76} is the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with pneumonic plague, k_{77} is the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected flea, k_{78} is the expected number of new cases of flea infested with *Yersinia pestis* caused by infected environment.

The k_{81} is the expected number of new cases of of new cases of infected soil/environment caused by one infected human with bubonic plague, k_{82} is the expected number of new cases of infected soil/environment caused by one infected human with septicemic plague, k_{83} is the expected number of new cases of infected soil/environment caused by one infected human with pneumonic plague, k_{84} is the expected number of new cases of infected soil/environment caused by one infected rodent with bubonic plague, k_{85} is the expected number of new cases of infected soil/environment caused by one infected rodent with septicemic plague, k_{86} is the expected number of new cases of infected soil/environment caused by one infected rodent with pneumonic plague, k_{87} is the expected number of new cases of infected soil/environment caused by one infected flea, k_{88} is the expected number of new cases of infected soil/environment caused by infected environment.

Some elements equal 0 as not all type at infection infect all other type at infection. Example human with bubonic plague I_{HB} (type at infection 1) do not produce type at infection 1 (human infected with bubonic plague), 4 (Rodent infected with bubonic plague), 5 (Rodent infected with septicemic plague), 6 (Rodent infected with pneumonic plague) and 8 (Pathogens in the environment). This means that k_{11}, k_{14}, k_{15}, k_{16} and k_{18} are 0. The type at infection 2 (Human infected with septicemic plague) also do not produce type at infection 1 (Human infected with bubonic plague), 4(Rodent infected with bubonic plague), 6(Rodent infected with pneumonic plague) and 8(Pathogens in the environment). This also means that k_{21}, k_{24}, k_{26} and k_{28} are zero (0). The type at infection 3 do not produce type at infection 1(Human infected with bubonic plague), 2(Human infected with septicemic plague), 4(rodent infected with bubonic plague), 5 and 7 which means that k_{31}, k_{32}, k_{34}, k_{35} and k_{37} are zero. Type at infection 4 do not produce type at infection 1, 2, 3, 4 or 8 which means that k_{41}, k_{42}, k_{43}, k_{44} and k_{48} are zero. Type at infection 5 do not produce type at infection 1, 3, 4, and 8 then k_{51}, k_{53}, k_{54} and k_{58} are zero. The type at infection 6 do not produce type at infection 1, 2, 4, 5 and 7 thus k_{61}, k_{62}, k_{64}, k_{65} and k_{67} are zero. Type at infection 7 also do not produce type at infection 3, 6, 7,and 8 thus k_{73}, k_{76}, k_{77}, and k_{78} are zero. And the type at infection 8 do not produce type at infection 1,2, 4,5, 7 and 8 which means that k_{81}, k_{82}, k_{84}, k_{85}, k_{87} and k_{88} are zero. Incorporating these, we modify the matrix K as shown in matrix (17)

$$\mathbf{K} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & k_{17} & 0 \\ k_{21} & k_{22} & 0 & 0 & k_{25} & 0 & k_{27} & 0 \\ k_{31} & k_{32} & k_{33} & 0 & 0 & k_{36} & 0 & k_{38} \\ 0 & 0 & 0 & 0 & 0 & 0 & k_{47} & 0 \\ 0 & 0 & 0 & k_{54} & k_{55} & 0 & k_{57} & 0 \\ 0 & 0 & 0 & k_{64} & k_{65} & k_{66} & 0 & k_{68} \\ k_{71} & k_{72} & 0 & k_{74} & k_{75} & 0 & 0 & 0 \\ 0 & 0 & k_{83} & 0 & 0 & k_{86} & 0 & 0 \end{pmatrix} \tag{17}$$

We will now explain the derivation of each matrix-elements in detail. We employ the derivation steps by Gail and Benichou (2000) to drive the expressions for k_{ij}. We mainly base our derivation on the adequate contact rate between the infected individual type j and the susceptible individual type i, the expected duration of infection of individual type j and the probability that the individual type j survive the duration between the latent stage to the time an individual experience the onset clinical disease as in (18)

$$\mathbf{K_{ij}} = \begin{pmatrix} \text{Effective} \\ \text{contact} \\ \text{Rate} \end{pmatrix} \times \begin{pmatrix} \text{Duration} \\ \text{of} \\ \text{infection} \end{pmatrix} \times \begin{pmatrix} \text{Probability that the} \\ \text{individual survive} \\ \text{the incubation period} \end{pmatrix} \tag{18}$$

The production of I_{HB}, depend on probability at which susceptible flea becomes infectious (β) and the infected immigrants survive the incubation period. We also consider the rate at which I_F adequately bites the susceptible human and the bite results to a human infected with bubonic plague I_{HB}. The total number of human infected with bubonic plague caused by one flea infested with pathogens is as given in (19).

$$k_{17} = \left(\frac{\beta}{\beta + \mu_2}\right) \frac{\nu_2 \Gamma_{fh}}{\mu_2 + \delta_2} \tag{19}$$

Septicemic plague in human may be produced in various way; progression of untreated human with bubonic plague to human with septcemic plague, adequate contact(including sexual contact) between humans with septicemic plague, adequate contact between rodent and human with septicemic plague and from the flea infested with pathogens. We consider the progression rate of infected human with bubonic to septicemic $\alpha_3\rho_3$, the adequate contact (it may be sexual contact) rate between humans with septicemic plague, rodent infected with septicemic plague and the infected flea to human with septicemic plague at the rates γ_{hsh}, γ_{rsh} and γ_{fh}. Then the number of human infected with septicemic plague from all the mentioned infectious agents is

as given in (20a), (20b), (20c) and (20d).

$$k_{21} = \frac{\alpha_2\alpha_3\nu_2\rho_3}{(\alpha_2\nu_2+\mu_1)(\mu_1+\alpha_3+\delta_{1b})} \tag{20a}$$

$$k_{22} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\Gamma_{hsh}}{(\alpha_4+\mu_1+\delta_{1s})} \tag{20b}$$

$$k_{25} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\Gamma_{rsh}}{(\gamma_4+\mu_3+\delta_{3s})} \tag{20c}$$

$$k_{27} = \left(\frac{\beta}{\beta+\mu_2}\right)\frac{\nu_1\Gamma_{fh}}{\mu_2+\delta_2} \tag{20d}$$

The proportion ρ_1 and ξ of untreated I_{HB} and I_{HS} may progress and become I_{HP} at the progression rate α_3 and α_3 respectively. We multiply the average period the I_{HB} remain infected with the rate at which they progress to I_{HP}. I_{HP} may also result from the airborne transmission from the human or rodent with pneumonic plague at the rate γ_{hph} or γ_{rph} respectively. And through the direct interaction with the environment at the rate ω_1. Then the total number of human infected with pneumonic plague from the stated five sources is given in (21a), (21b), (21c), (21d) and (21e)

$$k_{31} = \frac{\alpha_2\alpha_3\nu_2\rho_1}{(\alpha_2\nu_2+\mu_1)(\alpha_3+\mu_1+\delta_{1b})} \tag{21a}$$

$$k_{32} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\alpha_4\xi}{\alpha_4+\mu_1+\delta_{1s}} \tag{21b}$$

$$k_{33} = \left(\frac{\alpha_2\nu_1}{\alpha_2\nu_1+\mu_1} + \frac{\alpha_3\rho_1}{\alpha_3\rho_1+\mu_1} + \frac{\alpha_4\phi}{\alpha_4\phi+\mu_1}\right)\frac{\Gamma_{hph}}{\alpha_5+\mu_1+\delta_{1p}} \tag{21c}$$

$$k_{36} = \left(\frac{\gamma_2\tau_1}{\gamma_2\tau_1+\mu_3} + \frac{\gamma_3\phi}{\gamma_3\phi+\mu_3} + \frac{\gamma_4}{\gamma_4+\mu_3}\right)\frac{\Gamma_{rph}}{\mu_3+\delta_{3p}} \tag{21d}$$

$$k_{38} = \left(\frac{\lambda_4}{\lambda_4+\mu_4} + \frac{\eta_1}{\eta_1+\mu_4} + \frac{\eta_2}{\eta_2+\mu_4}\right)\frac{\omega_1}{\mu_4} \tag{21e}$$

Production of number of rodent with bubonic plague I_{RB} depend only on the flea infested with pathogens. The infection depends on the infection period of the flea that survive the incubation period and the proportion at which the adequate contact between infected flea and susceptible rodent causes bubonic plague $\tau_3\Gamma_{fr}$ as given in (22).

$$k_{47} = \left(\frac{\beta}{\beta+\mu_2}\right)\frac{\tau_3\Gamma_{fr}}{\mu_2+\delta_2} \tag{22}$$

The septicemic plague in rodent is produced in three ways; one is when untreated rodent with bubonic plague progresses and become septicemic plague infectives at the rate $\gamma_3(1-\phi)$. Two, is after adequate contact (it may also be a rodent eating or biting an infected individual) between the susceptible rodent and a rodent infected with septicemic plague or human at the rate Γ_{rsr}

or Γ_{hsr} respectively. Three is from the flea infested with pathogens with the proportion that the adequate contact between I_F and the susceptible rodent results to I_{RS}. The total number of I_{RS} infected from these infectious agent is as given in (23a), (23b), (23c) and (23d).

$$k_{52} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\Gamma_{hsr}}{\alpha_4+\mu_1+\delta_{1s}} \tag{23a}$$

$$k_{54} = \frac{\gamma_2\gamma_3\tau_3(1-\phi)}{(\gamma_2\tau_3+\mu_3)(\gamma_3+\mu_3+\delta_{3b})} \tag{23b}$$

$$k_{55} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\Gamma_{rsr}}{\gamma_4+\mu_3+\delta_{3s}} \tag{23c}$$

$$k_{57} = \left(\frac{\beta}{\beta+\mu_2}\right)\frac{\tau_2\Gamma_{fr}}{\mu_2+\delta_2} \tag{23d}$$

I_{RP} may be the result of airborne transmission between the susceptible rodent and the human and rodent with pneumonic plague at the rate Γ_{hpr} and Γ_{rpr} respectively. It may also occur from the progression of untreated I_{RB} and I_{RS} at the rate γ_3 and γ_4 respectively. The pathogens in soil/environment may also cause I_{RP} after the adequate rate of interaction ω_2. Now the total number of I_{RB} resulting from these interaction are in (24a), (24b), (24c), (24d) and (24e).

$$k_{63} = \left(\frac{\alpha_2\nu_1}{\alpha_2\nu_1+\mu_1} + \frac{\alpha_3\rho_1}{\alpha_3\rho_1+\mu_1} + \frac{\alpha_4\phi}{\alpha_4\phi+\mu_1}\right)\frac{\Gamma_{hpr}}{\alpha_5+\mu_1+\delta_{1p}} \tag{24a}$$

$$k_{64} = \frac{\gamma_2\gamma_3\tau_3\phi}{(\gamma_2\tau_3+\mu_3)(\gamma_3+\mu_3+\delta_{3b})} \tag{24b}$$

$$k_{65} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\gamma_4}{\gamma_4+\mu_3+\delta_{3s}} \tag{24c}$$

$$k_{66} = \left(\frac{\gamma_2\tau_1}{\gamma_2\tau_1+\mu_3} + \frac{\gamma_3\phi}{\gamma_3\phi+\mu_3} + \frac{\gamma_4}{\gamma_4+\mu_3}\right)\frac{\Gamma_{rpr}}{\mu_3+\delta_{3p}} \tag{24d}$$

$$k_{68} = \left(\frac{\lambda_4}{\lambda_4+\mu_4} + \frac{\eta_1}{\eta_1+\mu_4} + \frac{\eta_2}{\eta_2+\mu_4}\right)\frac{\omega_2}{\mu_4} \tag{24e}$$

Flea are infested with pathogens from human and rodent infected with bubonic and septicemic plague at the rate γ_{hbf}, γ_{hsf}, γ_{rbf} and γ_{rsf}. The infection is dictated by the probability that human and rodent with bubonic and septicemic plague survive the incubation period and the adequate rates of contact. From these interaction we get the total number of infectious flea is as given in (25a), (25b), (25c) and (25d).

$$k_{71} = \frac{\alpha_2\nu_2\Gamma_{hbf}}{(\alpha_2\nu_2+\mu_1)(\mu_1+\alpha_3+\delta_{1b})} \tag{25a}$$

$$k_{72} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\Gamma_{hsf}}{\alpha_4+\mu_1+\delta_{1s}} \tag{25b}$$

$$k_{74} = \frac{\gamma_2\tau_3\Gamma_{rbf}}{(\gamma_2\tau_3+\mu_3)(\gamma_3+\mu_3+\delta_{3b})} \tag{25c}$$

$$k_{75} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\Gamma_{rsf}}{\gamma_4+\mu_3+\delta_{3s}} \tag{25d}$$

The pathogens are released in the environment at the rates η_1 and η_1 from I_{HP} and I_{RP} respectively. The released number of pathogens at a given time depends on the infectious period of the rodent and human infected with pneumonic plague. And the probability that I_{HP} and I_{RP} survive the incubation period. The total pathogens in soil/environment is as given in (26a) and (26b).

$$k_{83} = \left(\frac{\alpha_2\nu_1}{\alpha_2\nu_1+\mu_1} + \frac{\alpha_3\rho_1}{\alpha_3\rho_1+\mu_1} + \frac{\alpha_4\xi}{\alpha_4\phi+\mu_1}\right)\frac{\eta_1}{\alpha_5+\mu_1+\delta_{1p}} \tag{26a}$$

$$k_{86} = \left(\frac{\gamma_2\tau_1}{\gamma_2\tau_1+\mu_3} + \frac{\gamma_3\phi}{\gamma_3\phi+\mu_3} + \frac{\gamma_4}{\gamma_4+\mu_3}\right)\frac{\eta_2}{\mu_3+\delta_{3p}} \tag{26b}$$

Each element in the matrix K represent the expected number of secondary cases produced by infected individual j during the entire infectious period of that particular individual into a completely susceptible population i (Hartemink *et al.*, 2008).

We obtain the basic reproduction number R_0 by computing the maximum modulus of the eigenvalues of the next-generation matrix K (Diekmann *et al.*, 1990; Heesterbeek, 2000). Now using mapple computing software package, the basic reproduction number is:

$$R_0 = \frac{k_{22}+k_{55}}{4} + \frac{1}{2}\sqrt{A_1 + \frac{1}{3\sqrt[3]{2}}A_4 + \frac{A_5}{3A_4}} + \frac{1}{2}\sqrt{A_2 - \frac{1}{3\sqrt[3]{2}}A_4 - \frac{A_5}{3A_4}} + \frac{A_3}{4\sqrt{A_1 + \frac{1}{3\sqrt[3]{2}}A_4 + \frac{L_3}{3A_4}}}$$

$$\vartheta_1 = k_{22}k_{55} - k_{17}k_{71} - k_{27}k_{72} - k_{57}k_{75}$$

$$\vartheta_2 = k_{17}k_{55}(k_{17}k_{71} + k_{21}k_{72}) - k_{47}(k_{25}k_{54}k_{72} + k_{22}(k_{55}k_{74} + k_{54}k_{75}))$$

$$\vartheta_3 = -k_{22} - k_{55}$$

$$\vartheta_4 = (k_{22}+k_{55})(k_{17}k_{71} + k_{47}k_{74}) - k_{72}(k_{17}k_{21} - k_{27}k_{55} + k_{25}k_{57}) - k_{75}(k_{47}k_{54} - k_{22}k_{57})$$

$$A_1 = \frac{3\vartheta_3 + 8\vartheta_1}{12}$$

$$A_2 = \frac{3\vartheta_3 - 8\vartheta_1}{6}$$

$$A_3 = 4\vartheta_1\vartheta_3 - \vartheta_3^3 - 8\vartheta_4$$

$$A_4 = \frac{1}{3\sqrt[3]{2}}((2\vartheta_1^3 - 72\vartheta_2\vartheta_1 - 9\vartheta_3\vartheta_4\vartheta_1 + 27\vartheta_4^2 + 27\vartheta_3^2\vartheta_2)) +$$
$$((2\vartheta_1^3 - 72\vartheta_2\vartheta_1 - 9\vartheta_3\vartheta_4\vartheta_1 + 27\vartheta_4^2 + 27\vartheta_3^2\vartheta_2^2 - 4(\vartheta_1^2 + 12\vartheta_2 - 3\vartheta_3\vartheta_4)^3)^{\frac{1}{3}})^{\frac{1}{2}}$$

$$A_5 = \sqrt[3]{2}(\vartheta_1^2 + 12\vartheta_2 - 3\vartheta_3\vartheta_4)$$

Since the system has multiple infectious types from multiple hosts then the next generation matrix produce the geometric mean of the number of infections per generation and the the basic

reproduction number is the average number of secondary infections (Li and Blakeley, 2011). It is shown that the basic reproduction number of plague disease depends on the expected number of new cases of human infected with bubonic plague caused by one infected flea (k_{17}), the expected number of new cases of human infected with septicemic plague caused by one infected human with bubonic plague (k_{21}), the expected number of new cases of human infected with septicemic plague caused by one infected human with septicemic plague (k_{22}), the expected number of new cases of rodent infected with bubonic plague caused by one infected flea (k_{47}), the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with bubonic plague (k_{54}), the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with septicemic plague (k_{55}), the expected number of new cases of rodent infected with septicemic plague caused by one infected flea (k_{57}), the expected number of new cases of of new cases of flea infested with *Yersinia pestis* caused by one infected human with bubonic plague (k_{71}), the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected human with septicemic plague (k_{72}), the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with bubonic plague (k_{74}) and the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with septicemic plague(k_{75}). The result may also be interpreted that, among all elements of the matrix K, the k_{ij} that appear in R_O gives more significant involvement in the dynamics and spread of plague disease.

5.4.3 Local stability of the Disease Free Equilibrium point

In this section, we prove the local stability of the Disease Free Equilibrium (DFE) point of plague disease system. We are requred to prove that the trajectories start arbitrary close to the equilibrium point but do not precisely reach it. We thus use Jacobian matrix $J(E^0)$ of system (8) - (11) at DFE point:
Then we have

$$\mathbf{J}(\mathbf{E^0}) = \begin{pmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{pmatrix} \tag{27}$$

where J_{11}, J_{12}, J_{21} and J_{22} are (7×7) matrices given by;

$$\mathbf{J_{11}} = \begin{pmatrix} -\mu_1 & 0 & 0 & \frac{-\alpha_1\Gamma_{hsh}S_H}{N_1} & \frac{-\alpha_1\Gamma_{hph}S_H}{N_1} & \varpi & 0 \\ 0 & -(\alpha_2+\mu_1) & 0 & \frac{\alpha_1\Gamma_{hsh}S_H}{N_1} & \frac{\alpha_1\Gamma_{hph}S_H}{N_1} & 0 & 0 \\ 0 & \alpha_2\nu_2 & -a_6 & 0 & 0 & 0 & \\ 0 & \alpha_2\nu_3 & \rho_3\alpha_3 & -a_7 & 0 & 0 & 0 \\ 0 & \alpha_2\nu_1 & \rho_1\alpha_3 & \alpha_4\xi & -a_8 & 0 & 0 \\ 0 & 0 & \rho_2\alpha_3 & \alpha_4(1-\xi) & \alpha_5 & -(\varpi+\mu_1) & 0 \\ 0 & 0 & 0 & \frac{-\gamma_1\Gamma_{hsr}S_R}{N_1} & \frac{-\gamma_1\Gamma_{hpr}S_R}{N_1} & 0 & -\mu_3 \end{pmatrix} \tag{28}$$

$a_6 = (\alpha_3+\mu_1+\delta_{1b})$, $a_7 = (\alpha_4+\mu_1+\delta_{1s})$, $a_8 = (\alpha_5+\mu_1+\delta_{1p})$

$$\mathbf{J_{21}} = \begin{pmatrix} 0 & 0 & 0 & \frac{\gamma_1\Gamma_{hsr}S_R}{N_1} & \frac{\gamma_1\Gamma_{hpr}S_R}{N_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{-\beta\Gamma_{hbf}S_F}{N_1} & \frac{-\beta\Gamma_{hsf}S_F}{N_1} & 0 & 0 & 0 \\ 0 & 0 & \frac{\beta\Gamma_{hbf}S_F}{N_1} & \frac{-\beta\Gamma_{hsf}S_F}{N_1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\eta_1}{N_1} & 0 & 0 \end{pmatrix} \tag{29}$$

$$\mathbf{J_{12}} = \begin{pmatrix} 0 & 0 & \frac{-\alpha_1\Gamma_{rsh}S_H}{N_3} & \frac{-\alpha_1\Gamma_{rph}S_H}{N_3} & 0 & \frac{-\alpha_1\Gamma_{fh}S_H}{N_2} & -\alpha_1\omega_1 S_H \\ 0 & 0 & \frac{\alpha_1\Gamma_{rsh}S_H}{N_3} & \frac{\alpha_1\Gamma_{rph}S_H}{N_3} & 0 & \frac{\alpha_1\Gamma_{fh}S_H}{N_2} & \alpha_1\omega_1 S_H \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{-\gamma_1\Gamma_{rsr}S_R}{N_3} & \frac{-\gamma_1\Gamma_{rpr}S_R}{N_3} & 0 & \frac{-\gamma_1\Gamma_{fr}S_R}{N_2} & -\gamma_2\omega_2 S_R \end{pmatrix} \tag{30}$$

$$\mathbf{J_{22}} = \begin{pmatrix} -a_3 & 0 & \frac{\gamma_1\Gamma_{rsr}S_R}{N_3} & \frac{\gamma_1\Gamma_{rpr}S_R}{N_3} & 0 & \frac{\gamma_1\Gamma_{fr}S_R}{N_2} & \gamma_2\omega_2 S_R \\ \tau_3\gamma_2 & -a_1 & 0 & 0 & 0 & 0 & 0 \\ \tau_2\gamma_2 & \gamma_3(1-\phi) & -a_2 & 0 & 0 & 0 & 0 \\ \gamma_2\tau_1 & \gamma_3\phi & \gamma_4 & -a_5 & 0 & 0 & 0 \\ 0 & \frac{-\beta\Gamma_{rbf}S_F}{N_3} & \frac{-\beta\Gamma_{rsf}S_F}{N_3} & 0 & -\mu_2 & 0 & 0 \\ 0 & \frac{\beta\Gamma_{rbf}S_F}{N_3} & \frac{\beta\Gamma_{rsf}S_F}{N_3} & 0 & 0 & -a_4 & 0 \\ 0 & 0 & 0 & \frac{\eta_2}{N_3} & 0 & 0 & -\mu_4 \end{pmatrix} \tag{31}$$

$a_1 = (\gamma_3 + \mu_3 + \delta_{3b})$, $a_2 = (\gamma_4 + \mu_3 + \delta_{3s})$, $a_3 = (\gamma_2 + \mu_3)$, $a_4 = (\mu_2 + \delta_2)$, $a_5 = (\mu_3 + \delta_{3p})$

From the combined matrix $J(E^0)$, the diagonal entries from the first,sixth, seventh and twelves column makes the four eigenvalues of the matrix (27). These are $-\mu_1$, $-(\varpi + \mu_1)$, $-\mu_3$ and $-\mu_2$. Now canceling their corresponding rows and columns we modify (27) and remain with a (10×10) matrix with the modified J_{11}, J_{12}, J_{21} and J_{22} as given in (32), (33), (34) and (35) respectively;

$$\mathbf{J_{11}} = \begin{pmatrix} -(\alpha_2 + \mu_1) & 0 & \frac{\alpha_1 \Gamma_{hsh} S_H}{N_1} & \frac{\alpha_1 \Gamma_{hph} S_H}{N_1} \\ \alpha_2 \nu_2 & -a_6 & 0 & \\ \alpha_2 \nu_3 & \rho_3 \alpha_3 & -a_7 & 0 \\ \alpha_2 \nu_1 & \rho_1 \alpha_3 & \alpha_4 \xi & -a_8 \end{pmatrix} \tag{32}$$

$a_6 = (\alpha_3 + \mu_1 + \delta_{1b})$, $a_7 = (\alpha_4 + \mu_1 + \delta_{1s})$, $a_8 = (\alpha_5 + \mu_1 + \delta_{1p})$

$$\mathbf{J_{21}} = \begin{pmatrix} 0 & 0 & \frac{-\gamma_1 \Gamma_{hsr} S_R}{N_1} & \frac{-\gamma_1 \Gamma_{hpr} S_R}{N_1} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \frac{\beta \Gamma_{hbf} S_F}{N_1} & \frac{-\beta \Gamma_{hsf} S_F}{N_1} & 0 \\ 0 & 0 & 0 & \frac{\eta_1}{N_1} \end{pmatrix} \tag{33}$$

$$\mathbf{J_{12}} = \begin{pmatrix} 0 & 0 & \frac{\alpha_1 \Gamma_{rsh} S_H}{N_3} & \frac{\alpha_1 \Gamma_{rph} S_H}{N_3} & \frac{\alpha_1 \Gamma_{hf} S_H}{N_2} & \alpha_1 \omega_1 S_H \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{34}$$

$$\mathbf{J_{22}} = \begin{pmatrix} -a_3 & 0 & \frac{\gamma_1 \Gamma_{rsr} S_R}{N_3} & \frac{\gamma_1 \Gamma_{rpr} S_R}{N_3} & \frac{\gamma_1 \Gamma_{fr} S_R}{N_2} & \gamma_2 \omega_2 S_R \\ \tau_3 \gamma_2 & -a_1 & 0 & 0 & 0 & 0 \\ \tau_2 \gamma_2 & \gamma_3 (1 - \phi) & -a_2 & 0 & 0 & 0 \\ \gamma_2 \tau_2 & \gamma_3 \phi & \gamma_4 & -a_5 & 0 & 0 \\ 0 & \frac{\beta \Gamma_{rbf} S_F}{N_3} & \frac{\beta \Gamma_{rsf} S_F}{N_3} & 0 & -a_4 & 0 \\ 0 & 0 & 0 & \frac{\eta_2}{N_3} & 0 & -\mu_4 \end{pmatrix} \tag{35}$$

$a_1 = (\gamma_3 + \mu_3 + \delta_{3b})$, $a_2 = (\gamma_4 + \mu_3 + \delta_{3s})$, $a_3 = (\gamma_2 + \mu_3)$, $a_4 = (\mu_2 + \delta_2)$, $a_5 = (\mu_3 + \delta_{3p})$

Doing further computations we find other negative eigenvalues of the matrix (27) are $-\mu_4$, $-(\mu_2+\delta_2)$, $\frac{-(\mu_2+\delta_2)(\gamma_2+\mu_3)\gamma_1\Gamma_{fr}S_R^0}{\mu_2}$, $-(\alpha_5+\mu_1+\delta_{1p})$, $-(\alpha_4+\mu_1+\delta_{1b})$ and $-(\alpha_3+\mu_1+\delta_{1b})$. Another eigenvalue is $\frac{\iota_1+\iota_2+\iota_3+\iota_4+\iota_5-\iota_6}{\mu_2\delta_1\alpha_1\mu_4\psi_1\Gamma_{fh}\delta_2\psi_3\mu_3}$ which is negative on the condition that $\frac{(\iota_1+\iota_2+\iota_3+\iota_4+\iota_5)}{\iota_6\mu_4\delta_2\psi_3\mu_3} < 1$

where;

$$\iota_1 = (\Gamma_{hph}\mu_4 + \omega_1\eta_1)\alpha_1\psi_{2s}(\mu_2+\delta_2)(\alpha_5+\mu_1+\delta_{1p})\alpha_2\mu_1\delta_2\psi_3\mu_3(\nu_1(\alpha_4+\mu_1+\delta_{1s})+\alpha_3\rho_1\nu_2)$$

$$\iota_2 = ((\mu_2+\delta_2)\Gamma_{hsh}+\beta\Gamma_{hsf}\Gamma_{fr})(\alpha_5+\mu_1+\delta_{1p})\alpha_1\psi_{2s}\mu_1\mu_4\delta_2\psi_3\mu_3((\alpha_3+\mu_1+\delta_{1b})+\alpha_3\rho_3\alpha_2\nu_2)$$

$$\iota_3 = (\Gamma_{rhp}\mu_4+\omega_1\eta_2)(\mu_2+\delta_2)(\alpha_3+\mu_1+\delta_{1b})\mu_3\alpha_2\nu_3\alpha_4\psi_{2s}\delta_1\psi_1\mu_3\xi$$

$$\iota_4 = (\alpha_5+\mu_1+\delta_{1p})(\alpha_4+\mu_1+\delta_{1s})\gamma_1\omega_2\alpha_2\nu_2\delta_2\psi_3\mu_2\delta_1\alpha_1\mu_4\psi_1\Gamma_{fh}\delta_2\psi_3$$

$$\iota_5 = (\alpha_1\Gamma_{rph}\mu_4+\alpha_2\omega_1\rho_2)\alpha_3\rho_3\alpha_4\xi\alpha_2\nu_2\psi_{2s}\mu_3\delta_1\psi_1\mu_3$$

$$\iota_6 = (\alpha_5+\mu_1+\delta_{1p})(\mu_2+\delta_2)(\alpha_2+\delta_1)(\alpha_4+\mu_1+\delta_{1b})(\alpha_3+\mu_1+\delta_{1b})\psi_{2s}\mu_1\mu_4\delta_2\psi_3\mu_3$$

The computation also gives two complex eigenvalues with very long expressions and negative real parts, which are named as $-p_1+q_1i$ and $-p_2+q_2i$ where p_1, p_2 and q_1, q_2 are real and imaginary parts respectively. The other and the last eigenvalue is negative if and only if $R_0 < 1$, where

$$R_0 = \frac{k_{22}+k_{55}}{4}+\frac{1}{2}\sqrt{A_1+\frac{1}{3\sqrt[3]{2}}A_4+\frac{A_5}{3A_4}}+\frac{1}{2}\sqrt{A_2-\frac{1}{3\sqrt[3]{2}}A_4-\frac{A_5}{3A_4}}+\frac{A_3}{4\sqrt{A_1+\frac{1}{3\sqrt[3]{2}}A_4+\frac{L_3}{3A_4}}}$$

These results verifies that the disease free equilibrium point E^0 is locally asymptotically stable (Morand *et al.*, 2011). It then leads to Theorem 5.13.

Theorem 5.13

The Disease Free Equilibrium E^0 of pneumonic plague is locally asymptotically stable if $R_0 <$ 1and unstable if $R_0 > 1$.

5.4.4 Global stability of the disease-free equilibrium point

We use Metzler matrix method by Castillo-Chavez *et al.* (2002), to verify the existence of global stability of disease free equilibrium point. We divide the system (8) - (11) into transmitting and non-transmitting components.

To do this we first let Y_n be the vector for non-transmitting compartments, Y_i be the vector for transmitting compartments and $Y_{E_0,n}$ be the vector of disease free point.

$$\begin{cases} \dfrac{dY_n}{dt} & = A_1(Y_n - Y_{E_0,n}) + A_2 Y_i \\ \\ \dfrac{dY_i}{dt} & = A_3 Y_i \end{cases} \tag{36}$$

Using the transmitting and non transmitting compartment, we modify equation (36) to have;

$$Y_n = (S_H, R_H, S_R, S_F)^T \qquad Y_i = (E_H, I_{HB}, I_{HS}, I_{HP}, E_R, I_{RB}, I_{RS}, I_{RS}, I_F, A)$$
$$Y_{E_0,n} = (\frac{\psi_1}{\mu_1}, 0, \frac{\psi_3}{\mu_3}, \frac{\psi_{2s}}{\mu_2})$$

$$\mathbf{Y_n} - \mathbf{Y_{E_0,n}} = \begin{pmatrix} S_H - \frac{\psi_1}{\mu_1} \\ R_H \\ S_R - \frac{\psi_3}{\mu_3} \\ S_F - \frac{\psi_{2s}}{\mu_2} \end{pmatrix}$$

To prove that the DFE point is globally and asymptotically stable, we need to show that Matrix A_1 has real negative eigenvalues and A_3 is a Metzler matrix that has non-negative off diagonal element. Now using (36) we have;

$$\begin{pmatrix} \psi_1 + \varpi R_H - \alpha_1 G_1 S_H - \mu_1 S_H \\ \alpha_3 \rho_2 I_{HB} + \alpha_4(1-\xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H \\ \psi_3 - \gamma_1 G_2 S_R - \mu_3 S_R \\ \psi_{2s} - \beta G_3 S_F - \mu_2 S_F \end{pmatrix} = \mathbf{A_1} \begin{pmatrix} S_H - \frac{\psi_1}{\mu_1} \\ R_H \\ S_R - \frac{\psi_3}{\mu_3} \\ S_F - \frac{\psi_{2s}}{\mu_2} \end{pmatrix} + \mathbf{A_2} \begin{pmatrix} E_H \\ I_{HB} \\ I_{HS} \\ I_{HP} \\ E_R \\ I_{RB} \\ I_{RS} \\ I_{RP} \\ I_F \\ A \end{pmatrix}$$

and

$$\begin{pmatrix} \psi_1 + \alpha_1 G_1 S_H - \alpha_2 E_H - \mu_1 E_H, \\ \alpha_2\nu_2 E_H - (\alpha_3 + \mu_1 + \delta_{1b}) I_{HB}, \\ \alpha_3\rho_3 I_{HB} + \alpha_2\nu_3 E_H - (\alpha_4 + \mu_1 + \delta_{1s}) I_{HS}, \\ \alpha_2\nu_1 E_H + \alpha_3\rho_1 I_{HB} + \alpha_4\xi I_{HS} - (\alpha_5 + \mu_1 + \delta_{1p}) I_{HP}, \\ \psi_3 + \gamma_1 G_2 S_R - \gamma_2 E_R - \mu_3 E_R, \\ \gamma_2\tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \\ \gamma_2\tau_2 E_R + \gamma_3(1-\phi) I_{RB} - (\gamma_4 + \mu_3 + \delta_{3s}) I_{RS}, \\ \gamma_2\tau_1 E_R + \gamma_3\phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \\ \beta G_3 S_F - (\mu_2 + \delta_2) I_F \\ \lambda_4 + \dfrac{\eta_1 I_{HP}}{N_1} + \dfrac{\eta_2 I_{RP}}{N_3} - \mu_4 A. \end{pmatrix} = \mathbf{A_3} \begin{pmatrix} E_H \\ I_{HB} \\ I_{HS} \\ I_{HP} \\ E_R \\ I_{RB} \\ I_{RS} \\ I_{RP} \\ I_F \\ A \end{pmatrix}$$

The matrices A_1, A_2 and A_3 are as below:

$$\mathbf{A_1} = \begin{pmatrix} -\mu_1 & \varpi & 0 & 0 \\ 0 & -(\varpi + \mu_1) & 0 & 0 \\ 0 & 0 & -\mu_3 & 0 \\ 0 & 0 & 0 & -\mu_2 \end{pmatrix} \tag{37}$$

$$\mathbf{A_2} = \begin{pmatrix} 0 & 0 & \frac{-\alpha_1\Gamma_{hsh}S_H^0}{N_1} & \frac{-\alpha_1\Gamma_{hph}S_H^0}{N_1} & 0 & 0 & \frac{-\alpha_1\Gamma_{rsh}S_H^0}{N_3} & \frac{-\alpha_1\Gamma_{rph}S_H^0}{N_3} & -a_{16} & -a_{12} \\ 0 & \alpha_3\rho_3 & (1-\xi)\alpha_4 & \alpha_5 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{-\gamma_1\Gamma_{hsr}S_R^0}{N_1} & \frac{-\gamma_1\Gamma_{hpr}S_R^0}{N_1} & 0 & 0 & \frac{-\gamma_1\Gamma_{rsr}S_R^0}{N_3} & \frac{-\gamma_1\Gamma_{rpr}S_R^0}{N_3} & -a_{15} & -a_{11} \\ 0 & -a_{10} & \frac{-\beta\Gamma_{hsf}S_F^0}{N_1} & 0 & 0 & -a_{13} & \frac{-\beta\Gamma_{rsf}S_F^0}{N_3} & 0 & 0 & 0 \end{pmatrix} \tag{38}$$

$$\mathbf{A_3} = \begin{pmatrix} -a_9 & 0 & \frac{\alpha_1\Gamma_{hsh}S_H^0}{N_1} & \frac{\alpha_1\Gamma_{hph}S_H^0}{N_1} & 0 & 0 & \frac{\alpha_1\Gamma_{rsh}S_H^0}{N_3} & \frac{\alpha_1\Gamma_{rph}S_H^0}{N_3} & a_{16} & a_{12} \\ \alpha_2\nu_2 & -a_6 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \alpha_2\nu_3 & \alpha_3\rho_3 & -a_7 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \alpha_2\nu_1 & \alpha_3\rho_1 & \alpha_4\xi & -a_8 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \dfrac{\gamma_1\Gamma_{hsr}S_R^0}{N_1} & \frac{\gamma_1\Gamma_{hpr}S_R^0}{N_1} & -a_3 & 0 & \frac{\gamma_1\Gamma_{rsr}S_R^0}{N_3} & \frac{\gamma_1\Gamma_{rpr}S_R^0}{N_3} & a_{15} & a_{11} \\ 0 & 0 & 0 & 0 & \tau_3\gamma_2 & -a_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \tau_2\gamma_2 & a_{14} & -a_2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_2\tau_1 & \gamma_3\phi & \gamma_4 & -a_5 & 0 & 0 \\ 0 & a_{10} & \frac{\beta\Gamma_{hsf}S_F^0}{N_1} & 0 & 0 & a_{13} & \frac{\beta\Gamma_{rsf}S_F^0}{N_3} & 0 & -a_4 & 0 \\ 0 & 0 & 0 & \frac{\eta_1}{N_1}0 & 0 & 0 & \frac{\eta_2}{N_3} & 0 & -\mu_4 & \end{pmatrix} \tag{39}$$

$$
\begin{array}{lll}
a_{16} = \frac{\alpha_1 \Gamma_{fh} S_H^0}{N_2} & n_2 = (\alpha_3 + \mu_1 + \kappa_1) & n_3 = (\alpha_4 + \mu_1 + \delta_1) \\
a_{13} = \frac{\beta \Gamma_{rbf} S_F^0}{N_3} & a_{13} = \gamma_3(1-\phi) & a_{15} = \frac{\gamma_1 \Gamma_{fr} S_R^0}{N_2} \\
a_{12} = \alpha_1 \omega_1 S_H & a_{11} = \gamma_1 \omega_2 S_R^0 & a_{10} = \dfrac{\beta \Gamma_{hbf} S_F^0}{N_1} \\
S_H^0 = \dfrac{\psi_1}{\mu_1} & S_R^0 = \frac{\psi_3}{\mu_3} & S_F^0 = \dfrac{\psi_{2s}}{\mu_2}
\end{array}
$$

The eigenvalues for matrix A_1 are $-\mu_1$, $-\mu_2$, $-\mu_3$ and $-(\varpi + \mu_1)$. This confirms that the system

$$\frac{dY_n}{dt} = A_1(Y_n - Y_{E_0,n}) + A_2 Y_i$$

is globally and asymptotically stable at Y_{E_0}. A_3 is a Metzler stable matrix since all its off-diagonal elements are non-negative. Therefore Disease Free Equilibrium point for Plague disease system is globally asymptotically stable thus we have the Theorem 5.14.

Theorem 5.14

The disease-free equilibrium point is globally asymptotically stable in E^0 if $R_0 < 1$and unstable if $R_0 > 1$.

5.5 Existence of Endemic Equilibrium

Here, we consider the situation in which the disease persists in a population. We investigate conditions for existence of the endemic equilibrium point of the system (8)-(11). The endemic equilibrium point $E^*(S_H^*, E_H^*, I_{HB}^*, I_{HS}^*, I_{HP}^*, R_H^*, S_R^*, E_R^*, I_{RB}^*, I_{RS}^*, I_{RP}^*, S_F^*, I_F^*, A^*)$ is obtained by solving the equations obtained by setting the derivatives of (8)-(11) equal to zero as in (40)-(43) which exist for $R_O > 1$.

Human Population

$$0 = \psi_1 + \varpi R_H - \alpha_1 G_1 S_H - \mu_1 S_H, \tag{40a}$$

$$0 = \alpha_1 G_1 S_H - \alpha_2 E_H - \mu_1 E_H, \tag{40b}$$

$$0 = \alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB}, \tag{40c}$$

$$0 = \alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS}, \tag{40d}$$

$$0 = \alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP}, \tag{40e}$$

$$0 = \alpha_3 \rho_2 I_{HB} + \alpha_4 (1-\xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H. \tag{40f}$$

Rodent population

$$0 = \psi_3 - \gamma_1 G_2 S_R - \mu_3 S_R, \tag{41a}$$

$$0 = \gamma_1 G_2 S_R - \gamma_2 E_R - \mu_3 E_R, \tag{41b}$$

$$0 = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \tag{41c}$$

$$0 = \gamma_2 \tau_2 E_R + \gamma_3 (1-\phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}, \tag{41d}$$

$$0 = \gamma_2 \tau_1 E_R + \gamma_3 \phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \tag{41e}$$

Fleas

$$0 = \psi_{2s} - \beta G_3 S_F - \mu_2 S_F, \tag{42a}$$

$$0 = \beta G_3 S_F - (\mu_2 + \delta_2) I_F \tag{42b}$$

Pathogens in the environment

$$0 = \lambda_4 + \frac{\eta_1 I_{HP}}{N_1} + \frac{\eta_3 I_{RP}}{N_3} - \mu_4 A. \tag{43}$$

We use the approach described in the studies by Tumwiine *et al.* (2007) and Massawe *et al.* (2015) to prove the existence of endemic equilibrium. For the endemic equilibrium to exist it must satisfy the condition $E_H \neq 0$ or $I_{HB} \neq 0$ or $I_{HS} \neq 0$ or $I_{HP} \neq 0$ or $E_R \neq 0$ or $I_{RB} \neq 0$ or $I_{RS} \neq 0$ or $I_{RP} \neq 0$ or $I_F \neq 0$ or $A \neq 0$ that is $S_H > 0$ or $E_H > 0$ or $I_{HB} > 0$ or $I_{HS} > 0$ or $I_{HP} > 0$ or $S_R > 0$ or $I_{RB} > 0$ or $I_{RS} > 0$ or $I_{RP} > 0$ or $E_R > 0$ or $S_F > 0$ or $I_F > 0$ or $A > 0$ must be satisfied. Now adding system (40)-(43) we have

$$\begin{aligned} &\psi_1 + \psi_{2s} + \psi_3 - \mu_1(S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H) - \mu_2(S_F + I_F) \\ &- \mu_3(S_R + E_R + I_{RB} + I_{RS} + I_{RP}) - \delta_{1b} I_{HB} - \delta_{1s} I_{HS} - \delta_{1p} I_{HP} - \delta_{3b} I_{RB} \\ &- \delta_{3s} I_{RS} - \delta_{3p} I_{RP} - \delta_2 I_F + \lambda_4 + \frac{\eta_1 I_{HP}}{N_1} + \frac{\eta_3 I_{RP}}{N_3} - \mu_4 A = 0 \end{aligned} \tag{44}$$

substituting equation (43), $N_1 = S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H$, $N_2 = S_F + I_F$ and $N_3 = S_R + E_R + I_{RB} + I_{RS} + I_{RP}$ into equation (44).
It follows that;

$$\psi_1 + \psi_{2s} + \psi_3 = \mu_1 N_1 + \mu_2 N_2 + \mu_3 N_3 + \delta_{1b} I_{HB} + \delta_{1s} I_{HS} + \delta_{1p} I_{HP} + \delta_{3b} I_{RB} + \delta_{3s} I_{RS} + \delta_{3p} I_{RP} + \delta_2 I_F$$

Since $\psi_1 + \psi_{2s} + \psi_3 > 0$, $\mu_1 > 0$, $\mu_2 > 0$, $\mu_3 > 0$, $\delta_{1b} > 0$, $\delta_{1s} > 0$, $\delta_{1p} > 0$, $\delta_2 > 0$, $\delta_{3b} > 0$, $\delta_{3s} > 0$ and $\delta_{3p} > 0$ we can discern that $\mu_1 N_1 > 0$, $\mu_2 N_2 > 0$, $\mu_3 N_3 > 0$, $\delta_{1b} I_{HB} > 0$, $\delta_{1s} I_{HS} > 0$, $\delta_{1p} I_{HP} > 0$, $\delta_2 I_F > 0$, $\delta_{3b} I_{RB} > 0$, $\delta_{3s} I_{RS} > 0$ and $\delta_{3p} I_{RP} > 0$ implying that $S_H > 0$, $E_H > 0$, $I_{HB} > 0$, $I_{HS} > 0$, $I_{HP} > 0$, $S_F > 0$, $I_F > 0$, $S_R > 0$, $E_R > 0$, $I_{RB} > 0$, $I_{RS} > 0$ and $I_{RP} > 0$.
Hence endemic equilibrium point of the plague disease model in human, rodent, flea and pathogens in the environment exists.

5.5.1 Stability of endemic equilibrium point

In this section, we derive the conditions under which the endemic equilibrium points are stable or unstable. That is the solution starting sufficiently close to the equilibrium remains close to the equilibrium and approaches the equilibrium as $t \to \infty$, or if there are solutions starting arbitrary close to the equilibrium point do not approach it. We only prove the global stability of the endemic equilibrium since we have already proven the local stability of the Disease free equilibrium which by Van den Driessche and Watmough (2002) it advocates for local stability of the Endemic Equilibrium for the reverse condition.

Global stability of Endemic equilibrium point

We prove the global stability of the endemic equilibrium point using Korobeinikov approach. We first formulate a suitable Lyapunov function for plague disease model (Korobeinikov, 2004, 2007)
The Lyapunov function is as given in the form below;

$$V = \sum a_i(y_i - y_i^* \ln y_i)$$

where a_i is defined as a properly selected positive constant, y_i defines the population of the i^{th} compartment, and y_i^* is the equilibrium point.
Now the Lyapunov function is,

$$\begin{aligned} V = \; & W_1(S_H - S_H^* \ln S_H) + W_2(E_H - E_H^* \ln E_H) + W_3(I_{HB} - I_{HB}^* \ln I_{HB}) \\ & + W_4(I_{HS} - I_{HS}^* \ln I_{HS}) + W_5(I_{HP} - I_{HP}^* \ln I_{HP}) + W_6(R_H - R_H^* \ln R_H) \\ & + W_7(S_R - S_R^* \ln S_R) + W_8(E_R - E_R^* \ln E_R) + W_9(I_{RB} - I_{RB}^* \ln I_{RB}) \\ & + W_{10}(I_{RS} - I_{RS}^* \ln I_{RS}) + W_{11}(I_{RP} - I_{RP}^* \ln I_{RP}) + W_{12}(S_F - S_F^* \ln S_F) \\ & + W_{13}(I_F - I_F^* \ln I_F) + W_{14}(A - A^* \ln A) \end{aligned}$$

The constants W_i are non negative in Φ for $i = 1, 2, 3...12$, V is Lyapunov function. The function V together with its constants $W_1, W_2...W_{14}$ are chosen such that V is continuous and differentiable in a space

We compute the time derivative of V this yields;

$$\begin{aligned} \frac{dV}{dt} = \; & W_1(1 - \tfrac{S_H^*}{S_H})\tfrac{dS_H}{dt} + W_2(1 - \tfrac{E_H^*}{E_H})\tfrac{dE_H}{dt} + W_3(1 - \tfrac{I_{HB}^*}{I_{HB}})\tfrac{dI_{HB}}{dt} + W_4(1 - \tfrac{I_{HS}^*}{I_{HS}})\tfrac{dI_{HS}}{dt} \\ & + W_5(1 - \tfrac{I_{HP}^*}{I_{HP}})\tfrac{dI_{HP}}{dt} + W_6(1 - \tfrac{R_H^*}{R_H})\tfrac{dR_H}{dt} + W_7(1 - \tfrac{S_R^*}{S_R})\tfrac{dS_R}{dt} + W_8(1 - \tfrac{E_R^*}{E_R})\tfrac{dE_R}{dt} \\ & + W_9(1 - \frac{I_{RB}^*}{I_{RB}})\frac{dI_{RB}}{dt} + W_{10}(1 - \frac{I_{RS}^*}{I_{RS}})\frac{dI_{RS}}{dt} + W_{11}(1 - \frac{I_{RP}^*}{I_{RP}})\frac{dI_{RP}}{dt} \\ & + W_{12}(1 - \frac{S_F^*}{S_F})\frac{dS_F}{dt} + W_{13}(1 - \frac{I_F^*}{I_F})\frac{dI_F}{dt} + W_{14}(1 - \frac{A^*}{A})\frac{dA}{dt} \end{aligned}$$

Using system (8) - (11) we will have

$$\begin{aligned}\frac{dV}{dt} = \; & W_1(1-\tfrac{S_H^*}{S_H})[\psi_1+\varpi R_H-\alpha_1 G_1 S_H-\mu_1 S_H,] \\ & +W_2(1-\tfrac{E_H^*}{E_H})[\alpha_1 G_1 S_H-\alpha_2 E_H-\mu_1 E_H,] \\ & +W_3(1-\frac{I_{HB}^*}{I_{HB}})[\alpha_2\nu_2 E_H-\alpha_3 I_{HB}-(\mu_1+\delta_{1b})I_{HB},\end{aligned}$$

$$\begin{aligned}&+W_4(1-\tfrac{I_{HS}^*}{I_{HS}})[\alpha_3\rho_3 I_{HB}+\alpha_2\nu_3 E_H-\alpha_4 I_{HS}-(\mu_1+\delta_{1s})I_{HS},] \\ &+W_5(1-\tfrac{I_{HP}^*}{I_{HP}})[\alpha_2\nu_1 E_H+\alpha_3\rho_1 I_{HB}+\alpha_4\xi I_{HS}-\alpha_5 I_{HP}-(\mu_1+\delta_{1p})I_{HP},] \\ &+W_6(1-\tfrac{R_H^*}{R_H})[\alpha_3\rho_2 I_{HB}+\alpha_4(1-\xi)I_{HS}+\alpha_5 I_{HP}-\varpi R_H-\mu_1 R_H,] \\ &+W_7(1-\tfrac{S_R^*}{S_R})[\psi_3-\gamma_1 G_2 S_R-\mu_3 S_R,] \\ &+W_8(1-\tfrac{E_R^*}{E_R})[\gamma_1 G_2 S_R-\gamma_2 E_R-\mu_3 E_R,] \\ &+W_9(1-\tfrac{I_{RB}^*}{I_{RB}})[\gamma_2\tau_3 E_R-\gamma_3 I_{RB}-(\mu_3+\delta_{3b})I_{RB},] \\ &+W_{10}(1-\tfrac{I_{RS}^*}{I_{RS}})[\gamma_2\tau_2 E_R+\gamma_3(1-\phi)I_{RB}-\gamma_4 I_{RS}-(\mu_3+\delta_{3s})I_{RS},] \\ &+W_{11}(1-\tfrac{I_{RP}^*}{I_{RP}})[\gamma_2\tau_1 E_R+\gamma_3\phi I_{RB}+\gamma_4 I_{RS}-(\mu_3+\delta_{3p})I_{RP},] \\ &+W_{12}(1-\tfrac{S_F^*}{S_F})[\psi_{2s}-\beta G_3 S_F-\mu_2 S_F,] \\ &+W_{13}(1-\tfrac{I_F^*}{I_F})[\beta G_3 S_F-(\mu_2+\delta_2)I_F] \\ &+W_{14}(1-\tfrac{A^*}{A})[\lambda_4+\tfrac{\eta_1 I_{HP}}{N_1}+\tfrac{\eta_2 I_{RP}}{N_3}-\mu_4 A.]\end{aligned}$$

Using system (8) - (11) at endemic equilibrium after simplification we can derive the following:

$$\begin{aligned}\frac{dV}{dt} = & -W_1(1-\frac{S_H^*}{S_H})^2-W_2(1-\frac{E_H^*}{E_H})^2-W_3(1-\frac{I_{HB}^*}{I_{HB}})^2-W_4(1-\frac{I_{HS}^*}{I_{HS}})^2 \\ & -W_5(1-\frac{I_{HP}^*}{I_{HP}})^2-W_6(1-\frac{R_H^*}{R_H})^2-W_7(1-\frac{S_R^*}{S_R})^2-W_8(1-\frac{E_R^*}{E_R})^2 \\ & -W_9(1-\frac{I_{RB}^*}{I_{RB}})^2-W_{10}(1-\frac{I_{RS}^*}{I_{RS}})^2-W_{11}(1-\frac{I_{RP}^*}{I_{RP}})^2-W_{12}(1-\frac{S_F^*}{S_F})^2 \\ & -W_{13}(1-\frac{I_F^*}{I_F})^2-W_{14}(1-\frac{A^*}{A})^2 \\ & +F(S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A)\end{aligned} \tag{45}$$

where the function $F(S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A)$ is non positive. We now follow the procedures by McCluskey (2006), and Korobeinikov and Wake (2002). We take:

$$F(S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A)\geq 0$$

for all

$$S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A.$$

Then $\frac{dV}{dt}\leq 0$ for all $S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A$ and it is zero when $S_H=S_H^*,E_H=E_H^*,I_{HB}=I_{HB}^*,I_{HS}=I_{HS}^*,I_{HP}=I_{HP}^*,R_H=R_H^*,S_R=S_R^*,E_R=E_R^*,I_{RB}=I_{RB}^*,I_{RS}=I_{RS}^*,I_{RP}=I_{RP}^*,S_F=S_F^*,I_F=I_F^*,A=A^*$. Hence the

largest compact invariant set in $S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A$ such that $\frac{dV}{dt} = 0$ is the singleton E^* which is Endemic Equilibrium point of the plague disease system (8) - (11). Using LaSalles's invariant principle by LaSalle (1976), it entails that endemic equilibrium point of plague disease system (E^*) is globally asymptotically stable in the interior of the region of $S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A$ and thus leads to Theorem 5.15.

Theorem 5.15
If $R_0 > 1$ then the model system (8) - (11) of plague disease has a unique endemic equilibrium point E^* which is globally asymptotically stable in S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F and A.

5.6 Sensitivity and Elasticity analysis and Numerical Simulation

In this section, we use sensitivity and elasticity analysis to determine the impact that expected number of new cases of i caused by one infected individual of j (k_{ij}) has on the basic reproduction number R_0 . This is vital as it will help to know what and where to prioritize in order to control the disease.

5.6.1 Parameter Estimation

We obtain the parameters from the literature that relate to this study, the present information on plague disease and through estimation using sensitivity analysis and simulations. Table 13 shows the values of the parameters as used in the model.

Table 13: Parameter values for plague disease model.

Parameters	Value/Range	Reference/Source
μ_3	0.2	Galtier and Mouchiroud (1998)
α_3	0.038	Keeling and Gilligan (2000*a*)
ψ_1	0.09	Ngeleja *et al.* (2016)
α_1	0.99	Estimated
α_2	0.23	Gani and Leach (2004)
ν_1	0.3	Estemated
ν_2	0.4	Estemated

Continued on next page

Table 13 – *Continued from previous page*

Parameters	**Value/Range**	**Reference/Source**
ν_3	0.3	Estemated
δ_{1b}	0.04	Keeling and Gilligan (2000*a*)
ρ_3	0.5	Estimated
δ_{3s}	0.09	Estemated
α_4	0.23	Estimated
δ_{1s}	0.069	Estimated
ρ_1	0.3	Estimated
α_5	0.4	Gani and Leach (2004)
δ_{1p}	0.63	Kugeler *et al.* (2015); Keeling and Gilligan (2000*a*)
ξ	0.71	Estimated
ρ_2	0.2	Estimated
Γ_{hph}	0.5	Estimated
Γ_{rsf}	0.1	Eisen *et al.* (2007)
Γ_{hsh}	0.85	Estimated
Γ_{rph}	0.805	Estimated
Γ_{rsh}	0.8	Estimated
ψ_3	0.03	Keeling and Gilligan (2000*a*)
δ_2	0.03	Benkirane *et al.* (2009)
Γ_{hbf}	0.1	Eisen *et al.* (2007)
Γ_{rbf}	0.99	Estimated
γ_1	0.92	Estimated
γ_2	0.98	Estimated
τ_3	0.4	Estimated
δ_{3b}	0.1	Estimated
ϖ	0.33	Kugeler *et al.* (2015)
Γ_{fh}	0.0641	Eisen *et al.* (2007)
τ_2	0.3	Estimated
ϕ	0.5	Estimated
γ_4	0.05	Estimated
τ_1	0.3	Estimated
δ_{3p}	0.14	Estimated
Γ_{hsf}	0.1	Eisen *et al.* (2007)
Γ_{fr}	0.0641	Eisen *et al.* (2007)
Γ_{hpr}	0.00005	Estimated

Continued on next page

Table 13 – *Continued from previous page*

Parameters	**Value/Range**	**Reference/Source**
Γ_{hsr}	0.00008	Estimated
Γ_{rpr}	0.9	Estimated
Γ_{rsr}	0.9	Estimated
ψ_{2s}	1000	Estimated
β	0.99	Estimated
μ_2	0.07	Benkirane *et al.* (2009)
μ_1	0.04	Keeling and Gilligan (2000*a*)
λ_4	50,000	Estimated
η_1	0.2	Estimated
η_2	0.4	Estimated
μ_4	0.1	Ngeleja *et al.* (2016)
γ_3	0.194	Tollenaere *et al.* (2010)

The dynamics of compartments in Human beings, Rodents, Fleas and Pathogens in the environment are shown in Fig. 36a, Fig. 36b, Fig. 36c and Fig. 36d respectively. In the human population we see the fast decrease of the susceptible and exposed population until it reaches its endemic equilibrium point. This result is due to the assumption that there will be all three forms of plague. The presence of all forms of plague results to many ways in which an individual may be infected and thus lead to a very high force of infection.

The number of recovered human beings will slightly increase and drop off to its endemic equilibrium point. This result is also cemented by Gani and Leach (2004) because as there is no treatment and with the presence all three forms of plague the recovery rate must be very small. The rapid decrease of the susceptible and exposed class will result to a rise of the infectious classes for a period within $0 - 5$ years before it decreases to its endemic point. As there is no any method introduced in the system to control the disease the infected classes I_{HB}, I_{HS} and I_{HP} will rise very fast in the first years before it drops to its the endemic point.

We assume no recovery in the rodent population, and therefore all infected individuals will end-up dying due to the disease after some time. That is to say with time the rodent population also experience the same dynamics as in human population. The number of infected classes I_{RB}, I_{RB} and I_{RB} rises within the time between $0 - 10$ years to its maximum and linger at its endemic equilibrium state. The susceptible and exposed rodent drops within the first ten years

to its endemic point.

As the disease becomes endemic to the community, the number of flea getting the disease and the number pathogens in the environment will significantly increase. The increase of I_F is mostly contributed by by the rise in number of I_{HB}, I_{HS}, I_{RB} and I_{RS}. Moreover the increase of A is due to the increase of the number of individuals (Human and Rodent) with pneumonic plague. The increase of individuals with bubonic and septicemic plague increases the rate at which the flea gets the infection. Then the number of susceptible fleas will decreases with time to its endemic point.

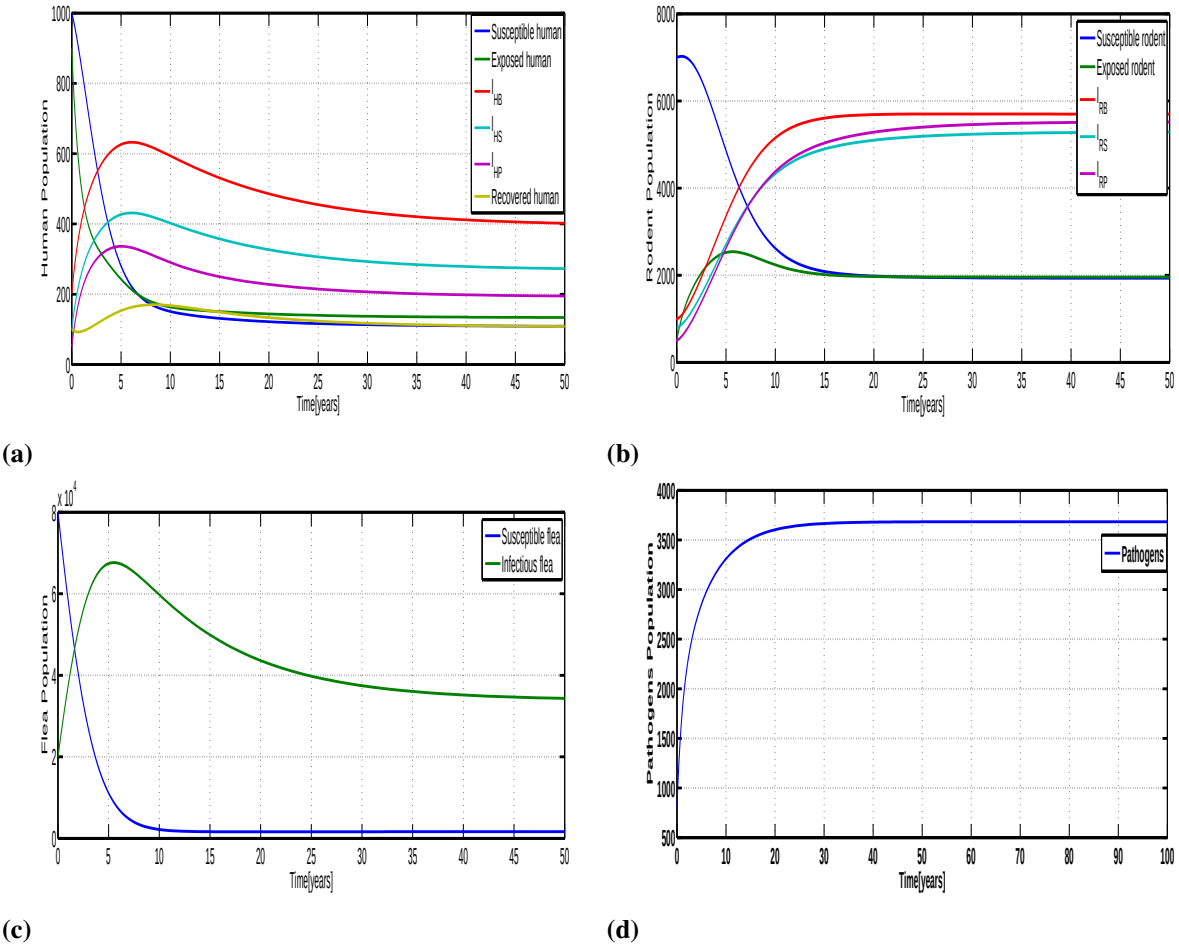


Figure 36: The dynamics of Human, Rodent, Flea and Pathogens in the environment with baseline parameter values given in Table 13.

The system consider vast ways of transmission between one individual to the other as it has all three forms of plague disease. But the infectious fleas still carries the very important role in the transmission and spread of plague disease (Bitam *et al.*, 2010). Fleas are the major player in the transmission of bubonic and septicemic plague. Which consequently makes it the very important agent in the transmission of plague disease.

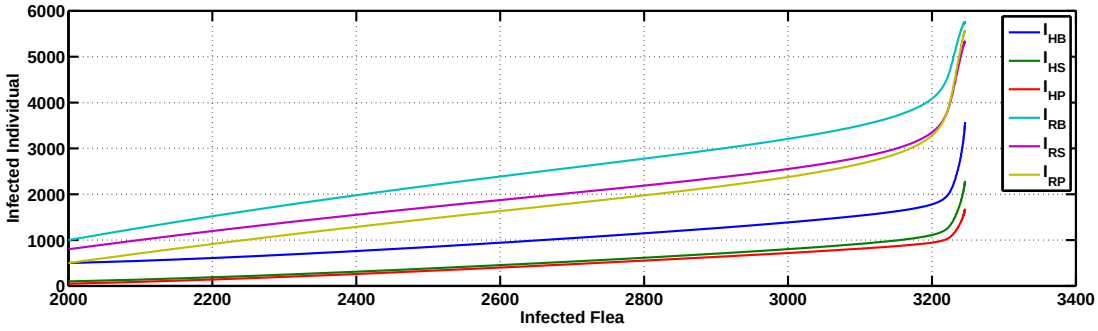
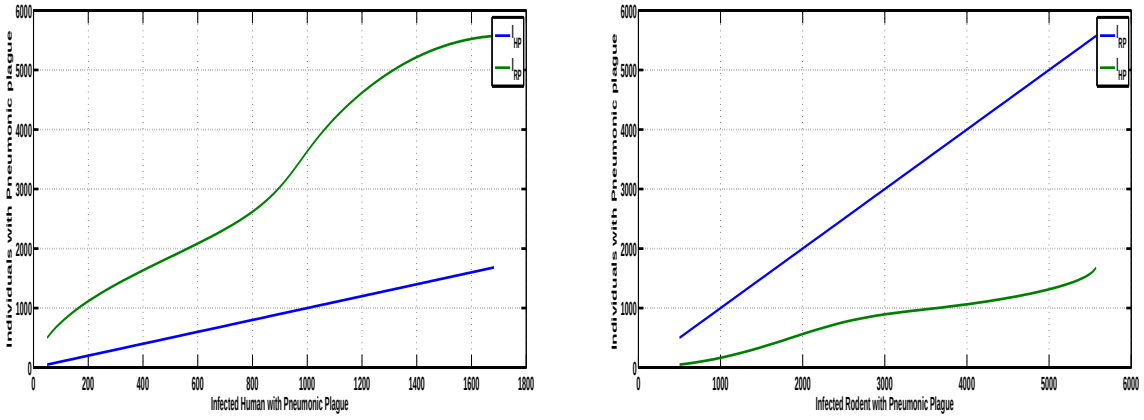


Figure 37: Effect of increased number of infected flea on Human and Rodent population.

Figure 37 illustrate the infect of flea to all three forms of plague in Human being and Rodent populations. Rodents being the primary host for the fleas, they are mostly affected by the infected flea followed by human population. In both populations, fleas mostly transmit bubonic plague followed by septicemic plague. Pneumonic plague in human and rodent shows to be least affected by the infected flea as the transmission is not direct. It depends on the progression of those with bubonic and septicemic plague if not treated they become Pneumonic plague infectives.

The increase of the number of individuals with pneumonic plague in both Human beings and Rodents is mainly due to the airborne transmission. An individual with pneumonic plague may cause infection within and outside the individual's population. Fig 38 shows the effect of increasing number of human beings and rodents with pneumonic plague to the human and rodent with pneumonic plague

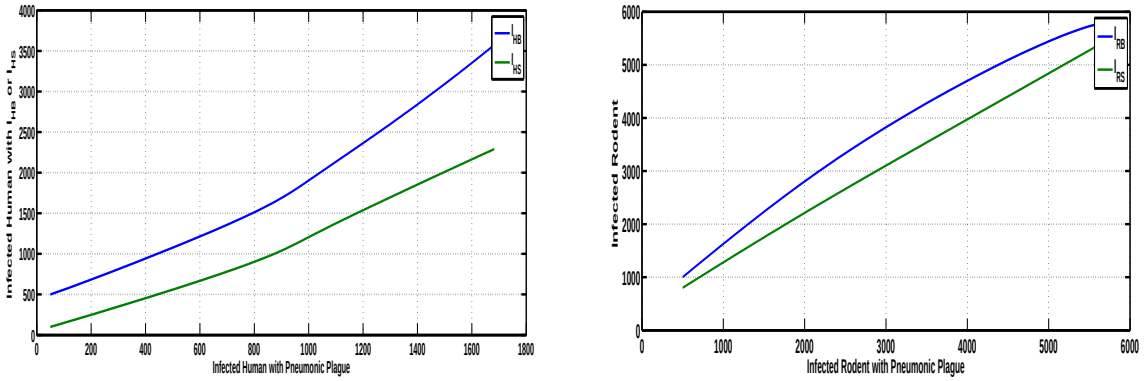


(a) **(b)**

Figure 38: Effect of increased number of Human and Rodent with pneumonic plague .

Increase of I_{HP} and I_{RP} is not limited to airborne transmission. When individuals with septicemic and bubonic are not treated, a fraction $\alpha_3\rho_1 I_{HB}$, $\gamma_3\phi I_{RB}$, $\gamma_4 I_{RS}$ and $\alpha_4\xi I_{HS}$ progresses and become pneumonic plague infectives. Figure 39 shows the effect of the increasing number of individuals with bubonic and septicemic plague in both human beings and rodents with

pneumonic plague.



(a) **(b)**

Figure 39: Effect of individual with I_{HB}, I_{HS},I_{RB} and I_{RS} to I_{HP} and I_{RP}.

The zoonotic nature of Plague gives it the very unique feature in terms of its spread and transmission. The force of infection in both human and rodent is positively affected by the increase of infection from the infectious flea and the pathogens in the environment. But it is also most significantly affected by the infection they transmit to one another.

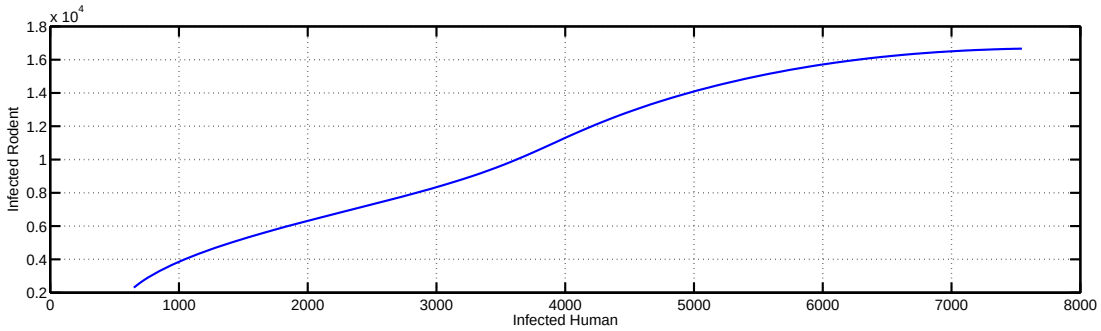


Figure 40: Effect of increased number of infected Human and Rodent.

Figure 40 shows the effect that infectious human and rodent have to one another. The figure shows a substantial effect that infectious rodent (plus other domestic animal) has to the infected human population and vice versa.

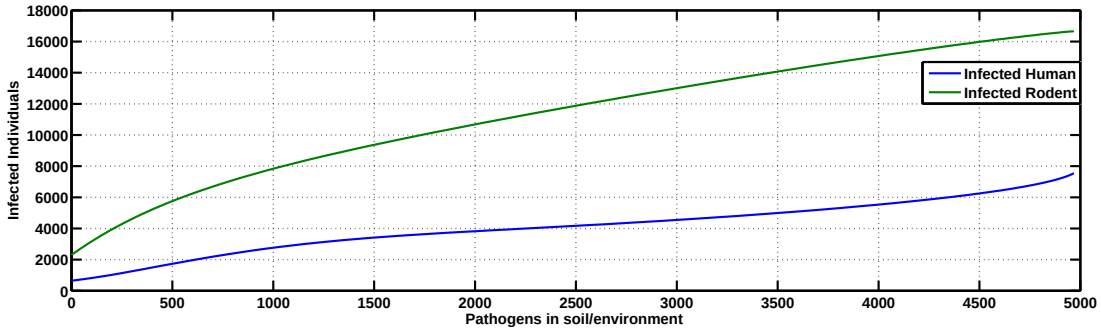


Figure 41: Effect of increased number of Pathogens in the environment to Human and Rodent.

When the environment is favorable, the pathogens grows in the natural condition. Pathogens in soil or air may infect a susceptible individuals upon a successful and adequate contact. Figure 41 shows the effects in the number of infected human and rodent as the number of pathogens in the environment increases. The prominence of A as the potential plague transmission agent depend solely on the weather condition. That is to say, when planning on the control strategies of plague disease especially when it is in pneumonic form much consideration should be on whether the condition is favorable or not for the pathogens to grow.

5.6.2 Sensitivity and Elasticity analysis of R_0,

We use sensitivity analysis to determine how the basic reproduction number (R_0) relates to changes in the parameters of the model. We also quantify the relative change in R_0 in response to the change in a parameter using the elasticity analysis. We use procedures described by Hartemink (2009) to study the sensitivity and elasticity of the basic reproduction number R_0 to the changes in elements k_{ij} or to the parameters in their expression.

Sensitivity

We define the sensitivity s_{ij} of a matrix K as the change in the basic reproduction number (R_0) in this case is the maximum modulus of the eigenvalues of the matrix K due to change in elements k_{ij} given by:

$$s_{ij} = \frac{\partial R_0}{\partial k_{ij}} \tag{46}$$

From the values s_{ij} we can forms a sensitivity matrix S_{ij}, obtained from the left and right eigenvectors of the next generation matrix corresponding to its dominant eigenvalue (Caswell, 2001).

The sensitivity of R_0 with respect to individual parameters $s(\lambda)$ is computed as:

$$s(\lambda) = \sum_{ij} \frac{\partial R_0}{\partial k_{ij}} \frac{\partial k_{ij}}{\partial \lambda} \tag{47}$$

Elasticity

The elasticity e_{ij} of a matrix element k_{ij} may also be obtained by:

$$e_{ij} = \frac{k_{ij}}{R_0} \frac{\partial R_0}{\partial k_{ij}} \tag{48}$$

For individual parameter the elasticity $e(\lambda)$ is given by

$$e(\lambda) = \frac{\lambda}{R_0} \sum_{ij} \frac{\partial R_0}{\partial k_{ij}} \frac{\partial k_{ij}}{\partial \lambda} \tag{49}$$

Table 14 shows the sensitivity and elasticity of the basic reproduction number R_0 for the given parameter values.

Table 14: Sensitivity and elasticity of R_0 for plague disease

Variable	**Sensitivity Index**	**Elasticity**
k_{21}	4.592	0.0001
k_{22}	56.467	1.123
k_{55}	50.462	1.123
k_{17}	202.805	0.318
k_{71}	15.603	0.297
k_{27}	64.41	0.072
k_{72}	-1.776	-0.029
k_{57}	-16.047	-0.017
k_{75}	3.302	0.081
k_{47}	43.174	0.061
k_{25}	-5.136	-0.103
k_{54}	-34.903	-0.004
k_{74}	3.913	0.065

From the Table 14 we can see the most sensitive element is the expected number of new cases of human infected with bubonic plague caused by one infected flea k_{17}. The most insensitive element is the expected number of new cases of rodent infected with septicemic plague caused by one infected untreated rodent with bubonic plague k_{54}. The positive sign entails that increasing (decreasing) of k_{ij} will result to the increase (decrease) the basic reproduction number. When the sensitivity index is negative it means that increasing (decreasing) one element while keeping the other constant decreases (increases) the value of basic reproduction number R_0 and hence decreases (increases) the persistence of plague disease. For example the sensitivity index of $k_{74} = 3.913$ indicates that increasing the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with bubonic plague by 10% will as a result increase the value of the basic reproduction number by 39%.

Figure 42 shows the the effect of the most sensitive element of the matrix K on the basic reproduction number. It entails that increasing (decrease) the expected number of

new cases of human infected with bubonic plague caused by one infected flea k_{17} consequently lead to the significant increase (decrease) on the basic reproduction number.

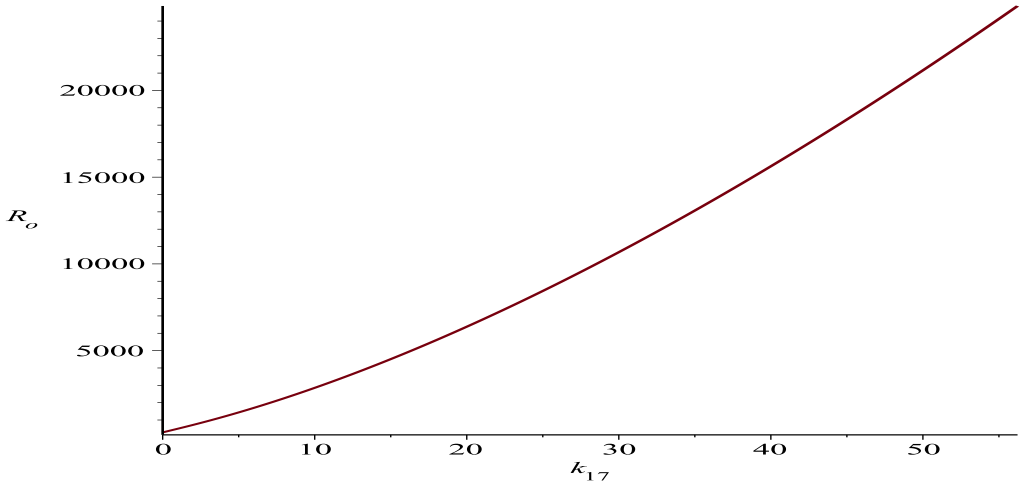
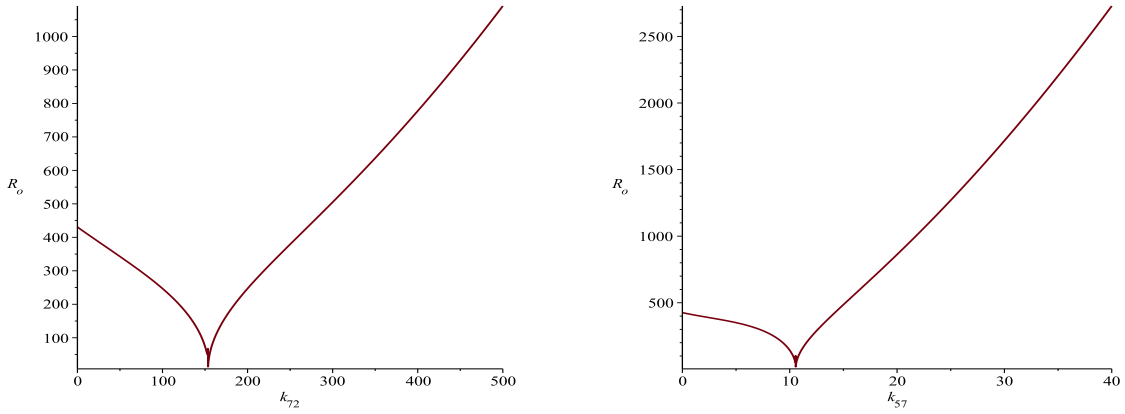
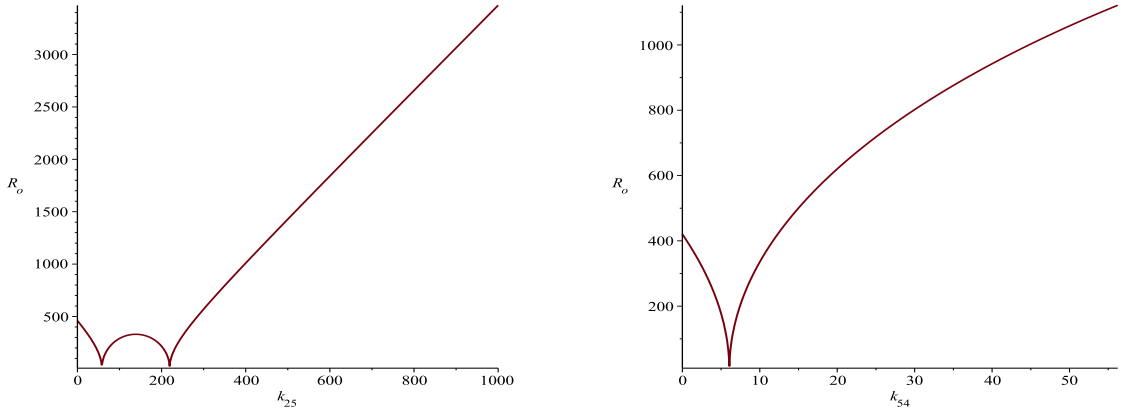


Figure 42: Effect of the most sensitive k_{17} on the basic reproduction number

Figure 43, shows the effect of k_{72}, k_{57}, k_{25} and k_{54} on the basic reproduction number R_O. We can see that, the k_{72}, k_{57}, k_{25} and k_{54} experience unstable endemic equilibrium when the values of k_{72} is between $[0\ \ 155]$, k_{57} is between $[0\ \ 15]$, k_{25} is between $[0\ \ 220]$ and k_{54} is between $[0\ \ 6]$ respectively. It then stabilize as the value of k_{72}, k_{57}, k_{25} and k_{54} increases above the stated interval. It is when the endemic is unstable where we can observe the sensitivity indices of k_{72}, k_{57}, k_{25} and k_{54} are negative and positive at some points. But when it is stable the sensitivity indices of each k_{ij} is positive. The results shows that when values of k_{ij} are positive, their increase lead to the increase of the value of the basic reproduction number as the element k_{ij} stands for expected number of new cases of i caused by one infected individual of j (Hartemink *et al.*, 2008).



(a) **(b)**

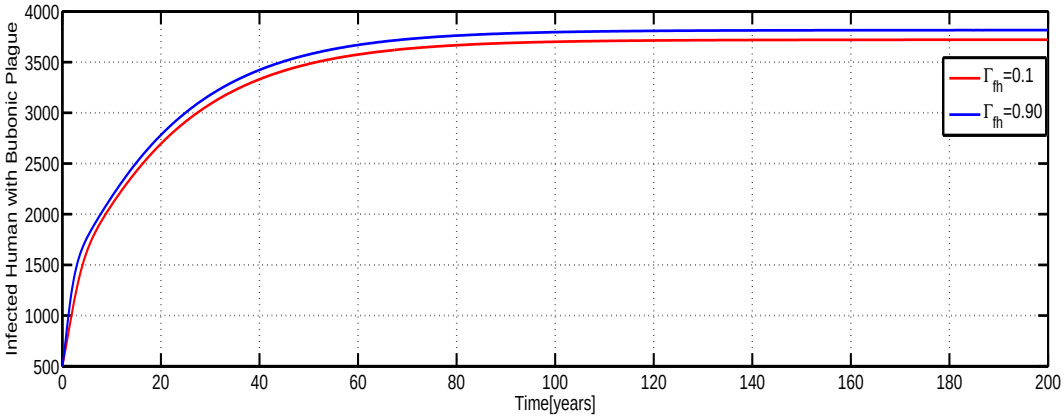


(c) **(d)**

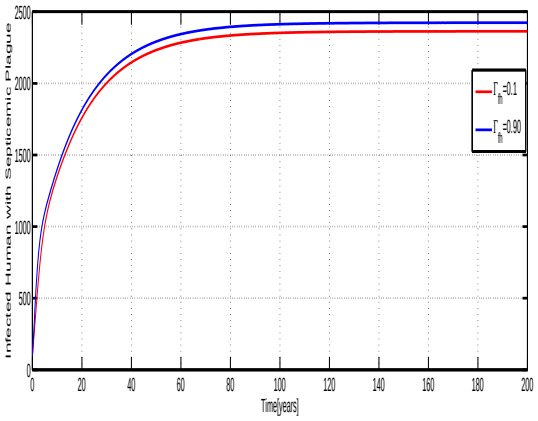
Figure 43: Effect of the most sensitive k_{ij} on the basic reproduction number.

The results also show that the expected number of new cases of human infected with bubonic plague caused by one infected flea is most sensitive to the basic reproduction number k_{17} depends mostly on the adequate contact between the susceptible human and the flea infested with pathogens. And as seen in Table 14 the increase in the adequate contact rate between the infected flea I_F and the susceptible human being (Γ_{fh}) will not only affect k_{17} but the entire basic reproduction number.

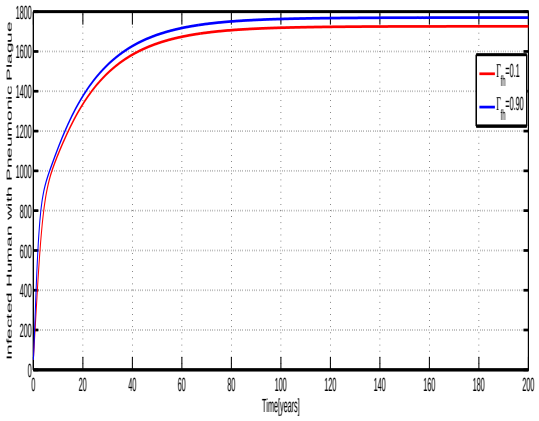
Machens *et al.* (2013) narrate that as we increase the adequate contact rate between the infected individuals and the susceptible, the number of infected classes also increase. Figure 44 shows the effect of the increased adequate contact rate between the flea infested with pathogens and the susceptible human being.



(a)



(b)



(c)

Figure 44: Effect of increased Γ_{fh} on the basic reproduction number.

Elements with large sensitive indices (especially those which constitute the basic reproduction number) should be considered first for the proper control strategy. Reducing the basic reproduction number in our case has the direct relation with reducing the individual element of the matrix K. Thus in order to have a disease free community we should work on reducing the number of individuals that an infected individual can affect in his/her entire life time. This is possible by always making $k_{ij} < 1$ which in turn will reduce the basic reproduction number of the plague disease.

Reducing the value of k_{ij} means touching several factors and parameters in the plague system model. It mainly entails reducing the contact rate between the infected and the susceptible individuals, reducing the infectious period of an individual and reducing the probability that individuals survive the incubation period. The strategies to reduce the contact rates must be based on the character of the pair of individuals under consideration . For example, we would do so by reducing the contact rate between the flea infested with pathogens and human or rodent. The best strategy will be fumigation in order to kill the infected fleas. The killing of the infected individuals in order to reduce contact rates may also work when it is between infected rodent and human and between flea and rodent. However when it is between human to human or between infected human to rodent, flea or the environment, fumigation may not be the best control strategy. The best strategy here may be either education or isolation.

5.7 Conclusion

In this work, we have developed and analyzed the deterministic SEIR model with modification for plague disease. We found the model is well posed and defined in the feasible region where disease free equilibrium points is found and the stability is examined. We use sensitivity and

elasticity analysis and numerical simulation to study the effect of most sensitive k_{ij} elements and the parameters to the transmission and spread of the disease.

The model analysis reveals that the expected number of secondary cases produced by a single infected individual during the entire infectious period of that particular individual into a completely susceptible population depends on several k_{ij}. It then entails that in order to be able to control the disease stakeholders should work on reducing the expected number of new cases of human infected with septicemic plague caused by one infected human with bubonic plague k_{21}, the expected number of new cases of human infected with septicemic plague caused by one infected human with septicemic plague k_{22}, the expected number of new cases of human infected with bubonic plague caused by one infected flea k_{17}, the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with septicemic plague k_{55}.

The endemicity of the disease may also be reduced by reducing the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected human with bubonic plague k_{71}, the expected number of new cases of human infected with septicemic plague caused by one infected flea k_{27}, the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected human with septicemic plague k_{72}, the expected number of new cases of rodent infected with septicemic plague caused by one infected flea k_{57}, the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with septicemic plague k_{75}, the expected number of new cases of rodent infected with bubonic plague caused by one infected flea k_{47}, the expected number of new cases of human infected with septicemic plague caused by one infected rodent with septicemic plague k_{25}, the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with bubonic plague k_{54} and the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with bubonic plague k_{74}.

From the analysis, it may be postulated that preventive measures, through reducing contact rates between the infected and susceptible individuals is necessary in order to control the disease. That is reduction of the contact rates will consequently reduce the transmission rates which in turn will lead to lower prevalence of the plague disease.

CHAPTER SIX

The Effect of Seasonal Weather Variation on the Dynamics of the Plague Disease [5]

Abstract: Plague is an historic disease which is also known to be the most devastating diseases ever occurred in human history, caused by gram -negative bacteria known as *Yersinia pestis*. The disease is mostly affected by variations of weather conditions as it disturb the normal behaviour of main plague disease transmission agents namely human beings, rodents, fleas and pathogens in the environment. This in-turn changes the way they interact with each other and ultimately lead to a periodic transmission of plague disease. In this paper we formulate a periodic epidemic model system by incorporating seasonal transmission rate in order to study the effect of seasonal weather variation on the dynamics of plague disease. We compute the basic reproduction number of a proposed model. We then use numerical simulation to illustrate the effect of different weather dependent parameters on the basic reproduction number. We are able to deduce that infection rate, progression rates from primary forms of plague disease to more severe forms of plague disease and the infectious flea abundance affect to a large extent the number of bubonic, septicemic and pneumonic plague infectives. We recommend that it is more reasonable to consider these factors that have shown to have a significant effect on R_T for effective control strategies.

Key words: Pneumonic plague; seasonal weather variation; Periodic-epidemic systems; Periodic transmission; septicemic plague; Evolution operator of periodic system; bubonic plague; Time averaged reproduction number; Periodic-force of infection

6.1 Introduction

Plague is the ancient disease caused by the bacterium *Yersinia pestis* and has had a splendid effects on human societies throughout the history (Wagner *et al.*, 2014). Dynamics of plague disease is the result of complex interactions between human beings, rodent population, flea population and pathogens in the environment. Seasonal variation particularly temperature, humidity, rainfall and precipitation greatly affect the normal transmission capacity of plague disease either by lowering it or rising it. It affects pathogen in the environment, fleas, rodents and even human behavior by altering their normal immigration rate, death rate, survival rate and infectious capability (Altizer *et al.*, 2006).

[5]This chapter is based on a research paper: Rigobert C. Ngeleja, Livingstone S. Luboobi, and Yaw Nkansah-Gyekye, "The Effect of Seasonal Weather Variation on the Dynamics of the Plague Disease," *International Journal of Mathematics and Mathematical Sciences*, vol. 2017, Article ID 5058085, 25 pages, 2017. https://doi.org/10.1155/2017/5058085.

6.1.1 Seasonality in flea development stages and behavior

Flea's survival is greatly affected by temperature and relative humidity (Cavanaugh and Marshall, 1972). The ecto-thermic characteristic of flea make them very sensitive to temperature fluctuations. *Xenopsylla cheopis* is the primary vector flea for Yersinia pestis. It is significantly affected by seasonal weather variation as most of its life stages depend on temperature, humidity and precipitation. The rate of metamorphosis of this kind of flea from egg to adult is also regulated by temperature.

Flea larvae feed on almost any organic debris but mostly they feed on adult excreta which consist of relatively undigested blood (Silverman *et al.*, 1981). These adult fecal matter when dried they falls from the host to serve as food for the larvae. Thus the availability of food (dried flea dirt) for a larvae to feed depends on the weather condition particularly temperature and humidity. The larvae develop well in areas where the relative humidity greater than 75 percent and the temperature between 21^0C and 32^0C (Zentko and Richman, 1997; Cavanaugh, 1971). At constant temperature flea becomes most sensitive to air saturation, and are massively killed when the air saturation is insufficiency (Bacot and Martin, 1924). The fact that all immature flea stages occur outside the host; development rates of flea increase with temperature until it reaches a critical value which makes flea most vulnerable. High temperature combined with low humidity hinders flea's survival at immature stages (Gage *et al.*, 2008).

The condition where relative humidity is below 50% is unfavorable for flea growth. It is at this condition the biting rate of flea onto the infected human and rodent or of the infected flea onto the susceptible human and rodent is significantly low. But when the relative humidity is 80% the flea becomes very active and as a result the biting rate and infection increase significantly. More over when temperature is above 27.5^0C the rapid disappearance of plague bacilli from the flea stomach occur, resulting in reduced rates of plague disease transmission. This in turn reduce the flea's efficiency in its ability to transmit the plague bacillus to human beings and rodents (Enscore *et al.*, 2002; Brooks, 1917)

When fleas are in rodent burrows, their survival of immature stages is affected by soil moisture that is partly controlled by outside precipitation (Eisen and Gage, 2009). As the way of getting rid of detrimental moisture losses and temperature swings, rodent normally shift to start living underground (Krasnov *et al.*, 2001*b*). On the other hand, when attached with a high organic load, excessively wet conditions in rodent burrows (e.g., relative humidity 95%) can stimulate the growth of destructive fungi that diminishes flea's larval and egg survival (Parmenter *et al.*, 1999).

Different studies justify the negative correlation between rainfall and plague epidemics. For example Cavanaugh and Marshall (1972) reported that areas where drains are absent, or where drainage is insufficient as a result of soil composition or impoundments of water, flooding unquestionably causes a drop in the flea population. In areas with improved drainage, such as those with sandy soils, the lessening of the flea population is minimal. Precipitation also influence plague infection for it influences the concentration of rodents, fleas and humans in the same shelter.

6.1.2 Seasonality in rodents

The direct effect posed on rodent population due to temperature change is minor. This is due to the fact that rodents are homoeothermic and hence do not respond immediately to changes in ambient temperatures (Korslund and Steen, 2006). Temperature indirectly affects the spread of plague in rodent population in different ways as follows: at a low mean temperature of 10^0C the bacteria within host (rodent) becomes very active as a result a large number of infected rodent die before even the plague bacilli appear in their blood. At this particular temperature rodent also lose the ability to infect other susceptible individuals.

Rainfall may pose positive or negative effect on the increase of rodent population depending on it's intensity (Eisen and Gage, 2009). A season of moderate rainfall may be considered to affect positively the increase of rodent abundance but when the amount of rainfall is extremely heavy it results in a tremendous rodent population decline (Roberts *et al.*, 2008). When it is moderate and upon a proper timing, rainfall may foster the increase of rodent population (Cavanaugh and Marshall, 1972). This is due to the fact that rodent's reproduction period normally follow wet seasons (Jaksic and Lima, 2003; Meserve *et al.*, 2001; Letnic *et al.*, 2005). That is to say the increase of rodent population during wet period is expected to be higher than during the dry seasons. This clearly concur with the result in the study by Leirs *et al.* (1996), which narrates that in Tanzania, rodent population densities show clear association with the annual rainfall and its seasonal distribution. However when rainfall is of high intensity, it causes flooding of rodent burrows. Large number of rodents population die and the remaining ones normally move from forest to the households where they can protect themselves (Gage *et al.*, 2008; Dickman *et al.*, 1999; Cavanaugh and Marshall, 1972). In other cases, increased precipitation or drought stalwartly disturb rodent population dynamics, as it deters food availability.

6.1.3 Seasonality in pathogens in the environment

When the bacteria are in lungs, the transmission of *Yersinia pestis* is possible through various ways: Contact transmission, in which one may be infected through physical contact with respiratory particles on the infected surface; Airborne transmission, which is through inhaling the bacteria causing the disease through successive contact with the nose or mouth of an infected individual; Respiratory particles, which is through respiratory droplets which is through shedding of respiratory particles (i.e., droplets or aerosols) from an infected human or rodent into the environment (Agar *et al.*, 2009).

Extreme temperatures regularly are ruinous to the survival of pathogens causing plague. The changes in temperature may lead to varying effects on the pathogens in the environment and vectors that lives in an environment. When the mean temperature approaches the maximum limit that can be endured by the pathogens, a small increase in temperature may be very dangerous to the pathogen survival. Conversely when pathogens are in the environment characterized by low mean temperature, a small increase in temperature may result in increased development, incubation and replication of the pathogen in the environment (Krasnov *et al.*, 2001*a*, 2002).

Davis (1953) compared the seasonal incidence of plague with usual atmospheric conditions in particular temperature and rainfall. It was depicted that human plague is more frequent in warm moist weather between $15^0C - 27^0C$ than in hot dry (over 27^0C), or cold weather (under 15^0C). Mitscherlich and Marth (2012) narrates that the solar exert a detrimental effect on bacterial aerosol and the decay rate of *Yersinia pestis* is proportion to the increase of UV light.

The reports by Ayyadurai *et al.* (2008) and Mollaret (1964) justifies the ability of the *Yersinia pestis* to culture the organism from deep within contaminated soil. Eisen *et al.* (2008) was able to show the great potential durability of *Yersinia pestis* in the soil substrate. The long duration of their survival in the soil supports indirectly the virulence maintenance.

Yersinia pestics, exhibit a very slow growth at the temperature between $35^0C - 37^0C$ but they grow very fast at the temperature 28^0C. They die very rapid if exposed to a UV light, temperature exceeding 40^0C or when exposed to intensive desiccation (Nozadze *et al.*, 2015; Koirala, 2006; Brubaker, 1972). Bacteria decrease their sensitivity when the level of humidity drops below 76% (Mitscherlich and Marth, 2012).

When an infected individual coughs or sneezes, thousands of the bacteria are released in air (Stenseth *et al.*, 2008). The released respiratory particles may be large and heavy that they can't remain suspended in the air. When respiratory particles are large the transmission can only occurs when these particles are expelled directly onto another close susceptible individual.

In some cases the release of smaller respiratory particles may occur; this is when the airborne transmission is possible. The smaller released particles are easily suspended in the air respired (i.e., pass into the lower respiratory tract) (Bevelacqua and Stilp, 2009).

Relative humidity and temperature affect the transmission of *yersinia pestis* from one individual to the other. Humidity affects the size of the respiratory particle (Meyer, 1961). When humidity is low the large drops partially evaporate to create smaller, lighter drops that are more likely to remain airborne for extended periods of time (Rose *et al.*, 2003). This is to say, when the air is sufficiently dry, the large sized particles shrink to a size that favours long-range transport which in turn leads to increased infection.

6.1.4 Seasonality in Human behavior

Human activities and behavior in plague-infected areas are also to be considered as important determinants of plague transmission to and by humans (Hunter, 2003). When occurrences of plague are due to human intrusions in natural plague areas, it is thus important to consider season variation as a second order variable that influences disease incidence through human behavior. In Tanzania, drought and famine which are the result of lack of rainfall and temperature fluctuation have a great impact to the farmers and pastoralists as it forces them to move from one area to another searching for food for themselves and their cattle. These human intrusions from one place to another may lead to the increase of plague disease transmission in rodents, fleas, human population and pathogens in the environment.

6.2 Model Formulation

We describe the complex interaction that leads to plague disease transmission and use it to formulate a model for the dynamics of the plague disease coupled with the effect of seasonal weather variation in its transmission. The model includes four populations namely human beings, rodents, fleas and pathogens in the environment. We generally assume that all individuals from each population are susceptible to the disease, the recovered individuals confer temporary immunity and return to be susceptible again, the infectious are all individuals with either bubonic plague, pneumonic or septicemic plague.

6.2.1 Variables and Parameters used in the model

In this section we present variables and parameters, their description and their values as used in the model. We obtained the parameter values from the literature that relate to this study, the present information on plague disease and through estimation using sensitivity analysis and simulations.

Table 15: Variables and their description for plague disease with weather variation.

Variable	Description
S_H	Susceptible Human population
E_H	Exposed human population
I_{HB}	Infectious human population infected with with bubonic plague
I_{HS}	Infectious human population with septicemic plague
I_{HP}	Infectious human population with Pneumonic plague
R_H	Recovered Human population
S_R	Susceptible rodents
E_R	Exposed rodents
I_{RB}	Infectious rodents with bubonic plague
I_{RS}	Infectious rodents with septicemic plague
I_{RP}	Infectious rodents with pneumonic plague
S_F	Susceptible fleas
I_F	Infected fleas
A	Pathogens in the soil/environment

Table 16: Parameters and their description for plague disease with weather variation.

Parameters	Description	Value	Reference/Source
$\Gamma_{rbf}(t)$	Adequate contact rate: between I_{RB} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{rsf}(t)$	Adequate contact rate: between I_{RS} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{fh}(t)$	Adequate contact rate: between I_F and human	0.0641	Eisen *et al.* (2007)
$\Gamma_{fr}(t)$	Adequate contact rate: between I_F and rodent	0.0641	Eisen *et al.* (2007)
$\Gamma_{hph}(t)$	Adequate contact rate: between I_{HP} and S_H	0.39	Estimated
$\Gamma_{hsh}(t)$	Adequate contact rate: between I_{HS} and S_H	0.12	Estimated
$\Gamma_{rbh}(t)$	Adequate contact rate: between I_{RB} and S_H		
$\Gamma_{rph}(t)$	Adequate contact rate:between I_{RP} and S_H	0.19	Estimated
$\Gamma_{rsh}(t)$	Adequate contact rate: between I_{RS} and S_H	0.21	Estimated
α_1	Progression rate of S_H to E_H population	0.99	Estimated
α_2	Progression rate out of E_H to infectious state	0.23	Gani and Leach (2004)
$\rho_1\alpha_3$	Progression rate out of I_{HB} to I_{HP}		
$\rho_2\alpha_3$	Progression rate out of I_{HB} to R_H		
$\rho_3\alpha_3$	Progression rate out of I_{HB} to I_{HS}		
δ_{1b}	Disease induced death rate of I_{HB}	0.04	Keeling and Gilligan (2000*a*)
α_4	Progression rate out of I_{HS} to I_{HP} and R_H	0.06	Estimated
δ_{1s}	Disease induced death rate of I_{HS}	0.04	Estimated
α_5	Progression rate out of I_{HP} to R_H	0.4	Gani and Leach (2004)
δ_{1p}	Disease induced death rate of I_{HP}	0.63	Kugeler *et al.* (2015)
γ_1	Progression rate of S_R to E_R	0.92	Estimated

Continued on next page

Table 16 – *Continued from previous page*

Parameters	Description	Value	Reference/Source
$\Gamma_{hbf}(t)$	Adequate contact rate: between I_{HB} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{hsf}(t)$	Adequate contact rate: between I_{HS} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{rpr}(t)$	Adequate contact rate: between I_{RP} and S_R	0.9	Estimated
$\Gamma_{rsr}(t)$	Adequate contact rate: between I_{RS} and S_R	0.9	Estimated
$\Gamma_{hpr}(t)$	Adequate contact rate: between I_{HP} and S_R	0.00005	Estimated
$\Gamma_{hsr}(t)$	Adequate contact rate: between I_{HS} and S_R	0.00008	Estimated
γ_2	The rate at which rodent become infectious	0.98	Estimated
γ_3	Progression rate out of I_{RB} to I_{RS} and I_{RP}	0.194	Tollenaere *et al.* (2010)
δ_{3b}	Disease induced death rate of I_{RB}	0.1	Estimated
γ_4	Progression rate out of I_{RS} to I_{RP}	0.05	Estimated
δ_{3s}	Disease induced death rate of I_{RS}	73	Tollenaere *et al.* (2010)
δ_{3p}	Disease induced death rate of I_{RP}	0.14	Estimated
ϖ	Progression rate of R_H to S_H	0.33	Kugeler *et al.* (2015)
μ_1	Natural death rate for Human being	0.04	Keeling and Gilligan (2000*a*)
μ_2	Natural death rate for Flea	0.2	Bacot and Martin (1924)
μ_3	Natural death rate for rodent	1	Morand and Harvey (2000)
$\omega_1(t)$	Adequate contact rate: A and Human being		
$\omega_2(t)$	Adequate contact rate: A and rodent		
$\eta_1(t)$	Recruitment rate of A by I_{HP}	0.2	Estimated
$\eta_2(t)$	Recruitment rate of A by I_{RP}	0.4	Estimated
μ_4	Natural death rate for Pathogens	0.1	Estimated
ψ_1	Recruitment rate of human beings	0.09	Estimated
ψ_2	Recruitment rate of fleas		
ψ_3	Recruitment rate of rodents		

6.2.2 Model description

The human population is divided into six subgroups: the subgroup of people who have not contracted the disease to be referred to as susceptible and denoted by S_H but may get it if they get into contact with I_{HS}, I_{HP}, I_{RS}, I_{HP}, I_F or A, People who have the disease but haven't shown any symptom and incapable of transmitting the disease to be referred to as Exposed and denoted by E_H; those who are infected and capable of transmitting the disease are divided into three subgroups: there are those who have bubonic plague denoted by I_{HB}, those with septicemic plague denoted by I_{HS} and those who have Pneumonic plague disease denoted by I_{HP}. The fraction of population in I_{HB} if treated may recover and move to subgroup R_H otherwise they progress either to a septicemic disease infectives I_{HS}, or to pneumonic plague disease infective I_{HP} or else they die. The population in the subgroup I_{HS} if treated they recover and progress to the subgroup R_H and if not treated they progress and join subgroup I_{HP} otherwise they die. The population of the subgroup I_{HP} is considered as a very dangerous stage of plague disease, it is very fatal stage of plague disease with the fatality rate of about 100%, however if treated they recover and join subgroup R_H otherwise they die. So the total

human population N_1 is as given by (1);

$$N_1 = S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H \tag{1}$$

Fleas are divided into two sub-groups, those who have not contracted the disease but may get it if they get in contact with infectious agent (rodent or human) referred to as susceptible flea and denoted by S_F and those who are infected and are capable of transmitting the disease referred to as infectives and denoted by I_F. The total flea population N_2 is as given by (2)

$$N_2 = S_F + I_F \tag{2}$$

The rodents are divided into five sub-groups: those who have not contracted the disease but may get it if they get in contact with I_{HS}, I_{HP}, I_{RS}, I_{HP}, I_F or A, referred to as susceptible rodents and denoted by S_R; those who have the disease but haven't shown any symptom and incapable of transmitting the disease referred to as Exposed and denoted by E_R, those who are infected and capable of transmitting the disease are divided into three subgroups, there are those who have bubonic plague denoted by I_{RB}, those with septicemic plague denoted by I_{RS} and those who have Pneumonic plague I_{RP}. The fraction of population in I_{RB} may progress to either a septicemic plague disease infectives I_{RS}, or to preneumonic plague disease infectives I_{RP}. The rodent population in the subgroup I_{RS} may either progress to preneumonic plague disease infectives I_{RP} otherwise they die. The population in the subgroup I_RP is considered as a very dangerous stage of plague disease and very fatal so the mortality due to disease in this subgroup is approximated to be 100% . Then the total rodent population N_3 is as given by (3)

$$N_3 = S_R + E_R + I_{RB} + I_{RS} + I_{RP} \tag{3}$$

The individuals with pneumonic plague may release pathogens causing plague disease to the environment denoted by A through coughing or sneezing. When the condition in soil/environment is favorable, pathogens may remain infectious in the environment for long time. When a susceptible individual adequately interact with the environment infested with *yersinia pestis* gets the disease even in the absence of any vector.

6.2.3 Description of interactions

The susceptible fleas in sub-group S_F get *Yersinia pestis* bacteria through biting the infected rodent I_{RB} or I_{RS} who are the primary reservoir for the bacteria and become infected at the rates Γ_{rbf} and Γ_{rsf} respectively. Flea may also get the disease when they bite the infected human being with bubonic plague I_{HB} or septicemic plague I_{HS} at the rates Γ_{hbf} and Γ_{hsf} respectively. Thus the flea population gets plague infection with the force of infection given in

(4)

$$G_3(t) = \frac{\Gamma_{hbf}(t)I_{HB} + \Gamma_{hsf}(t)I_{HS}}{N_1} + \frac{\Gamma_{rbf}(t)I_{RB} + \Gamma_{rsf}(t)I_{RS}}{N_3} \quad (4)$$

The human population may get the disease in one of the following ways: when the infected flea I_F bites and infect the susceptible human being S_H at a rate Γ_{fh}, when they interact with one another; this can be with either a person with pneumonic plague I_{HP} through airborne transmission or septicemic plague I_{HS} through physical or sexual contact at the rates Γ_{hph} and Γ_{hsh}, respectively. Other infection is through airborne transmission through interaction with rodent infected with pneumonic plague I_{RP} or through touching or eating the infected rodent with septicemic plague I_{RS} at rates of Γ_{rph} and Γ_{rsh}, respectively. Human beings may also get the infection from the environment when they breath in the bacteria or physically contact the infected material at the rate of ω_1. This is to say human population acquire plague disease following effective contact with infected human, rodent, flea and the environment with force of infection G_1 given by (5)

$$G_1(t) = \frac{\Gamma_{hph}(t)I_{HP} + \Gamma_{hsh}(t)I_{HS}}{N_1} + \Gamma_{fh}(t)\frac{I_F}{N_2} + \frac{\Gamma_{rph}(t)I_{RP} + \Gamma_{rsh}(t)I_{RS}}{N_3} + \omega_1(t)A \quad (5)$$

The subgroup S_H, after the infection, progress and become latent to the disease at a rate α_1. After 2 to 7 days the sub-groups E_H become infected into one of the three infectious classes I_{HB}, I_{HS} or I_{HP} (depending on the mode of transmission an individual is exposed to) and capable of transmitting the disease. The proportional of E_H progress and become infected by bubonic plague I_{HB}, septicemic plague I_{HS} or Pneumonic plague I_{HP} at the rate α_2 and proportional to ν_1, ν_2 or ν_3 respectively. If the individuals in the compartment I_{HB} get treatment they would recover and move to sub-group R_H at a rate α_3 otherwise they either progress to subgroups I_{HP} or I_{HS} at a rate α_3 or die either naturally at a rate μ_1 or due to the disease at a rate δ_{1b}. The fraction of human with septicemic plague I_{HS} if treated they recover at a rate α_4 and join R_H otherwise they either progress to subgroup I_{HP} at a rate α_4 or die due to the disease at a rate δ_{1s} or naturally at a rate μ_1. The compartments I_{HP} if treated they recover at a rate α_5 otherwise they die either naturally at a rate μ_1 or due to the disease at a rate δ_{1p}. The subgroup R_H attain temporally immunity then return and become susceptible S_H at a rate ϖ.

The rodent population may get a disease in one of the following ways: when the infected flea I_F bites and infect the susceptible rodent S_R at a rate Γ_{fr}, through interaction between rodent themselves, which may be with rodent infected by pneumonic plague I_{RP} or septicemic plague I_{RS} at the rates Γ_{rpr} and Γ_{rsr}, respectively. The other infection may be through interaction with human infected with either pneumonic plague I_{HP}, or septicemic plague I_{HS} at a rates of Γ_{hpr} and Γ_{hsr}, respectively. When the susceptible rodent sufficiently interact with the pathogens in environment through breathing in the bacteria or physically touch the infected material gets the infections at the rate of ω_2. Rodent also gets the disease through adequate interaction with

Rodent, Human, Flea and Pathogens in the environment with force of infection G_2 given by (6)

$$G_2(t) = \frac{\Gamma_{hpr}(t)I_{HP} + \Gamma_{hsr}(t)I_{HS}}{N_1} + \Gamma_{fr}(t)\frac{I_F}{N_2} + \frac{\Gamma_{rpr}(t)I_{RP} + \Gamma_{rsr}(t)I_{RS}}{N_3} + \omega_2(t)A \quad (6)$$

The subgroup S_R, after the infection, they progress and become latent to the disease at a rate γ_1. After 2 to 7 days the sub-groups E_R become infected and capable of transmitting the disease, the fraction of it progress and become infected by bubonic plague I_{RB}, septicemic plague I_{RS} or Pneumonic plague I_{RP} at the rate γ_2 and proportional to τ_1,τ_2 or τ_3 respectively. The rodent in subgroup I_{RB} may either progress to subgroups I_{RP} or I_{RS} at a rate γ_3 or die either naturally at a rate μ_3 or due to the disease at a rate δ_{3b}. The compartment I_{RS} may either progress to I_{RP} at a rate γ_4 or die due to a disease at a rate δ_{3s} or naturally at a rate μ_3 and the compartments I_{RP} die either naturally at a rate μ_3 or due to the disease at a rate δ_{3p}.

With regard to the pathogens in the environment, we assume that the adequate interaction with S_H and S_R has a negligible effect on the dynamics of pathogens population size in the environment. The pathogens in the environment are populated at a constant rate λ_4. The infected human with pneumonic plague I_{HP} and Rodent with pneumonic plague I_{RP} also populate the environment A with the bacteria at the rate η_1 and η_2 respectively. Thus the environment is populated with pathogens causing plague disease with the force of infection G_4 given by (7)

$$G_4(t) = \lambda_4(t) + \eta_1(t)\frac{I_{HP}}{N_1} + \eta_2(t)\frac{I_{RP}}{N_3} \quad (7)$$

The pathogens within the environment suffer natural mortality at a rate μ_4. Human population in sub-groups S_H and E_H, flea population in sub-group S_F and rodent population in sub-groups S_R and E_R suffer natural mortality at rates μ_1, μ_2 and μ_3 respectively. The compartments I_{HB}, I_{HS}, I_{HP} , I_F, I_{RB}, I_{RS} and I_{RP} suffer both natural death at the rates μ_1, μ_2 and μ_3 and disease induced mortality at rates δ_{1b}, δ_{1s}, δ_{1p}, δ_2, δ_{3b}, δ_{3s} and δ_{3p} respectively. Human, Flea and rodent are recruited at the rate ψ_1, ψ_2 and ψ_3 respectively.

6.2.4 Model Equations for Plague Disease

Now we assume that the variation of infection capability from one individual to the other, migration of individuals from one place to another, recruitment and death rates of individuals in different stages due to seasonal weather variation affect only the rate at which the disease is transmitted from one infected individuals to the other. We now use the variables and parameters and their description given in Table 15 and Table 16 and the description of interactions we drive the following system of differential equations as given in (8) - (11).

Human beings

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1 G_1(t) S_H - \mu_1 S_H, \tag{8a}$$
$$\frac{dE_H}{dt} = \alpha_1 G_1(t) S_H - \alpha_2 E_H - \mu_1 E_H, \tag{8b}$$
$$\frac{dI_{HB}}{dt} = \alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB}, \tag{8c}$$
$$\frac{dI_{HS}}{dt} = \alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS}, \tag{8d}$$
$$\frac{dI_{HP}}{dt} = \alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP}, \tag{8e}$$
$$\frac{dR_H}{dt} = \alpha_3 \rho_2 I_{HB} + \alpha_4 (1 - \xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H. \tag{8f}$$

Rodents

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1 G_2(t) S_R - \mu_3 S_R, \tag{9a}$$
$$\frac{dE_R}{dt} = \gamma_1 G_2(t) S_R - \gamma_2 E_R - \mu_3 E_R, \tag{9b}$$
$$\frac{dI_{RB}}{dt} = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \tag{9c}$$
$$\frac{dI_{RS}}{dt} = \gamma_2 \tau_2 E_R + \gamma_3 (1 - \phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}, \tag{9d}$$
$$\frac{dI_{RP}}{dt} = \gamma_2 \tau_1 E_R + \gamma_3 \phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \tag{9e}$$

Fleas

$$\frac{dS_F}{dt} = \psi_{2s} - \beta G_3(t) S_F - \mu_2 S_F, \tag{10a}$$
$$\frac{dI_F}{dt} = \beta G_3(t) S_F - (\mu_2 + \delta_2) I_F \tag{10b}$$

Pathogens

$$\frac{dA}{dt} = \lambda_4(t) + \frac{\eta_1(t) I_{HP}}{N_1} + \frac{\eta_3(t) I_{RP}}{N_3} - \mu_4(t) A. \tag{11}$$

6.3 Basic properties of the model

In this section, we discuss the feasible region and positivity of the plague disease model. For convenience purpose and easy presentation of the result we let C denote all continuous functions on the real line. If f is a periodic function in C then we use $\overline{f}$ for the average value of f on time interval $[0, T]$ defined by (12).

$$\overline{f} = \frac{1}{T} \int_0^T f(t) dt \tag{12}$$

for a continuous T - periodic function $f(t)$.

6.3.1 Invariant region

Plague disease affects Human, Rodent, Flea and pathogens in the environment populations. For the possible modeling process all state variables and parameters of the model must be non-negative for $\forall t \geq 0$. We thus need to verify whether the solution of the model system (8) - (11) are in suitable feasible region where all state variables are positive. Inspired by Dumont *et al.* (2008) and Mpeshe *et al.* (2014) we first write the system (8) - (11) in the following compact form

$$\frac{dX}{dt} = A(x)X + F \tag{13}$$

where $X = (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A)^T$, $A(x)$ is a 14×14 matrix and F is a column vector.

We then have

$$A(x) = \begin{pmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{pmatrix} \tag{14}$$

where

$$\mathbf{A_{11}} = \begin{pmatrix} -g_1 & 0 & 0 & 0 & 0 & \varpi & 0 \\ \alpha_1 G_1(t) & -(\alpha_2+\mu_1) & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha_2\nu_2 & -a_1 & 0 & 0 & 0 & 0 \\ 0 & \alpha_2\nu_3 & \rho_3\alpha_3 & -a_2 & 0 & 0 & 0 \\ 0 & \alpha_2\nu_1 & \rho_1\alpha_3 & \alpha_4\xi & -a_3 & 0 & 0 \\ 0 & 0 & \rho_2\alpha_3 & \alpha_4(1-\xi) & \alpha_5 & -(\varpi+\mu_1) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -g_2 \end{pmatrix} \tag{15}$$

$$\mathbf{A_{12}} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{16}$$

$$\mathbf{A_{22}} = \begin{pmatrix} -(\gamma_2+\mu_3) & 0 & 0 & 0 & 0 & 0 & 0 \\ \gamma_2\tau_3 & -a_4 & 0 & 0 & 0 & 0 & 0 \\ \gamma_2\tau_2 & \gamma_3(1-\phi) & -a_5 & 0 & 0 & 0 & 0 \\ \gamma_2\tau_1 & \gamma_3\phi & \gamma_4 & -(\mu_3+\delta_{3p}) & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -g_3 & 0 & 0 \\ 0 & 0 & 0 & 0 & \beta G_3(t) & -(\mu_2+\delta_2) & 0 \\ 0 & 0 & 0 & \frac{\eta_2(t)}{N_3} & 0 & 0 & -\mu_4 \end{pmatrix} \tag{17}$$

$$\mathbf{A_{21}} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & \gamma_1 G_2(t) \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\eta_1(t)}{N_1} & 0 & 0 & 0 & 0 \end{pmatrix} \tag{18}$$

and

$$F = (\psi_1, 0, 0, 0, 0, 0, \psi_3, 0, 0, 0, 0, \psi_{2s}, 0, \lambda_4)^T$$

where $a_1 = (\alpha_3 + \mu_1 + \delta_{1b})$, $a_2 = (\alpha_4 + \mu_1 + \delta_{1s})$, $a_3 = (\alpha_5 + \mu_1 + \delta_{1p})$, $a_4 = (\gamma_3 + \mu_3 + \delta_{3b})$, $a_5 = (\gamma_4 + \mu_3 + \delta_{3s})$, $g_1 = (\alpha_1 G_1(t) + \mu_1)$, $g_2 = (\gamma_1 G_2(t) + \mu_3)$ and $g_3 = (\beta G_3(t) + \mu_2)$.

Now from sub-matrix A_{11}, A_{12}, A_{21} and A_{22} we can deduce that matrix $A(x)$ is a Metzler matrix such that all its off-diagonal elements are non-negative $\forall x \in \mathbb{R}^{14}_+$ and $F \geq 0$ is Lipschitz continuous. Thus the feasible region for the model system (8)-(11) is the set

$$\Phi = \left\{(S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A) \geq 0 \in \mathbb{R}^{14}_+\right\}$$

This means that any trajectory of the system starting from an initial state in the positive orthant of $\mathbb{R}^{14}_+$ remains forever in Φ.

6.3.2 Positivity of the solution

We need to show that all variables and parameters of the model are non-negative $\forall t \geq 0$. We now solve the equations of the system in their patches for testing the positivity. We found that by letting the initial values of the systems (8), (9), (10) and (11) be: $S_H(0) > 0$, $S_R(0) > 0$,$S_F(0) > 0$ and $A_0 \geq 0$ $E_H(0) \geq 0$, $I_{HB}(0) \geq 0$, $I_{HS}(0) \geq 0$, $I_{HP}(0) \geq 0$, $R_H(0) \geq 0$, $E_R(0) \geq 0$, $I_{RB}(0) \geq 0$, $I_{RS}(0) \geq 0$, $I_{RP}(0) \geq 0$, $I_F(0) \geq 0$. Then in the solution set $S_H(t)$, $S_R(t)$, $S_F(t)$, $A(t)$, $E_H(t)$, $I_{HB}(t)$, $I_{HS}(t)$, $I_{HP}(t)$, $R_H(t)$, $E_R(t)$, $I_{RB}(t)$, $I_{RS}(t)$, $I_{RP}(t)$ and $I_F(t)$ are non-negative $\forall t \geq 0$.

6.4 Model Analysis

6.4.1 Disease free equilibrium solution

The periodic model system (8) - (11) with non-negative, continuous periodic functions has disease free equilibrium solution in which we consider equations (19), (20) and (21)

$$\frac{dS_H}{dt} = \psi_1 - \mu_1 S_H \tag{19}$$

$$\frac{dS_R}{dt} = \psi_3 - \mu_3 S_R \tag{20}$$

$$\frac{dS_F}{dt} = \psi_{2s} - \mu_2 S_F \tag{21}$$

Now given initial conditions $S_H = S_{H0} \in \mathbb{R}_+$, $S_R = S_{R0} \in \mathbb{R}_+$ and $S_F = S_{F0} \in \mathbb{R}_+$ for (19), (20) and (21) respectively, we will have

$$S_H = \frac{\psi_1}{\mu_1} + \left(S_{H0} - \frac{\psi_1}{\mu_1} \right) e^{-\mu_1 t} \tag{22}$$

$$S_R = \frac{\psi_3}{\mu_3} + \left(S_{R0} - \frac{\psi_3}{\mu_3} \right) e^{-\mu_3 t} \tag{23}$$

$$S_R = \frac{\psi_{2s}}{\mu_2} + \left(S_{F0} - \frac{\psi_{2s}}{\mu_2} \right) e^{-\mu_2 t} \tag{24}$$

As $t \longrightarrow \infty$ (19), (20) and (21) admit unique solution $S_H \equiv \frac{\psi_1}{\mu_1}$, $S_R \equiv \frac{\psi_3}{\mu_3}$ and $S_F \equiv \frac{\psi_{2s}}{\mu_2}$ respectively, which is globally attractive in $\mathbb{R}^3_+$.

To find the disease free equilibrium point we set the derivatives of the system (8)-(11) equal zero. Then the model system has disease free solution which is obtained by setting $I_{HB} = I_{HS} = I_{HP} = E_H = R_H = 0$, $I_{RB} = I_{RS} = I_{RP} = E_R = 0$, $I_F = 0$ and $A = 0$ for human, Rodent, Flea and pathogen system respectively. Hence system (8)-(11) has a disease free equilibrium point

$$\begin{aligned} &E^0(S^0_H, E^0_H, I^0_{HB}, I^0_{HS}, I^0_{HP}, R^0_H, S^0_R, E^0_R, I^0_{RB}, I^0_{RS}, I^0_{RP}, S^0_F, I^0_F, A^0) \\ &= \left(\tfrac{\psi_1}{\mu_1}, 0, 0, 0, 0, 0, \tfrac{\psi_3}{\mu_3}, 0, 0, 0, 0, \tfrac{\psi_{2s}}{\mu_2}, 0, 0 \right) \end{aligned} \tag{25}$$

6.5 Basic Reproduction Number

Let ($\mathbb{R}^k$, $\mathbb{R}^k$) be the standard ordered k-dimensional Euclidean space with a norm $\| \ . \ \|$. For $u, v \in \mathbb{R}^k$ we write $u \geq v$ provided $u - v \in \mathbb{R}^k_+$, $u > v$ provided $u - v \in \mathbb{R}^k_+ \setminus \{0\}$, and $u \gg v$ if $u - v \in \text{Int}(\mathbb{R}^k_+)$.

Now let $A(t)$ be the continuous, cooperative, irreducible, and T-periodic $k \times k$ matrix function with period $T > 0$, $\Phi_{A(.)}(t)$ be the fundamental solution matrix of the linear ordinary differential system

$$\frac{dx}{dt} = A(t)x, \tag{26}$$

and $\rho(\Phi_{A(.)}(T))$ be the spectral radius of $\Phi_{A(.)}(T)$. By Aronsson and Kellogg (1978) it follows that $\Phi_{A(.)}(t)$ is a matrix with all elements positive for each $t > 0$. By the Perron Frobenius theorem, $\rho(\Phi_{A(.)}(T))$ is the principal eigenvalue of $\Phi_{A(.)}(t)$ in the sense that it is simple and admits an eigenvector $v^* \gg 0$. The following result is important for our subsequent comparison argument

Proposition 1. *let $\iota = \frac{1}{T} ln(\rho(\Phi_A(T)))$, and then there exist a positive , T-periodic function $v(t)$ such that $e^{\iota t} v(t)$ is a solution of $x' = A(t)x$*

Proof. Let $v^* \gg 0$ be the eigenvector associated with the spectral radius $\rho\Phi_{A(.)}(T)$

By the change of variable

$$x(t) = e^{\mu t}v(t)$$

the system 26 becomes

$$\frac{dv}{dt} = A(t)v - \mu v = (A(t) - \mu I)v \tag{27}$$

where I is an identity matrix.
Thus $v(t) = \Phi_{(A(.)-\mu I)}(t)v^*$ is a positive solution of (27). We can easily see that

$$e^{\mu t}\Phi_{(A(.)-\mu I)}(t) = \Phi_{A(.)}(t)$$

Moreover

$$v(T) = \Phi_{(A(.)-\mu I)}(t)v^* = e^{-\mu T}\Phi_{A(.)}(T)v^* = e^{-\mu T}\rho(\Phi_{A(.)}(T))v^* = v^* = v(0)$$

Thus, v(t) is a positive T-periodic solution of (27) and hence, $x(t) = e^{\mu t}v(t)$ is a solution of (26) □

The plague disease model system (8)- (11) has unique disease free equilibrium point given in (25)

We consider a heterogeneous population whose individuals are distinguishable by stage of the disease, and hence identifiable and put into epidemiological compartments which are S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F and A. We sort the compartments so that the first m compartments correspond to infected individuals.
We now let
$\mathcal{F}_i(x)$ be the rate of appearance of new infections in the i^{th} compartments;
$\mathcal{V}_i^+(x)$ be the rate of transfer of individuals into compartment i by all other means, other than the epidemic;
$\mathcal{V}_i^-(x)$ be the rate of transfer of individuals out of compartment i.

Then the plague disease transmission model in (8) - (11) is governed by a periodic ordinary differential system given in (28)

$$\frac{dx_i}{dt} = \mathcal{F}_i(t,x) - \mathcal{V}_i(t,x) \triangleq f_i(t,x), \tag{28}$$

where $\mathcal{V}_i(x) = \mathcal{V}_i^-(x) - \mathcal{V}_i^+(x)$.

We rearrange the system by sorting the infectious classes (E_H, I_{HB}, I_{HS}, I_{HP}, E_R, I_{RB}, I_{RS},

I_{RP}, I_F, A) come first. We then have:

$$\mathcal{F}(x) = \begin{pmatrix} \alpha_1\overline{G_1(t)}S_H \\ 0 \\ 0 \\ 0 \\ \gamma_1\overline{G_2(t)}S_R \\ 0 \\ 0 \\ 0 \\ \beta\overline{G_3(t)}S_R \\ 0 \end{pmatrix} \tag{29}$$

$$\mathcal{V}(x) = \begin{pmatrix} \alpha_2 E_H + \mu_1 E_H \\ (\alpha_3 + \mu_1 + \delta_{1b})I_{HB} - \alpha_2\nu_2 E_H \\ (\alpha_4 + \mu_1 + \delta_{1s})I_{HS} - \alpha_3\rho_3 I_{HB} - \alpha_2\nu_3 E_H \\ (\alpha_5 + \mu_1 + \delta_{1p})I_{HP} - \alpha_2\nu_1 E_H - \alpha_3\rho_1 I_{HB} - \alpha_4\xi I_{HS} \\ \gamma_2 E_R + \mu_3 E_R \\ (\gamma_3 + \mu_3 + \delta_{3b})I_{RB} - \gamma_2\tau_3 E_R \\ (\gamma_4 + \mu_3 + \delta_{3s})I_{RS} - \gamma_2\tau_2 E_R - \gamma_3(1-\theta)I_{RB} \\ (\mu_3 + \delta_{3p})I_{RP} - \gamma_2\tau_1 E_r - \gamma_3\theta I_{RB} - \gamma_4 I_{RS} \\ (\mu_2 + \delta_2)I_F \\ \mu_4 A - \frac{\eta_1(t)I_{HP}}{N_1} - \frac{\eta_2(t)I_{RP}}{N_3} + \lambda_4 \end{pmatrix} \tag{30}$$

Then we have:

$$F(t) = \left(\frac{\partial \mathcal{F}_i}{\partial x_j}(x_0)\right), \qquad V(t) = \left(\frac{\partial \mathcal{V}_i}{\partial x_j}(x_0)\right) \tag{31}$$

with $1 \leq i, j \leq 10$.

Now using (31) the matrices F and V as given below:

$$F(x) = \begin{pmatrix} 0 & 0 & \alpha_1\overline{\Gamma_{hsh}} & \alpha_1\overline{\Gamma_{hph}} & 0 & 0 & \frac{\alpha_1\overline{\Gamma_{rsh}}S_H^0}{N_3} & \frac{\alpha_1\overline{\Gamma_{rph}}S_H^0}{N_3} & \frac{\alpha_1\overline{\Gamma_{fh}}S_H^0}{N_2} & \alpha_1\overline{\omega_1}S_H^0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\gamma_1\overline{\Gamma_{hsr}}S_R^0}{N_1} & \frac{\gamma_1\overline{\Gamma_{hpr}}S_R^0}{N_1} & 0 & 0 & \gamma_1\overline{\Gamma_{rsr}} & \gamma_1\overline{\Gamma_{rpr}} & \frac{\gamma_1\overline{\Gamma_{fr}}S_R^0}{N_2} & \gamma_1\overline{\omega_2}S_R^0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta\overline{\Gamma_{hbf}}S_F^0}{N_1} & \frac{\beta\overline{\Gamma_{hsf}}S_F^0}{N_1} & 0 & 0 & \frac{\beta\overline{\Gamma_{rbf}}S_F^0}{N_3} & \frac{\beta\overline{\Gamma_{rsf}}S_F^0}{N_3} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{32}$$

$$V(x) = \begin{pmatrix} v_{11} & v_{12} \\ v_{21} & v_{22} \end{pmatrix} \tag{33}$$

where:

$$V_{11} = \begin{pmatrix} \alpha_2 + \mu_1 & 0 & 0 & 0 & 0 \\ -\alpha_2\nu_2 & \alpha_3 + \mu_1 + \delta_{1b} & 0 & 0 & 0 \\ -\alpha_2\nu_3 & -\alpha_3\rho_3 & \alpha_4 + \mu_1 + \delta_{1s} & 0 & 0 \\ -\alpha_2\nu_1 & -\alpha_3\rho_1 & -\alpha_4\xi & \alpha_5 + \mu_1 + \delta_{1p} & 0 \\ 0 & 0 & 0 & 0 & \gamma_2 + mu_3 \end{pmatrix}$$

$$V_{22} = \begin{pmatrix} \gamma_3 + \mu_3 + \delta_{3b} & 0 & 0 & 0 & 0 & 0 \\ -\gamma_3(1-\theta) & \gamma_4 + \mu_3 + \delta_{3s} & 0 & 0 & 0 & \\ -\gamma_3\theta & -\gamma_4 & \mu_3 + \delta_{3p} & 0 & 0 & \\ 0 & 0 & 0 & \mu_2 + \delta_2 & 0 & \\ 0 & 0 & -\frac{\eta_2}{N_3} & 0 & \mu_4 & \end{pmatrix}$$

$$V_{21} = \begin{pmatrix} 0 & 0 & 0 & 0 & -\gamma_2\tau_3 \\ 0 & 0 & 0 & 0 & -\gamma_2\tau_2 \\ 0 & 0 & 0 & 0 & -\gamma_2\tau_1 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\frac{\eta_1}{N_1} & 0 \end{pmatrix}$$

$$V_{12} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

Following the setting by Wang and Zhao (2008) and Van den Driessche and Watmough (2002) for epidemic models we check the condition (A1) - (A7) for plague disease epidemic model. The system (8) - (11) is equivalent to periodic ordinary differential system (28). Now considering this system we can easily see that the condition (A1) - (A5) stated below are satisfied.

A1 Since each function represents a directed transfer of individuals (human, rodent, flea and pathogens in the environment), they are all non-negative. Thus, for each $1 \leq i \leq n$ the function $\mathcal{F}_i(t,x)$, $\mathcal{V}_i^+(t,x)$ and $\mathcal{V}_i^-(t,x)$ are non-negative and continuous on $\mathbb{R} \times \mathbb{R}_+^n$ and continuously differentiable with respect to x

A2 There is a real number $T > 0$ such that for each $1 \leq i \leq n$ the functions $\mathcal{F}_i(t,x)$, $\mathcal{V}_i^+(t,x)$ and $\mathcal{V}_i^-(t,x)$ are T- periodic in t

A3 If a compartment is empty, there will be no transfer of individuals out of the compartment any means. That is to say if $x_i = 0$ then $\mathcal{V}_i^- = 0$. In particular if $x \in X_s$, then $\mathcal{V}_i^- = 0$ for $i = 1, \ldots, m$

A4 The incidence of infection for uninfected compartments is zero. That is to say $\mathcal{F}_i = 0$ for $i > m$.

A5 If the population is disease free then the population will remain free of disease. Thus if $x \in X_s$, then $\mathcal{F}_i = 0$ and $\mathcal{V}_i^+ = 0$ for $i = 1, \ldots, m$.

We know that the system (28) has disease free periodic solution given in (25). Now we define $f(t, x(t)) = \mathcal{F}(t, x(t)) - \mathcal{V}(t, x(t))$ and $M(t) = \left(\frac{\partial f_i(t_i, E^0)}{\partial x_j}\right)$, $11 \leq i, j \leq 14$ where $f_i(t, x(t))$ and x_i is the $i - th$ component of $f(t, x(t))$ and x respectively. Now

from (29) and (30) we obtain a 4×4 matrix given in (34)

$$\mathbf{A(t)} = \begin{pmatrix} -\mu_1 & \varpi & 0 & 0 \\ 0 & -(\varpi + \mu_1) & 0 & 0 \\ 0 & 0 & -\mu_3 & 0 \\ 0 & 0 & 0 & -\mu_2 \end{pmatrix} \tag{34}$$

We then let $\Phi_{A(.)}(t)$ be the monodromy matrix of the linear T- periodic system $\frac{dz}{dt} = A(t)z$. Then $\rho\Phi_{A(.)}(T) < 1$ which implies that E^0 is linearly asymptotically stable in the in the disease free subspace $X_s = \{x \geq 0 : x_i = 0, \forall i = 1 \dots m\}$ where $i = 1 \dots m$ are the infected compartments. Thus the condition (A6) stated below holds.

A6 The disease free periodic solution is asymptotically stable in a disease free subspace X_s that is $\rho\Phi_{A(.)}(T) < 1$ where $\rho\Phi_{A(.)}(T)$ is the principal eigenvalue of $\Phi_{A(.)}(t)$.

Next we set $F(t)$ and $V(t)$ are two 10×10 matrices defined by (31), then using (29) and (30) we get matrices $F(t)$ and $V(t)$ given in (32) and (33) respectively. We can further see that matrix $F(t)$ is non-negative, and $-V(t)$ is cooperative in the sense that the off-diagonal elements are non negative. Let $Y(t, s), t \geq s$, be the evolution operator of our T-periodic system

$$\frac{dy}{dt} = -V(t)y. \tag{35}$$

That is for each $s \in \mathbb{R}$ the 10×10 matrix $Y(t, s)$ satisfies

$$\frac{dY(t,s)}{dt} = -V(t)Y(t,s), \forall t \geq s, Y(s,s) = Id \tag{36}$$

where Id is a 10×10 identity matrix. Thus the monodromy matrix $\Phi_{V(t)}$ of (35) equals $Y(t, 0), t \geq 0$. Therefore the condition $(A7)$ stated below holds.

A7 The evolution of individuals in the infectious compartments decays exponentially due to natural and disease induced mortalities. Thus $\rho\Phi_V(T) < 1$

Now using the standard theory of linear periodic system by Hale (1980) there exist $K > 0$ and $\wp > 0$ such that

$$\| Y(t,s) \| \leq Ke^{-\wp(t-s)}, \quad \forall t \geq s, \quad s \in \mathbb{R}. \tag{37}$$

We then have

$$\| Y(t, t-a)F(t-a) \| \leq K \| F(t-a) \| e^{-\wp a}, \quad \forall t \in \mathbb{R}, \quad a \in [0, \infty) \tag{38}$$

Considering the periodic environment we suppose that $\Phi(s)$, T- periodic in s, is the distribution of the new infection at a rate $F(s)\Phi(s)$ produced by the infected individual who were introduced

at time s. Given $t \geq s$ then $Y(t,s)F(s)\Phi(s)$ yields the distribution of those infected individuals who were newly infected at time s and remain in the infected class at t. We then have

$$\Psi(t) = \int_{-\infty}^{t} Y(t,s)F(s)\Phi(s)ds = \int_{0}^{\infty} Y(t,t-a)F(t-a)\Phi(t-a)da \tag{39}$$

which is the distribution of accumulative new infections at time t produced by all those infected individual $\Phi(s)$ introduce at previous time s to t $(s \leq t)$.

Let C_T be the ordered Banach space of all T- periodic function from $\mathbb{R}$ to $\mathbb{R}^n$, which is equipped with the maximum norm $\| \, . \, \|_\infty$ and the positive cone $C_T^+ = \{\Phi \in C_T \Phi(t) \geq 0, t \in \mathbb{R}\}$. Define a linear operator $L : C_T \longrightarrow C_T$ by

$$(L\Phi)(t) = \int_{0}^{\infty} Y(t,t-a)F(t-a)\Phi(t-a)da, \quad \forall t \in \mathbb{R}, \;\; \Phi \in C_T \tag{40}$$

Now by Wang and Zhao (2008), Diekmann *et al.* (1990) and Van den Driessche and Watmough (2002) we name L as the next infection operator, then the basic reproduction number R_T of the periodic system (8) - (11) is given (41).

$$R_T = \rho(L) \tag{41}$$

where $\rho(L)$ is the spectral radius of L.

6.5.1 Characterization of R_T

In this subsection, we investigate whether the basic reproduction number in our periodic system can characterize the threshold of the disease invasion. To do this we consider the following linear T-periodic equation

$$\frac{dw}{dt} = \left[-V(t) + \frac{F(t)}{\lambda}\right] w, \quad \forall t \in \mathbb{R} \tag{42}$$

with parameter $\lambda \in (0, \infty)$. Let $W(t,s,\lambda), t \geq s, s \in \mathbb{R}$, be the evolution operator of the system (42) on $\mathbb{R}^{10}$. We can clearly see that $\Phi_{F-V}(t) = W(t,0,1)$, $\forall t \geq 0$. Considering matrix (32) and (33) we note that for each $\lambda \in (0, \infty)$, all off-diagonal element of matrix $-V(t) + \frac{F(t)}{\lambda}$ are non negative (cooperative matrix). It follows that the linear operator $W(t,s,\lambda)$ is positive in $\mathbb{R}^{10}$ for each $t \geq s$, $s \in \mathbb{R}$. Now using Perron-Forobenius theorem by Smith and Waltman (1995) it entails that $\rho(W(T,0,\lambda))$ is an eigen value of $W(T,0,\lambda)$ with a non-negative eigenvector. Also using matrix similarity concept by Shores (2007) we can easily verify that matrix $W(s+T,0,\lambda)$ is similar to the matrix $W(T,0,\lambda)$ and hence $\sigma(W(s+T,0,\lambda)) = \sigma(W(T,0,\lambda))$ for any $s \in \mathbb{R}$ where $\sigma(D)$ is a spectrum of the matrix D.

Proposition 2 ((Wang and Zhao, 2008)). *We let* $(A1) - (A7)$ *holds for system (8) - (11) then*

(i) If $\rho(W(T, 0, \lambda)) = 1$ *has a positive solution* λ_0*, then* λ_0 *is an eigenvalue of* L*, and hence* $R_T > 0$.

(ii) If $R_T > 0$*, then* $\lambda = R_T$ *is the unique solution of* $\rho(W(T, 0, \lambda)) = 1$

(iii) $R_T = 0$ *if and only if* $\rho(W(T, 0, \lambda)) < 1 \forall \lambda > 0$

This result shows that in order to find the basic reproduction number, we need to find the monodromy matrix $\Phi_{F-V}(t)$ of the system (42) and evaluate it. We then find the spectral radius of $\Phi_{F-V}(T)$ and solve the equation $\rho(\Phi_{F-V}(T)) = 1$ for λ which is the basic reproduction number.

6.5.2 Computation of the Basic Reproduction Number

We compute a time-averaged basic reproduction number R_0 using the next generation matrix as outlined by Wesley and Allen (2009), Heesterbeek (2000) and Diekmann *et al.* (1990). The method has the advantage over the usual next generation method in that, the steps to reach an estimate of R_0 and the matrix elements of the next-generation matrix have a clear biological basis. It is easy to handle complex diseases like plague disease which has multiple transmission roots from different infections agents.

To do this, we first categorize individuals by their state at the moment they become infected (type at infection). These types-at-infection refers specifically to the birth of the infection in the individual. These categories (type at infection) differs in the way they transmit plague disease which in-turn differentiate their ability to produce secondary cases.

In our case, we categorize the individuals into eight states and label them as follows: Human infected with bubonic plague (type 1), Human infected with septsemic plague (type 2), Human infected with pneumonic plague (type 3), Rodent infected with bubonic plague (type 4), Rodent infected with septcemic plague (type 5), Rodent infected with pneumonic plague (type 6) Flea infested with pathogens (type 7) and the Pathogens in the environment (type 8).

We assume and label individual with bubonic plague as stage one of the disease, septsemic plague as stage two and pneumonic plague as stage three. We also assume that when an individual in stage one graduates to stage two we only consider the current stage and ignore the latter. We assume that the infection only goes in ascending direction that is from stage one to two, or two to three, but not in the reverse of it.

Since the system has eight types-at-infection, the next-generation matrix, K, will be a 8×8 matrix with elements k_{ij}'s. Each of the element k_{ij} stands for expected number of new cases of i caused by one infected individual of j. For example k_{11} is the expected number of new cases of human infected with bubonic plague caused by one infected human with bubonic plague.

We now define a matrix K whose entries are k_{ij}. The resulting next generation matrix is as given in (43).

$$\mathbf{K} = \begin{pmatrix} k_{11} & k_{12} & k_{13} & k_{14} & k_{15} & k_{16} & k_{17} & k_{18} \\ k_{21} & k_{22} & k_{23} & k_{24} & k_{25} & k_{26} & k_{27} & k_{28} \\ k_{31} & k_{32} & k_{33} & k_{34} & k_{35} & k_{36} & k_{37} & k_{38} \\ k_{41} & k_{42} & k_{43} & k_{44} & k_{45} & k_{46} & k_{47} & k_{48} \\ k_{51} & k_{52} & k_{53} & k_{54} & k_{55} & k_{56} & k_{57} & k_{58} \\ k_{61} & k_{62} & k_{63} & k_{64} & k_{65} & k_{66} & k_{67} & k_{68} \\ k_{71} & k_{72} & k_{73} & k_{74} & k_{75} & k_{76} & k_{77} & k_{78} \\ k_{81} & k_{82} & k_{83} & k_{84} & k_{85} & k_{86} & k_{87} & k_{88} \end{pmatrix} \tag{43}$$

Then, $R_0 = \rho(K)$ where $\rho(K)$ is spectral radius of K.

Some elements equal 0 because not all types of infections cause all other types of infection. Example human with bubonic plague I_{HB} (type at infection 1) does not produce type at infection 1 (human infected with bubonic plague), 4 (rodent infected with bubonic plague), 5 (rodent infected with septicemic plague), 6 (rodent infected with pneumonic plague) and 8 (pathogens in the environment). This means that k_{11}, k_{14}, k_{15}, k_{16} and k_{18} are 0. The type at infection 2 (human being infected with septicemic plague) also does not produce Type at infection 1 (human being infected with bubonic plague), 4(rodent infected with bubonic plague), 6 (rodent infected with pneumonic plague) and 8(Pathogens in the environment). This also means that k_{21}, k_{24}, k_{26} and k_{28} are zero (0). The type at infection 3 does not produce type at infection 1(human being infected with bubonic plague), 2 (human being infected with septicemic plague), 4 (rodent infected with bubonic plague), 5 and 7 which means that k_{31}, k_{32}, k_{34}, k_{35} and k_{37} are zero. Type at infection 4 does not produce type at infection 1, 2, 3, 4 or 8 which means that k_{41}, k_{42}, k_{43}, k_{44} and k_{48} are zero. Type at infection 5 does not produce type at infection 1, 3, 4, and 8 then k_{51}, k_{53}, k_{54} and k_{58} are zero. The type at infection 6 does not produce type at infection 1, 2, 4, 5 and 7 thus k_{61}, k_{62}, k_{64}, k_{65} and k_{67} are zero. Type at infection 7 also does not produce type at infection 3, 6, 7,and 8 thus k_{73}, k_{76}, k_{77}, and k_{78} are zero. And the type at infection 8 does not produce type at infection 1,2, 4,5, 7 and 8 which means that k_{81}, k_{82}, k_{84}, k_{85}, k_{87} and k_{88} are zero. Incorporating these, we modify the matrix K as shown in matrix (44)

$$\mathbf{K} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & 0 & k_{17} & 0 \\ k_{21} & k_{22} & 0 & 0 & k_{25} & 0 & k_{27} & 0 \\ k_{31} & k_{32} & k_{33} & 0 & 0 & k_{36} & 0 & k_{38} \\ 0 & 0 & 0 & 0 & 0 & 0 & k_{47} & 0 \\ 0 & 0 & 0 & k_{54} & k_{55} & 0 & k_{57} & 0 \\ 0 & 0 & 0 & k_{64} & k_{65} & k_{66} & 0 & k_{68} \\ k_{71} & k_{72} & 0 & k_{74} & k_{75} & 0 & 0 & 0 \\ 0 & 0 & k_{83} & 0 & 0 & k_{86} & 0 & 0 \end{pmatrix} \tag{44}$$

We will now explain the derivation of each matrix-elements in detail. We employ the derivation steps by Gail and Benichou (2000) to drive the expressions for k_{ij}. We mainly base our derivation on the adequate contact rate between the infected individual type j and the susceptible individual type i, the expected duration of infection of individual type j and the probability that the individual type j survive the duration between the latent stage to the time an individual experience the onset clinical disease as in (45)

$$\mathbf{K_{ij}} = \begin{pmatrix} \text{Effective} \\ \text{contact} \\ \text{Rate} \end{pmatrix} \times \begin{pmatrix} \text{Duration} \\ \text{of} \\ \text{infection} \end{pmatrix} \times \begin{pmatrix} \text{Probability that the} \\ \text{individual survive} \\ \text{the incubation period} \end{pmatrix} \tag{45}$$

The production of I_{HB}, depend on probability that the susceptible flea becomes infectious (β). We also consider the rate at which I_F adequately bites the susceptible human and the bite results to a human infected with bubonic plague I_{HB} at the average value of transmission rate $\overline{\Gamma_{fh}}$. The total number of human infected with bubonic plague caused by one flea infested with pathogens is as given in (46).

$$k_{17} = \left(\frac{\beta}{\beta + \mu_2}\right) \frac{\nu_2 \overline{\Gamma_{fh}}}{\mu_2 + \delta_2} \tag{46}$$

Septicemic plague in human may be produced in various way; progression of untreated human with bubonic plague to human with septcemic plague, adequate contact(including sexual contact) between humans with septicemic plague, adequate contact between rodent and human with septicemic plague and from the flea infested with pathogens. We consider the progression rate of infected human with bubonic to septicemic $\alpha_3\rho_3$, the adequate contact (it may be sexual contact) rate between humans with septicemic plague, rodent infected with septicemic plague and the infected flea to human with septicemic plague at the average rates $\overline{\gamma_{hsh}}$, $\overline{\gamma_{rsh}}$ and $\overline{\gamma_{fh}}$. Then the number of human infected with septicemic plague from all the mentioned infectious

agents is as given in (47a), (47b), (47c) and (47d).

$$k_{21} = \frac{\alpha_2\alpha_3\nu_2\rho_3}{(\alpha_2\nu_2+\mu_1)(\mu_1+\alpha_3+\delta_{1b})} \tag{47a}$$

$$k_{22} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\overline{\Gamma_{hsh}}}{(\alpha_4+\mu_1+\delta_{1s})} \tag{47b}$$

$$k_{25} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\overline{\Gamma_{rsh}}}{(\gamma_4+\mu_3+\delta_{3s})} \tag{47c}$$

$$k_{27} = \left(\frac{\beta}{\beta+\mu_2}\right)\frac{\nu_1\overline{\Gamma_{fh}}}{\mu_2+\delta_2} \tag{47d}$$

The proportions ρ_1 and ξ of untreated I_{HB} and I_{HS} may progress and become I_{HP} at the progression rates α_3 and α_4 respectively. We multiply the average period the I_{HB} remain infected with the rate at which they progress to I_{HP}. I_{HP} may also result from the airborne transmission from the human or rodent with pneumonic plague at the average rate $\overline{\gamma_{hph}}$ or $\overline{\gamma_{rph}}$ respectively. And through the direct interaction with the environment at the average rate $\overline{\omega_1}$. Then the total number of human infected with pneumonic plague from the stated five sources is given in (48a), (48b), (48c), (48d) and (48e)

$$k_{31} = \frac{\alpha_2\alpha_3\nu_2\rho_1}{(\alpha_2\nu_2+\mu_1)(\alpha_3+\mu_1+\delta_{1b})} \tag{48a}$$

$$k_{32} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\alpha_4\xi}{\alpha_4+\mu_1+\delta_{1s}} \tag{48b}$$

$$k_{33} = \left(\frac{\alpha_2\nu_1}{\alpha_2\nu_1+\mu_1} + \frac{\alpha_3\rho_1}{\alpha_3\rho_1+\mu_1} + \frac{\alpha_4\phi}{\alpha_4\phi+\mu_1}\right)\frac{\overline{\Gamma_{hph}}}{\alpha_5+\mu_1+\delta_{1p}} \tag{48c}$$

$$k_{36} = \left(\frac{\gamma_2\tau_1}{\gamma_2\tau_1+\mu_3} + \frac{\gamma_3\phi}{\gamma_3\phi+\mu_3} + \frac{\gamma_4}{\gamma_4+\mu_3}\right)\frac{\overline{\Gamma_{rph}}}{\mu_3+\delta_{3p}} \tag{48d}$$

$$k_{38} = \left(\frac{\overline{\lambda_4}}{\overline{\lambda_4}+\overline{\mu_4}} + \frac{\overline{\eta_1}}{\overline{\eta_1}+\overline{\mu_4}} + \frac{\overline{\eta_2}}{\overline{\eta_2}+\overline{\mu_4}}\right)\frac{\overline{\omega_1}}{\overline{\mu_4}} \tag{48e}$$

Production of number of rodent with bubonic plague I_{RB} depend only on the flea infested with pathogens. The infection depends on the infection period of the flea that survive the incubation period and the proportion at which the adequate contact between infected flea and susceptible rodent causes bubonic plague at the average rate $\tau_3\overline{\Gamma_{fr}}$ as given in (49).

$$k_{47} = \left(\frac{\beta}{\beta+\mu_2}\right)\frac{\tau_3\overline{\Gamma_{fr}}}{\mu_2+\delta_2} \tag{49}$$

The septicemic plague in rodent is produced in three ways; one is when infected rodent with bubonic plague progresses and become septicemic plague infectives at the rate $\gamma_3(1-\phi)$. Two, is after adequate contact (it may also be a rodent eating or biting an infected individual) between the susceptible rodent and a rodent infected with septicemic plague or human at the average rate

$\overline{\Gamma_{rsr}}$ or $\overline{\Gamma_{hsr}}$ respectively. Three is from the flea infested with pathogens with the proportion that the adequate contact between I_F and the susceptible rodent results to I_{RS}. The total number of I_{RS} infected from these infectious agent is as given in (50a), (50b), (50c) and (50d).

$$k_{52} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\overline{\Gamma_{hsr}}}{\alpha_4+\mu_1+\delta_{1s}} \tag{50a}$$

$$k_{54} = \frac{\gamma_2\gamma_3\tau_3(1-\phi)}{(\gamma_2\tau_3+\mu_3)(\gamma_3+\mu_3+\delta_{3b})} \tag{50b}$$

$$k_{55} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\overline{\Gamma_{rsr}}}{\gamma_4+\mu_3+\delta_{3s}} \tag{50c}$$

$$k_{57} = \left(\frac{\beta}{\beta+\mu_2}\right)\frac{\tau_2\overline{\Gamma_{fr}}}{\mu_2+\delta_2} \tag{50d}$$

I_{RP} may be the result of airborne transmission between the susceptible rodent and the human and rodent with pneumonic plague at the average rate $\overline{\Gamma_{hpr}}$ and $\overline{\Gamma_{rpr}}$ respectively. It may also occur from the progression of untreated I_{RB} and I_{RS} at the rate γ_3 and γ_4 respectively. The pathogens in environment may also cause I_{RP} after the adequate interaction at the average rate $\overline{\omega_2}$. Now the total number of I_{RB} resulting from these interaction are in (51a), (51b), (51c), (51d) and (51e).

$$k_{63} = \left(\frac{\alpha_2\nu_1}{\alpha_2\nu_1+\mu_1} + \frac{\alpha_3\rho_1}{\alpha_3\rho_1+\mu_1} + \frac{\alpha_4\phi}{\alpha_4\phi+\mu_1}\right)\frac{\overline{\Gamma_{hpr}}}{\alpha_5+\mu_1+\delta_{1p}} \tag{51a}$$

$$k_{64} = \frac{\gamma_2\gamma_3\tau_3\phi}{(\gamma_2\tau_3+\mu_3)(\gamma_3+\mu_3+\delta_{3b})} \tag{51b}$$

$$k_{65} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\gamma_4}{\gamma_4+\mu_3+\delta_{3s}} \tag{51c}$$

$$k_{66} = \left(\frac{\gamma_2\tau_1}{\gamma_2\tau_1+\mu_3} + \frac{\gamma_3\phi}{\gamma_3\phi+\mu_3} + \frac{\gamma_4}{\gamma_4+\mu_3}\right)\frac{\overline{\Gamma_{rpr}}}{\mu_3+\delta_{3p}} \tag{51d}$$

$$k_{68} = \left(\frac{\lambda_4}{\lambda_4+\mu_4} + \frac{\overline{\eta_1}}{\overline{\eta_1}+\mu_4} + \frac{\overline{\eta_2}}{\overline{\eta_2}+\mu_4}\right)\frac{\overline{\omega_2}}{\mu_4} \tag{51e}$$

Flea are infested with pathogens from human and rodent infected with bubonic and septicemic plague at the average rate $\overline{\gamma_{hbf}}$, $\overline{\gamma_{hsf}}$, $\overline{\gamma_{rbf}}$ and $\overline{\gamma_{rsf}}$. The infection is dictated by the probability that human and rodent with bubonic and septicemic plague survive the incubation period and the adequate rates of contact. From these interaction we get the total number of infectious flea is as given in (52a), (52b), (52c) and (52d).

$$k_{71} = \frac{\alpha_2\nu_2\overline{\Gamma_{hbf}}}{(\alpha_2\nu_2+\mu_1)(\mu_1+\alpha_3+\delta_{1b})} \tag{52a}$$

$$k_{72} = \left(\frac{\alpha_3\rho_3}{\alpha_3\rho_3+\mu_1} + \frac{\alpha_2\nu_3}{\alpha_2\nu_3+\mu_1}\right)\frac{\overline{\Gamma_{hsf}}}{\alpha_4+\mu_1+\delta_{1s}} \tag{52b}$$

$$k_{74} = \frac{\gamma_2\tau_3\overline{\Gamma_{rbf}}}{(\gamma_2\tau_3+\mu_3)(\gamma_3+\mu_3+\delta_{3b})} \tag{52c}$$

$$k_{75} = \left(\frac{\gamma_2\tau_2}{(\gamma_2\tau_2+\mu_3)} + \frac{\gamma_3(1-\phi)}{\gamma_3(1-\phi)+\mu_3}\right)\frac{\overline{\Gamma_{rsf}}}{\gamma_4+\mu_3+\delta_{3s}} \tag{52d}$$

The pathogens are released in the environment at the average rates $\overline{\eta_1}$ and $\overline{\eta_1}$ from I_{HP} and I_{RP} respectively. The released number of pathogens at a given time depends on the infectious period of the rodent and human infected with pneumonic plague. And the probability that I_{HP} and I_{RP} survive the incubation period. The total pathogens in soil/environment is as given in (53a) and (53b).

$$k_{83} = \left(\frac{\alpha_2\nu_1}{\alpha_2\nu_1+\mu_1} + \frac{\alpha_3\rho_1}{\alpha_3\rho_1+\mu_1} + \frac{\alpha_4\xi}{\alpha_4\phi+\mu_1}\right)\frac{\overline{\eta_1}}{\alpha_5+\mu_1+\delta_{1p}} \tag{53a}$$

$$k_{86} = \left(\frac{\gamma_2\tau_1}{\gamma_2\tau_1+\mu_3} + \frac{\gamma_3\phi}{\gamma_3\phi+\mu_3} + \frac{\gamma_4}{\gamma_4+\mu_3}\right)\frac{\overline{\eta_2}}{\mu_3+\delta_{3p}} \tag{53b}$$

Each element in the matrix K represent the expected number of secondary cases produced by infected individual j during the entire infectious period of that particular individual into a completely susceptible population i (Hartemink *et al.*, 2008).

Basic Reproduction Number R_0

We obtain the average basic reproduction number R_0 by computing the maximum modulus of the eigenvalues of the next-generation matrix K (Diekmann *et al.*, 1990; Heesterbeek, 2000). Now using Maple computing software package, the basic reproduction number is:

$$R_0 = \frac{1}{T}\int_0^T \frac{k_{22}(s)+k_{55}(s)}{4} + \frac{1}{2}\sqrt{A_1 + \frac{1}{3\sqrt[3]{2}}A_4 + \frac{A_5}{3A_4}} + \frac{1}{2}\sqrt{A_2 - \frac{1}{3\sqrt[3]{2}}A_4 - \frac{A_5}{3A_4}}$$
$$+ \frac{A_3}{4\sqrt{A_1 + \frac{1}{3\sqrt[3]{2}}A_4 + \frac{A_5}{3A_4}}}ds$$

in which:

$$A_1 = \frac{3\vartheta_3+8\vartheta_1}{12}, \qquad A_2 = \frac{3\vartheta_3-8\vartheta_1}{6}, \qquad A_3 = 4\vartheta_1\vartheta_3 - \vartheta_3^3 - 8\vartheta_4$$
$$A_4 = \frac{1}{3\sqrt[3]{2}}((2\vartheta_1^3 - 72\vartheta_2\vartheta_1 - 9\vartheta_3\vartheta_4\vartheta_1 + 27\vartheta_4^2 + 27\vartheta_3^2\vartheta_2)) +$$
$$((2\vartheta_1^3 - 72\vartheta_2\vartheta_1 - 9\vartheta_3\vartheta_4\vartheta_1 + 27\vartheta_4^2 + 27\vartheta_3^2\vartheta_2^2 - 4(\vartheta_1^2 + 12\vartheta_2 - 3\vartheta_3\vartheta_4)^3)^{\frac{1}{3}})^{\frac{1}{2}}$$
$$A_5 = \sqrt[3]{2}(\vartheta_1^2 + 12\vartheta_2 - 3\vartheta_3\vartheta_4)$$

where

$$\vartheta_1 = k_{22}(s)k_{55}(s) - k_{17}(s)k_{71}(s) - k_{27}(s)k_{72}(s) - k_{57}(s)k_{75}(s)$$
$$\vartheta_2 = k_{17}(s)k_{55}(s)(k_{17}(s)k_{71}(s) + k_{21}(s)k_{72}(s)) - k_{47}(s)(k_{25}(s)k_{54}(s)k_{72}(s)$$
$$+ k_{22}(s)(k_{55}(s)k_{74}(s) + k_{54}(s)k_{75}(s)))$$
$$\vartheta_3 = -k_{22}(s) - k_{55}(s)$$
$$\vartheta_4 = (k_{22}(s)+k_{55}(s))(k_{17}(s)k_{71}(s) + k_{47}(s)k_{74}(s)) - k_{72}(s)(k_{17}(s)k_{21}(s) - k_{27}(s)k_{55}(s)$$
$$+ k_{25}(s)k_{57}(s)) - k_{75}(s)(k_{47}(s)k_{54}(s) - k_{22}(s)k_{57}(s))$$

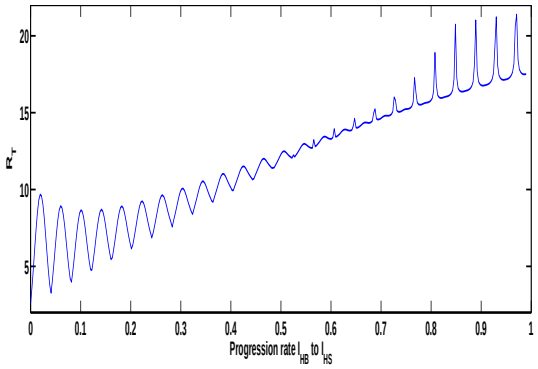
Since the system has multiple infectious types from multiple hosts then the next generation matrix produce the average value of the geometric mean of the number of infections per generation and the the basic reproduction number is the average number of secondary infections (Li and Blakeley, 2011). It is shown that the basic reproduction number of plague disease depends on the expected number of new cases of human infected with bubonic plague caused by one infected flea (k_{17}), the expected number of new cases of human infected with septicemic plague caused by one infected human with bubonic plague (k_{21}), the expected number of new cases of human infected with septicemic plague caused by one infected human with septicemic plague (k_{22}), the expected number of new cases of rodent infected with bubonic plague caused by one infected flea (k_{47}), the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with bubonic plague (k_{54}), the expected number of new cases of rodent infected with septicemic plague caused by one infected rodent with septicemic plague (k_{55}), the expected number of new cases of rodent infected with septicemic plague caused by one infected flea (k_{57}), the expected number of new cases of of new cases of flea infested with *Yersinia pestis* caused by one infected human with bubonic plague (k_{71}), the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected human with septicemic plague (k_{72}), the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with bubonic plague (k_{74}) and the expected number of new cases of flea infested with *Yersinia pestis* caused by one infected rodent with septicemic plague(k_{75}). The result may also be interpreted as: among all elements of the matrix K, the k_{ij}, that appear in R_O gives more significant involvement in the dynamics and spread of plague disease.

6.6 Numerical Results and Discussion

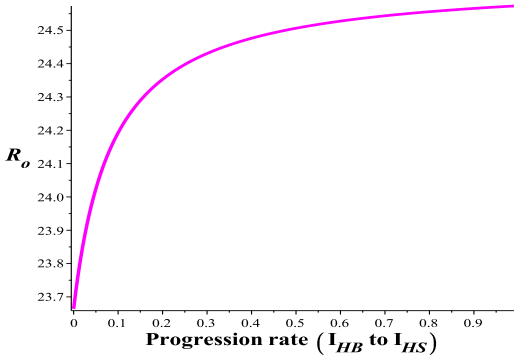
Here we use the parameters values of model system (8) - (11) given in Table 16 to study the transmission trend of plague disease. Simulation results are given to show the effect of different parameters on the periodic reproduction number. We also chose temperature data obtained from Tanga region from January to December 2013 to show the seasonal distribution in the the number of secondary cases of plague infections. It is observed that simulation results from time averaged seasonal parameters and those seasonal parameters treated mathematically as sinusoidal functions matches the real seasonal fluctuation data (Temperature).

Results shows that the increase in number of individuals infected with bubonic plague, to a large extent affects the increases in number of individuals with septicemic and pneumonic plague disease. This is due to the fact that, individual with bubonic plague progresses and become either septicemic or pneumonic plague infectives. This in turn leads to the significant increase of plague disease transmission rate and the average number of secondary infections. Figure 46

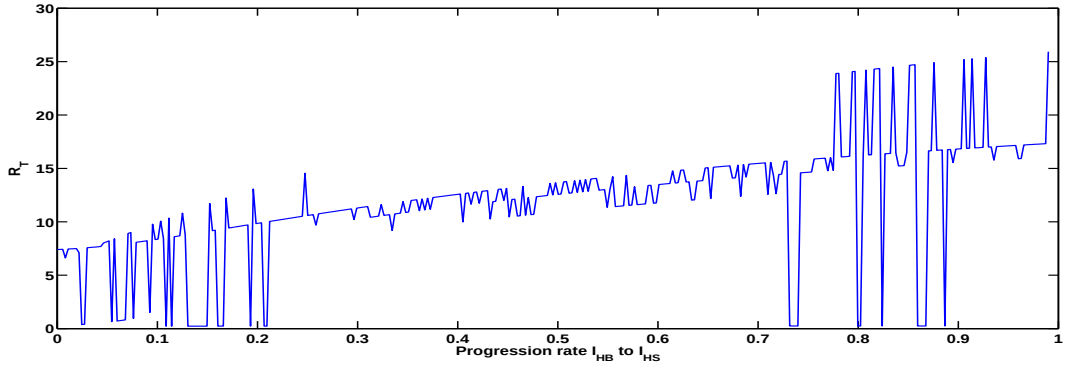
and Fig. 45 show how the progression rates from individuals with bubonic plague to individuals with septicemic plague affects the average number of secondary infections in human beings and rodent respectively. It is illustrated that the increase of human beings and Rodents progressing to become septicemic plague infectives, affects the disease dynamics by increasing the average number of secondary infections. We see similar result when we evaluate the periodic reproduction number basing on the temperature data from Tanga region (Sub-Fig 45c) and (Sub-Fig 46c) and time averaged parameters (Sub-Fig 45b) and (Sub-Fig 46b) for human beings and rodents respectively. These findings necessitate the need for early treatment of plague disease infectives especially the primary forms (Bubonic and septicemic plague) before they progress to a highly fatal and fast spreading plague forms like pneumonic plague disease. It is thus important for the government and other health stake holders to ensure the availability of effective plague disease treatment especially in high risk areas.



(a)



(b)



(c)

Figure 45: Effect of progression rates from I_{HB} to I_{HS} on the Periodic reproduction number.

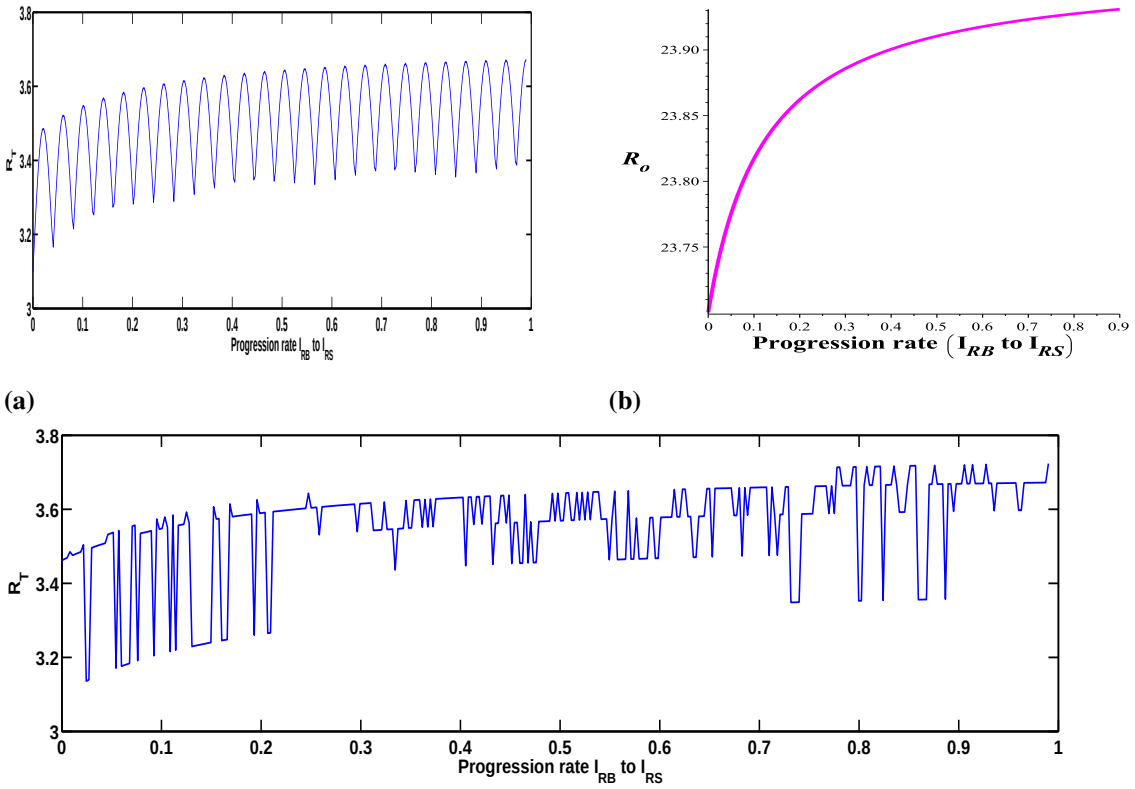
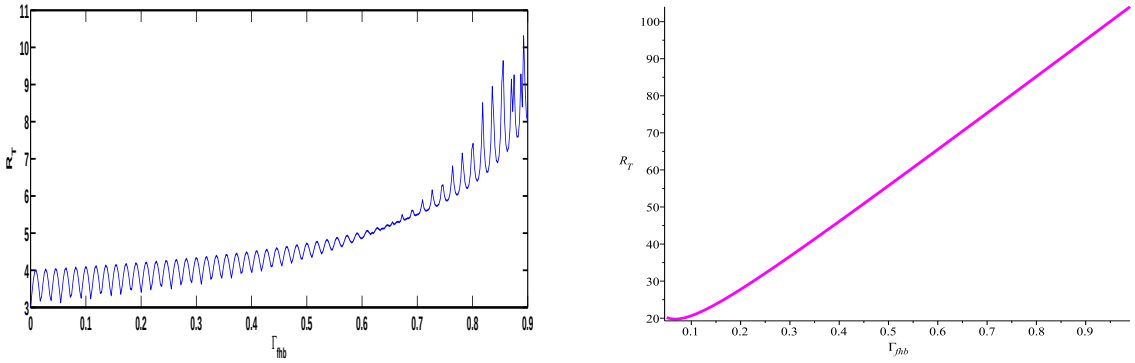
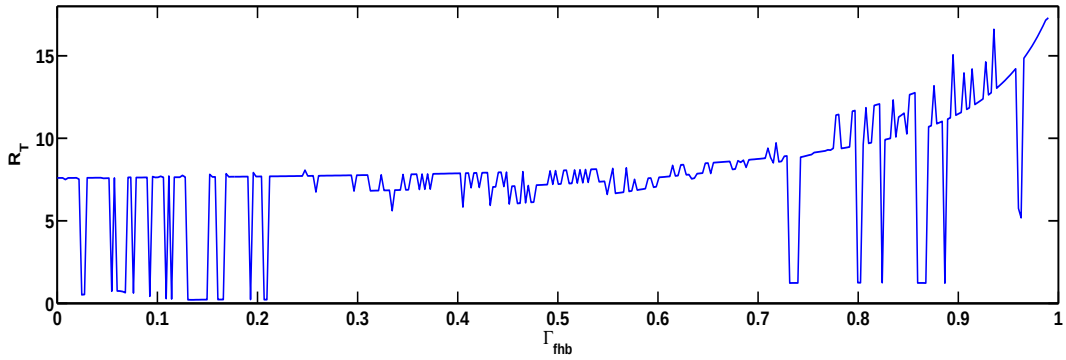


Figure 46: Effect of progression rates from I_{RB} to I_{RS} on the Periodic reproduction number.

Increase of plague disease transmission through flea bite in Human beings and Rodents populations alter the whole dynamics of plague disease. Results in Fig. 47 and Fig. 48 shows the effect of infection from infectious flea to Human beings with bubonic and septicemic plague on the average number of secondary infections. The infection from flea to rodents with bubonic and septicemic plague disease also shows the significant effect on R_T as illustrated in Fig. 49 and Fig. 50 respectively. The results generally shows that when the periodic infection rates from flea increases the infectious human beings and rodent increases as well, this in-turn affect the general plague disease periodic transmission and spread. These results are in conjuncture with what is observed when R_T is evaluated using the temperature data and time averaged seasonal parameter as in Sub-Fig. 47c and Sub-Fig. 47b and Sub-Fig. 49c and Sub-Fig. 49b for human beings and rodents respectively

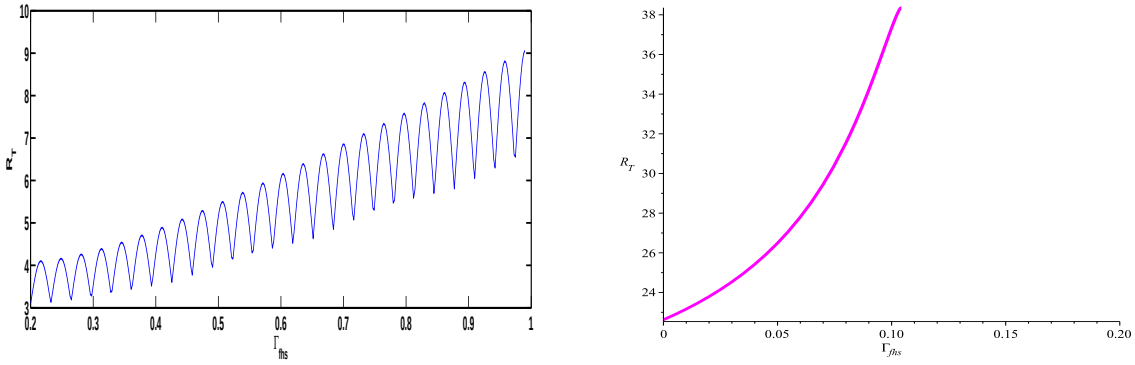


(a) **(b)**

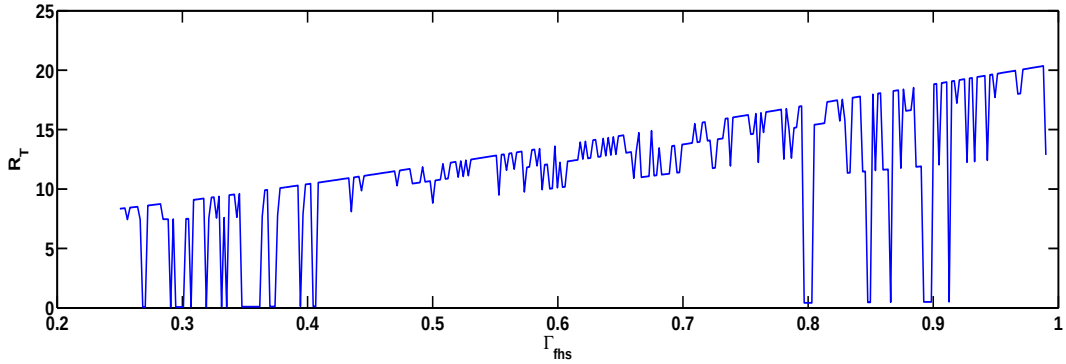


(c)

Figure 47: The effect of infection from I_F to Human beings with bubonic plague on the Periodic Reproduction Number.

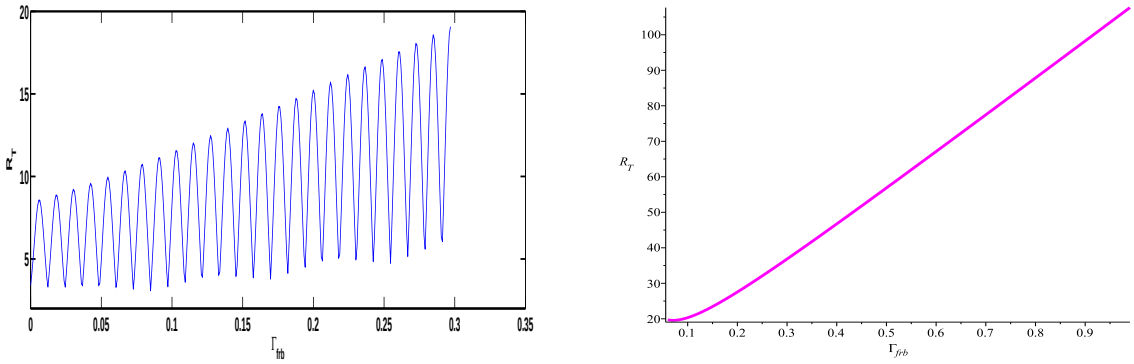


(a) **(b)**

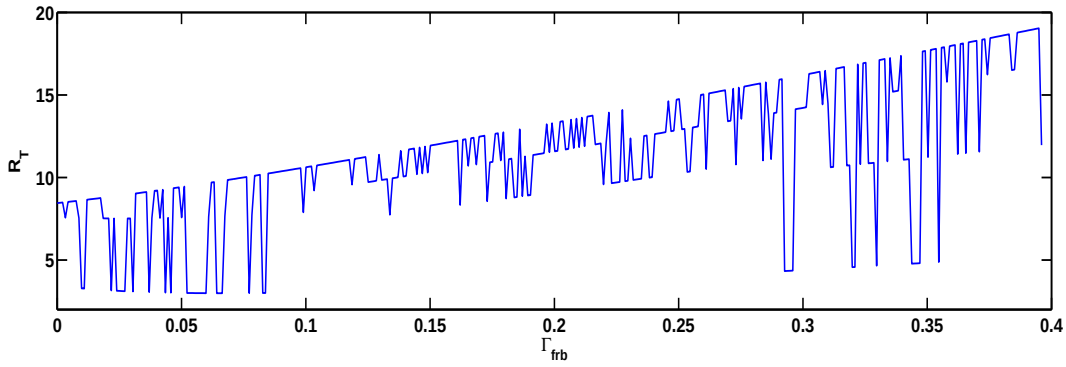


(c)

Figure 48: The effect of infection from I_F to Human beings with Septicemic plague on the Periodic Reproduction Number.

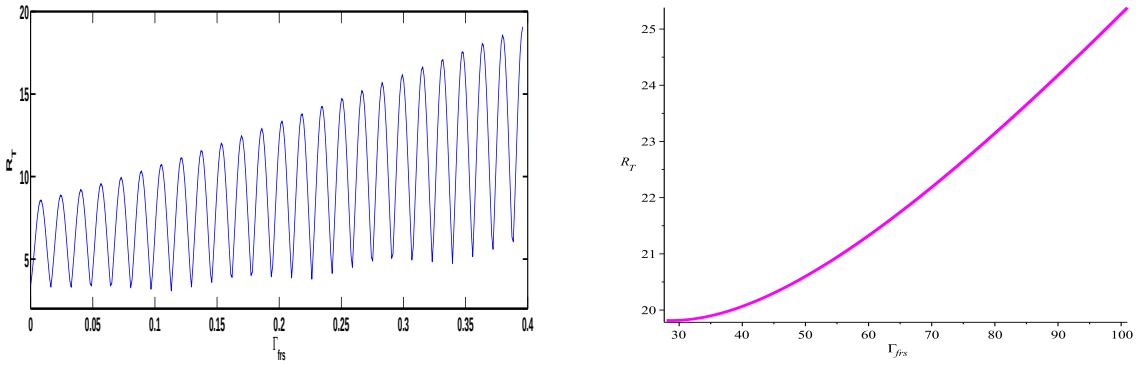


(a) **(b)**

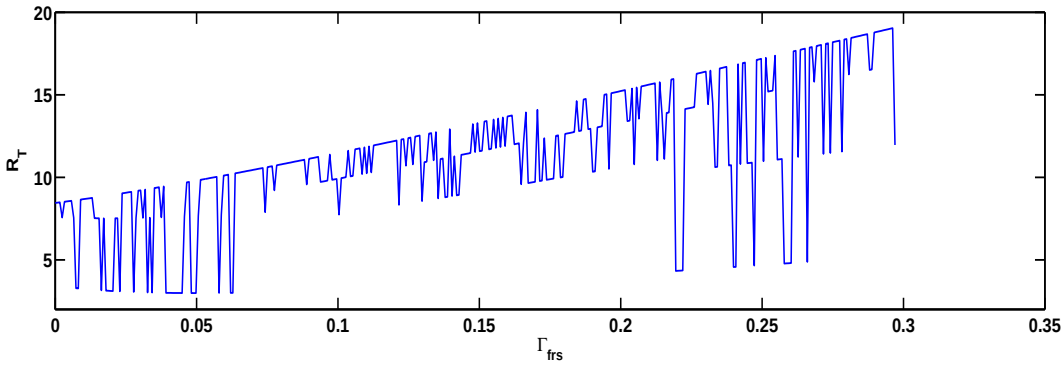


(c)

Figure 49: The effect of infection from I_F to Rodents with bubonic plague on the Periodic Reproduction Number.



(a) **(b)**



(c)

Figure 50: The effect of infection from I_F to rodents with septicemic plague on the Periodic Reproduction Number.

The result calls attention for the need to control the number of infectious flea and flea population in general as the way of controlling the plague disease. The study recommends that for the appropriate and most effective way to control flea population we first need to study the flea's ecology and its local patterns of disease transmission. One of the most important and cost effective strategy of controlling the vector flea is environmental management strategies that can reduce or eliminate vector breeding grounds. For example in residential areas people must be educated to improve their surrounding environment in a way that do not fevers the survival and growth of vector flea. This may be through improving the design of water systems, improve waste disposal and water storage, discourage deforestation and loss of biodiversity and living in a well ventilated housing that is not close to animals.

There are also biological controls tools like bacterial larvicides and larvivorous fish may be used to control flea population (Rozendaal, 1997). These control methods aim at killing vector larvae without generating the ecological impacts as they don't use chemicals. Another strategy is using chemical methods, which mainly shorten the lifespan of vectors. These tools are such as indoor residual sprays, space spraying, and use of chemical larvicides and adulticides. Since most of these methods have side effects to the environmental ecology they are recommended to be used when other safe strategies fail. Moreover, even though these chemicals are not environmentally friendly we argue to the environmental stake holders to recommended the use of chemical methods of vector control that reinforces linkages between health and environment.

Reducing the number of flea population will reduce the infection rates to human beings and rodents and ultimately reduce the number of secondary infections. Sub-Fig 51a shows how reducing the number of infectious flea reduce the number of secondary infections. This is also true when the parameters that are affected by seasonal weather variation are evaluated using the temperature data in Tanga (Sub-Fig 51c) and using the time averaged seasonal parameters (Sub-

Fig 51b). This result is in light of the fact that, the reduction of flea population will reduce the number of individual with bubonic and septicemic and as a result reduce number of pneumonic plague infectives that result from the progression of individual with bubonic and septicemic plague.

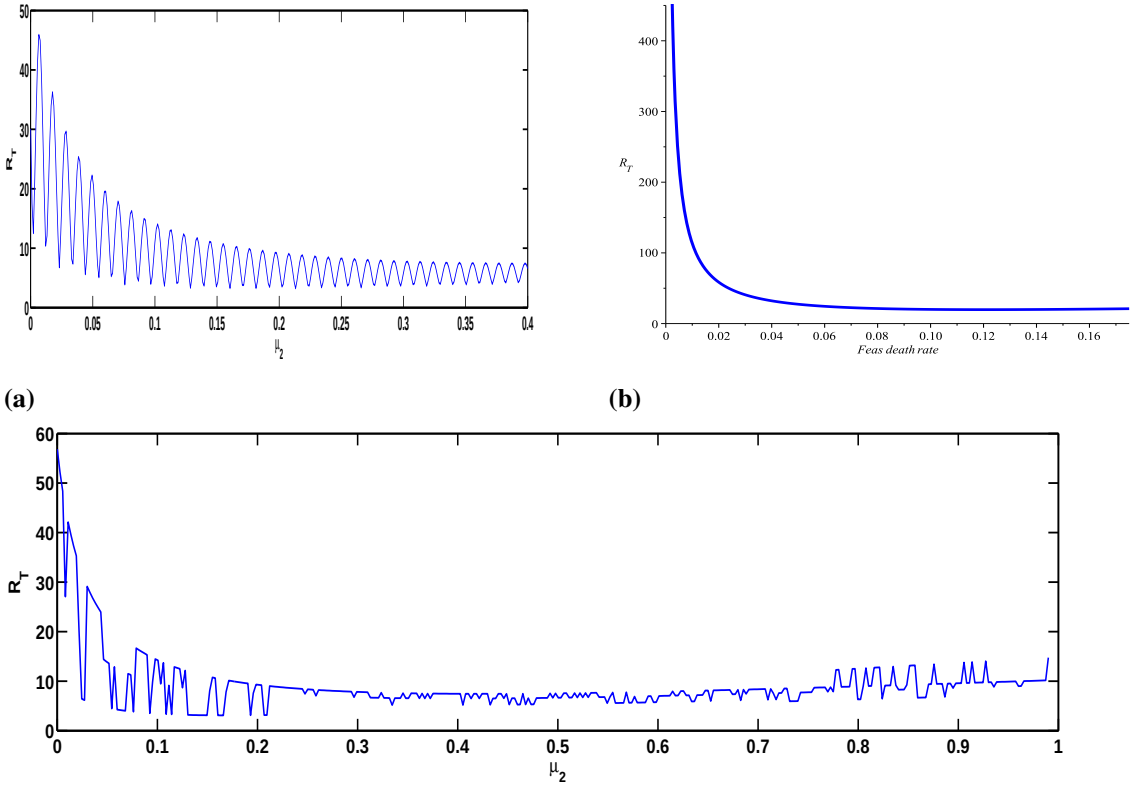
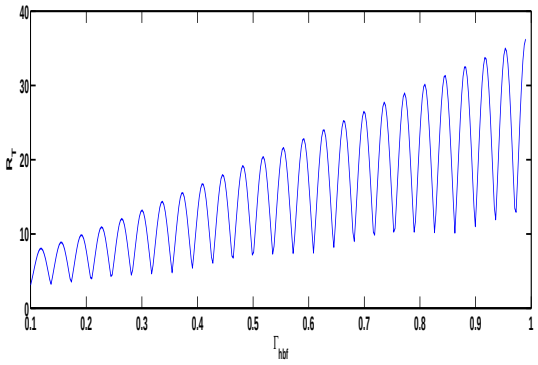


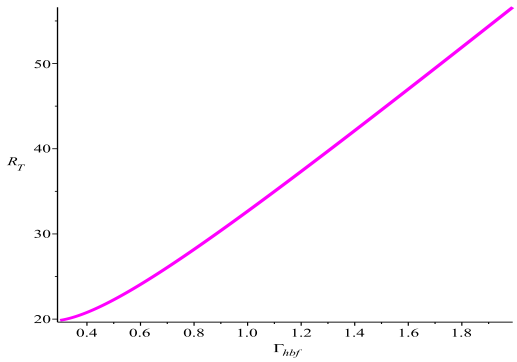
Figure 51: Effect of increased number of flea's death rate on the periodic reproduction number.

The reduction of flea population will not only reduce the infection from flea to other individual but also the rate at which flea gets the disease from other individuals (Human beings and Rodents). When the flea population is reduced it will as a result reduce the interaction between susceptible flea and other infectious individual and vice-versa. The number of fleas getting the disease increases with the increase with the rate at which flea acquire infection from infectious human beings with bubonic plague (see Sub-Fig 52a) and those with septicemic plague (see Sub-Fig 53a). We further observe that the increase of infectious flea may be contributed by the infectious rodents with bubonic plague (see Sub-Fig 54a) and those with septicemic plague (see Sub-Fig 55a). We can also observe the similar results when the parameters are are evaluated basing on the temperature data in Tanga region and when the parameters are timely averaged as in Sub-Fig 52c and Sub-Fig 52b and Sub-Fig 54c and Sub-Fig 54b for human beings and rodents respectively. Therefore, using these results, we settle to the point that increasing transmission rate in flea population from Human beings and Rodents with bubonic and septicemic

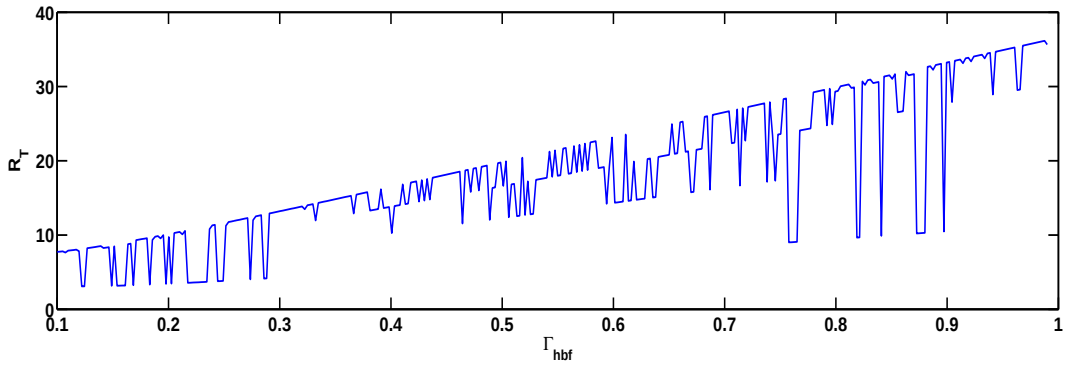
plague raises the average number of secondary plague disease infections.



(a)

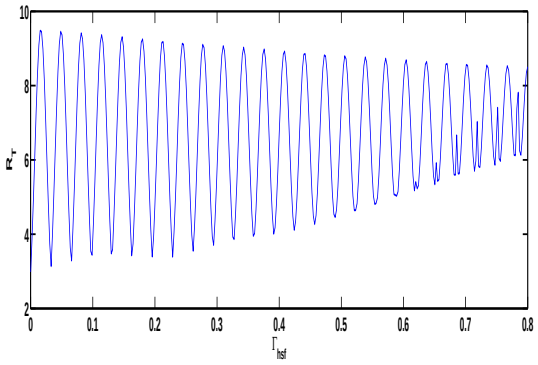


(b)

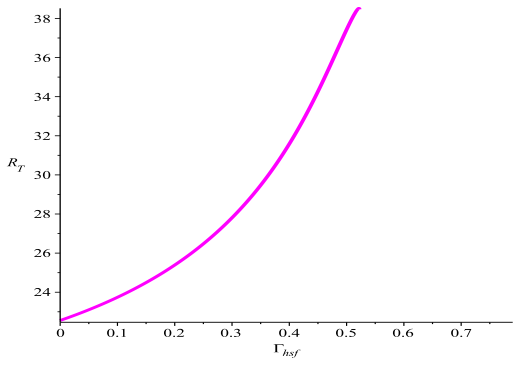


(c)

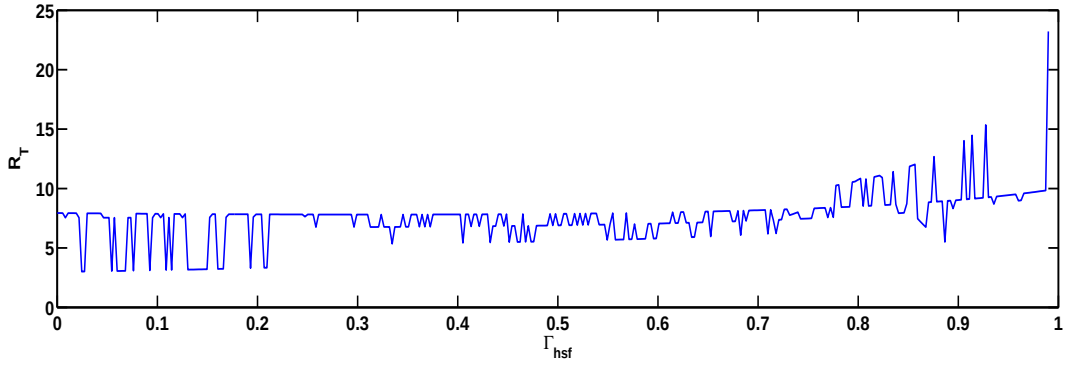
Figure 52: The effect of increased infection rate to Fleas from the infectious Human beings (I_{HB}) on the Periodic Reproduction Number



(a)

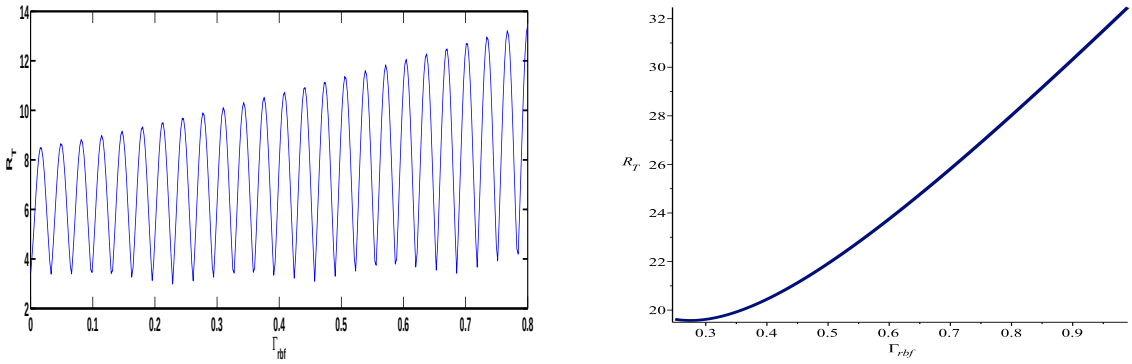


(b)

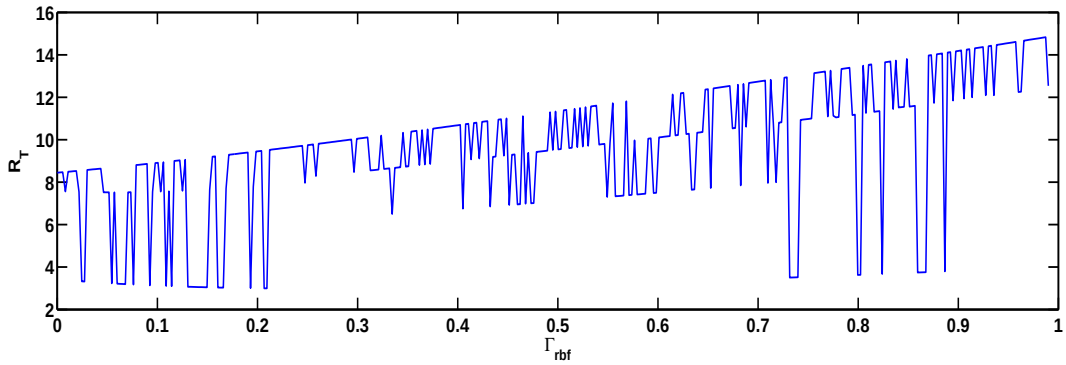


(c)

Figure 53: The effect of increased infection rate to Fleas from the infectious Human beings (I_{HS}) on the Periodic Reproduction Number



(a) **(b)**



(c)

Figure 54: The effect of increased infection rate to Fleas from the infectious rodents (I_{RB}) on the Periodic Reproduction Number

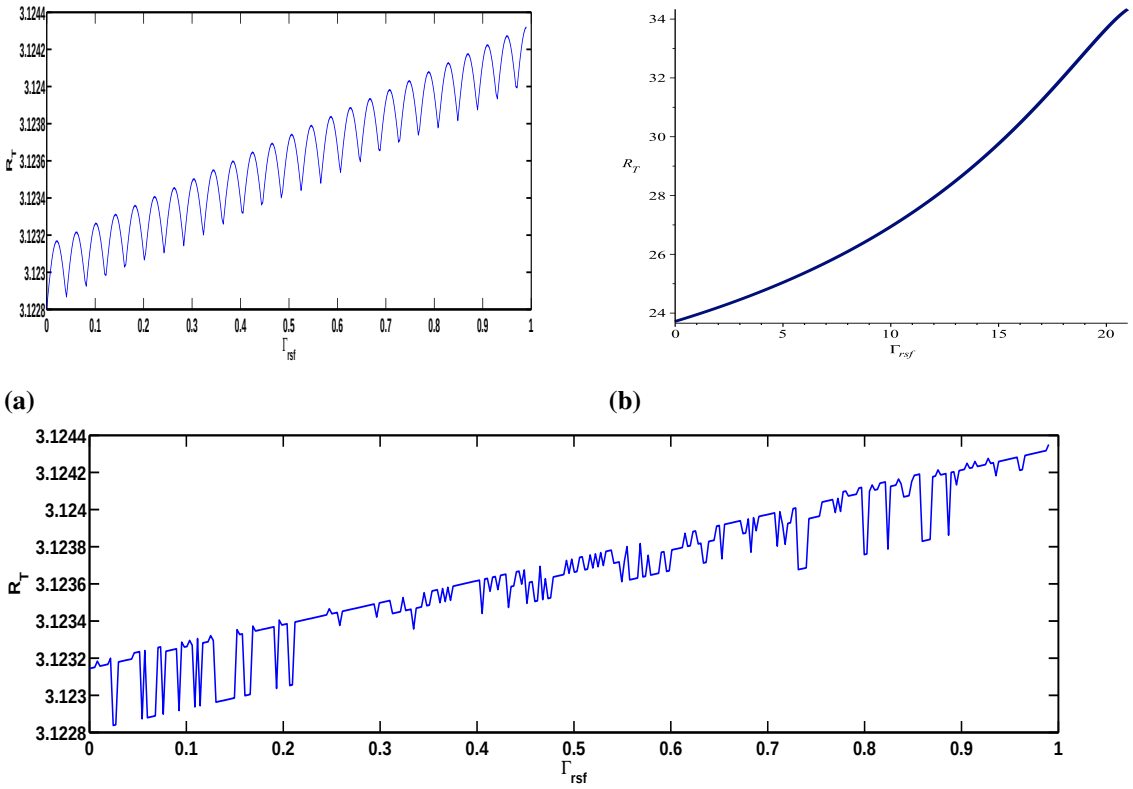
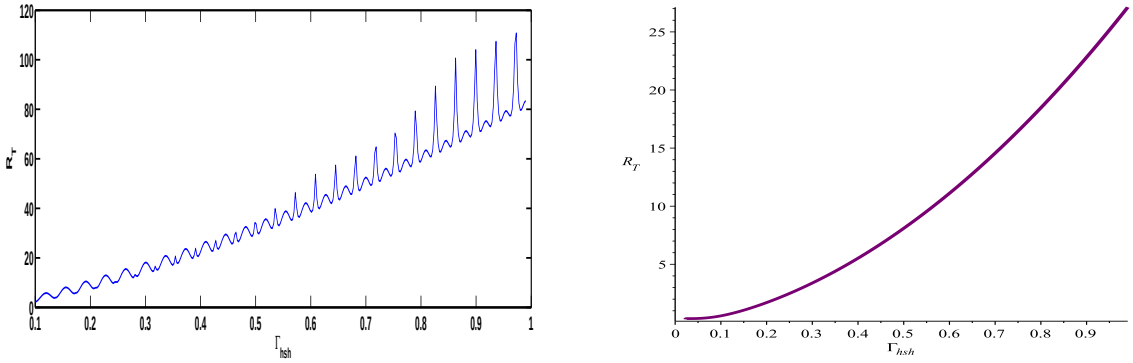
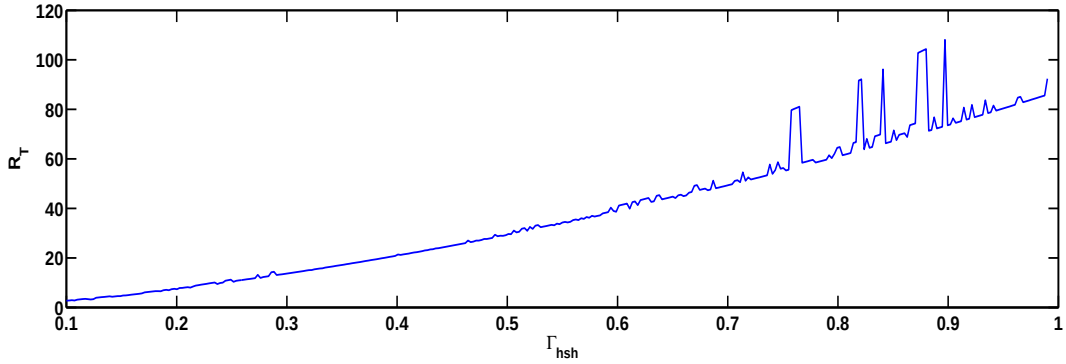


Figure 55: The effect of increased infection rate to Fleas from the infectious rodents (I_{RS}) on the Periodic Reproduction Number

Physical contact that include sexual contact between two infectious individual (Human beings and Rodents) may lead to septicemic plague. The increase in the number of individual with septicemic plague affects the general dynamics of plague disease particularity the average number of secondary infections. It is illustrated that increasing infection rate from a Human beings with septicemic plague to the other susceptible Human (see Sub-Fig 56a) and from Rodent with septicemic plague to the susceptible Rodents (see Sub-Fig 57a) increases the average number of secondary infections. The result again shows a clear correlation when parameters are evaluated based on the Temperature data from Tanga region (see Sub-Fig 56c and Sub-Fig 57c) and when are averaged (see Sub-Fig 56b and Sub-Fig 57b) for human beings and rodents respectively. This shows the necessity to educate human beings practice safe sex using protective gears and taking necessary precaution when handling people or animals with septicemic plague. It also tells us that, there is a necessity to quarantine people and animals that immigrate from areas that are infected by septicemic plague so that they do not affect other Human beings or animals and thus increases the endemicity of the disease.

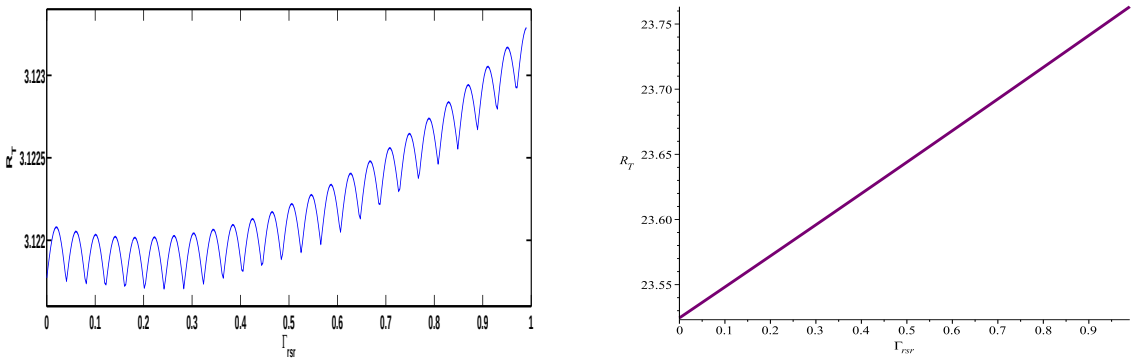


(a) **(b)**

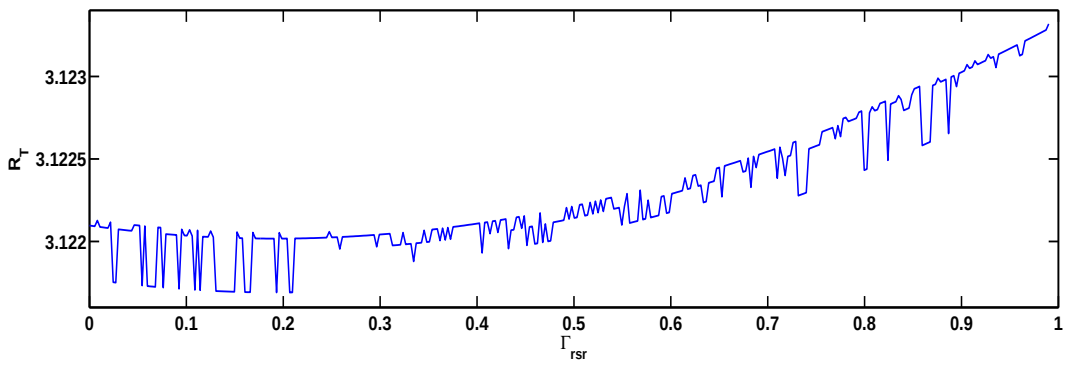


(c)

Figure 56: Effect of infection rate (Γ_{hsh}) on the Periodic reproduction number.



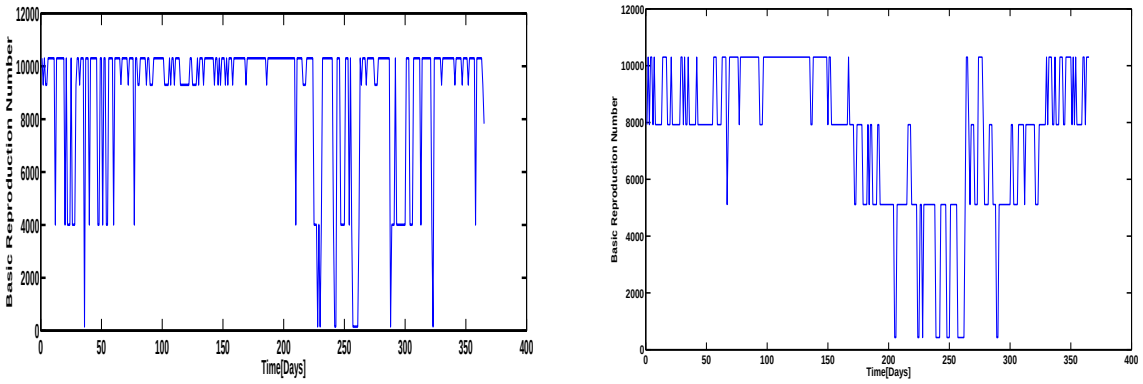
(a) **(b)**



(c)

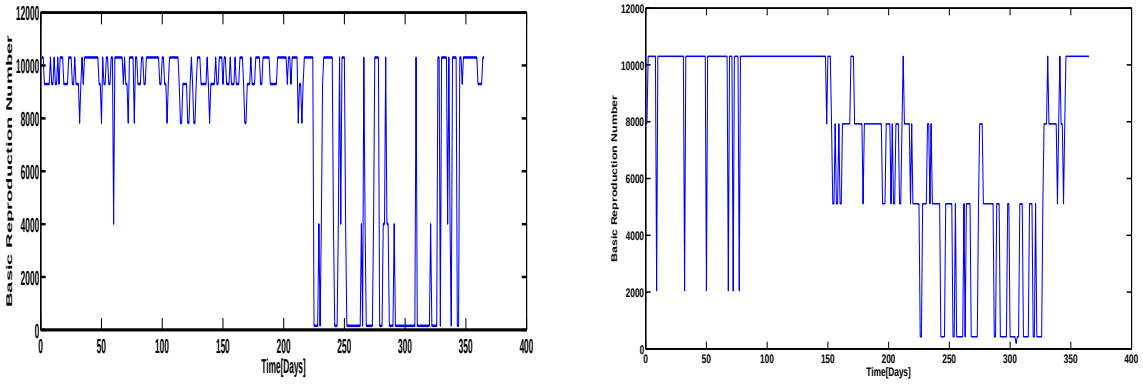
Figure 57: Effect of infection rate (Γ_{rsr}) on the Periodic reproduction number.

The distribution of the basic reproduction number is based on the seasonal weather condition of a particular area at a particular time. This is what causes the unpredictability of the number of secondary cases of plague disease infection (Bubonic, septicemic and pneumonic plague) as it will change whenever the weather conditions changes. We evaluate the distribution of the basic reproduction number based on the data we obtained on daily temperature (^0C) and humidity($\%$) from five regions in Tanzania from January to December, 2013. Figure 58, Fig. 59, Fig. 60, Fig. 61 and Fig. 62 shows the seasonal distribution of basic reproduction number when evaluated based on the Temperature and Humidity data from Kigoma, Mbeya, Mtwara, Singida and Tanga regions respectively.



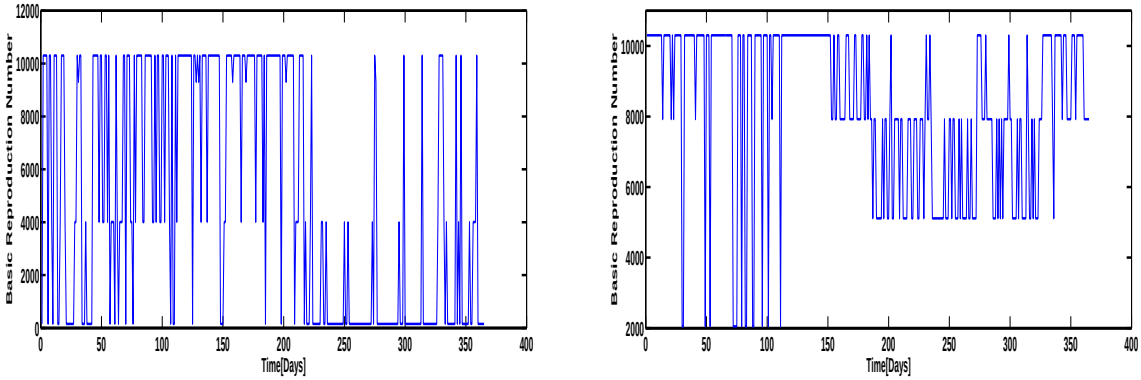
(a) **(b)**

Figure 58: Distribution of R_0 based on fluctuation of Temperature (Sub-Fig 58a) and Relative Humidity (Sub-Fig 58b) data in Kigoma



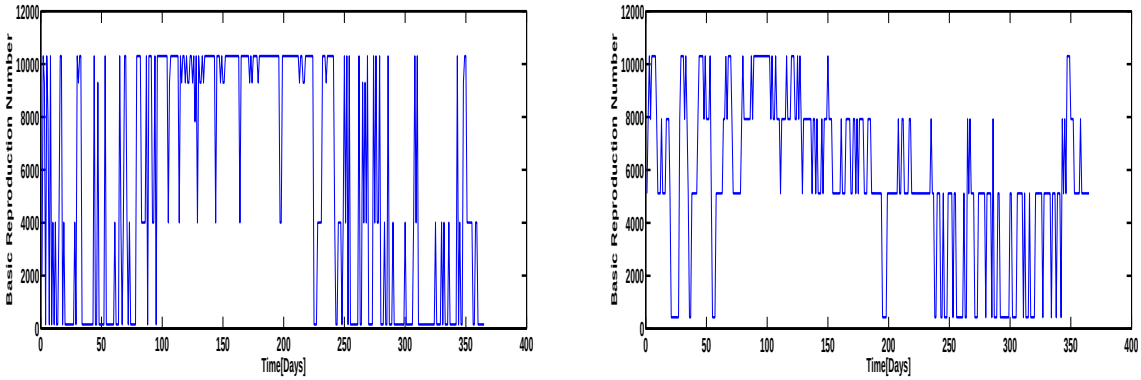
(a) **(b)**

Figure 59: Distribution of R_0 based on fluctuation of Temperature (Sub-Fig 59a) and Relative Humidity (Sub-Fig 59b) data in Mbeya



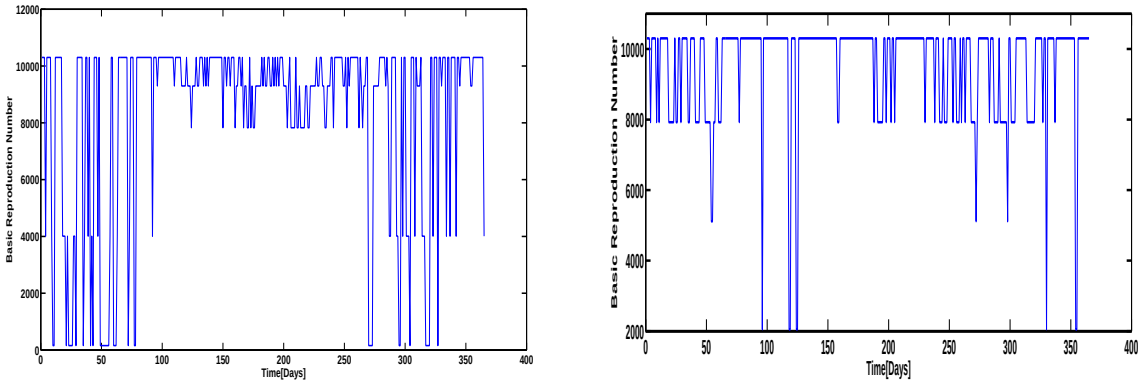
(a) **(b)**

Figure 60: Distribution of R_0 based on fluctuation of Temperature (Sub-Fig 60a) and Relative Humidity (Sub-Fig 60b) data in Mtwara



(a) **(b)**

Figure 61: Distribution of R_0 based on fluctuation of Temperature (Sub-Fig 61a) and Relative Humidity (Sub-Fig 61b) data in Singida



(a) **(b)**

Figure 62: Distribution of R_0 based on fluctuation of Temperature (Sub-Fig 62a) and Relative Humidity (Sub-Fig 62b) data in Tanga

The features displayed in these results clearly show how seasonal weather fluctuation can be

of significant effects on the number of secondary cases of plague disease. It can be noted that there is a seasonal pattern in new plague disease infection cases. We therefore vindicate that the number plague disease infectives peaks whenever the weather condition is favorable for plague disease transmission and it drops when the weather condition do not favor plague disease transmission.

6.7 Conclusion

The transmission of plague disease occurs in several pathways which makes the modeling of the disease challenging and very complex. Moreover all ways that lead to plague disease transmission are directly or indirectly affected by seasonal weather variation which cause seasonality in plague disease epidemic. The effect of seasonal weather variation has been a glowing concern in different epidemiological studies. This in-turn dictate that in order to study the dynamics and propose the effective control strategies of the plague disease we must incorporate the effect of seasonal weather variation. In this study we have analysed the plague disease model incorporated with the factors that are affected by the seasonal weather variation in order to study its effects on the dynamics of the plagues disease. We have computed basic reproduction number and depict how it can be affected by seasonal weather variation through numerical simulation. We were able to deduce that, progression rates from one primary form to secondary form of plague infection, flea's infection rate and the vector flea abundance pose the significant effect on the increase of the average number of secondary cases of plague infection. Therefore the effective control strategies must take into account these factors as they have shown to have a significant contribution on the increase of the average number of secondary cases of plague infection.

CHAPTER SEVEN

Plague Disease Model with Weather Seasonality [6]

Abstract: The plague disease model that include the effect of seasonal weather variation in its transmission is investigated in this paper. The disease is caused by an extremely virulent bacteria *Yersinia pestis* named after a French bacteriologist Alexandre Yersin. The analysis shows that, when the periodic reproduction number (R_T) is greater than one there exist a globally asymptotically stable disease free equilibrium solution (DFS). Using fundamental existence-uniqueness theorem we were able to prove the existence of positive periodic solutions. The analysis further shows that when $R_T > 1$ then there is at least one positive periodic solution. We additionally establish the conditions for global stability of periodic solutions of the model and finally using numerical simulation we depict the behavioral dynamics of plague disease and justify the theoretical solutions.

Key words: Periodic solutions; disease free equilibrium; local stability; global stability; Lyapunov function;

7.1 Introduction

Plague disease is a severe, frequently lethal and potentially epidemic re-imaging disease caused by infection with the gram negative bacterium called *Yersinia pestis* (Wagner *et al.*, 2014). It is greatly affected by seasonal weather variation as it influences all components involved in plague disease system (Ari *et al.*, 2011). In most cases, seasonal fluctuation of weather condition is regarded as the primary factors that cause the recurrent of plague disease circle and is probably the factor that enlighten the reasons for variability of plague disease from small to large scales (Patz *et al.*, 2000, 2003). Weather variation dictates the infection rate of the plague disease, as it affect natural demographic behaviour of the populations involved in its dynamics (Stenseth *et al.*, 2006; Gage *et al.*, 2008).

The environmental condition varies due to seasonal fluctuation of weather parameters which naturally are subjected to fluctuation in time. Recently the issue of effect of seasonal weather variation in the dynamics of infectious disease has become the key point to many epidemiological researchers due to the fact that many infectious disease are affected by different element of

[6]This chapter is based on a research paper: Ngeleja, R. C., Luboobi, L. S., & Nkansah-Gyekye, Y. (2018). Plague Disease Model with Weather Seasonality. *Mathematical biosciences.*

weather conditions in the environment (Altizer *et al.*, 2006). The variation in disease dynamics caused by season weather variation may be due to its ability to alter infection rate of the disease, birth and death rates and immigration rates (Ma and Ma, 2006; Lou and Zhao, 2010). Now if the desired disease dynamics is affected by these fluctuations it changes from being an autonomous disease model system to non-autonomous which is a bit tough in analyzing (Bai and Zhou, 2011).

To better understand the dynamics of infectious diseases we use mathematical models, which are the powerful tools for studying the wide range of phenomena in real world (Hannon and Ruth, 2014). In most cases mathematical epidemiology results reflect the reality and may be useful in predicting the dynamics of the disease in the particular range of time (Keeling and Rohani, 2008). However in most epidemic models, the model parameters such as transmission rates, migration rates and birth and death rates are mostly considered to be constants regardless of the seasonal behavior of most of the infectious diseases due to weather conditions fluctuations (Altizer *et al.*, 2006). Therefore for more realistic disease dynamics and result, we must take into account the seasonal variation of the epidemic due to weather fluctuation. In this paper we study the dynamics of non-autonomous model system of plague disease with periodic transmission rate. We therefore assume the seasonal transmission to be sinusoidal, in a form as given in (1).

$$\lambda(t) = \lambda_0(1 + \sigma cos(2\pi t)) \tag{1}$$

where σ is the amplitude of seasonal variation in transmission also known as strength of seasonal forcing and λ_0 is the average transmission rate.

We discuss the plague disease system dynamics in terms of global stability of the disease-free equilibrium, the existence of positive periodic solutions and the stability of positive periodic solution. We further use numerical simulations to illustrate the theoretical results.

7.2 Model formulation

The model has four settings: Human population, rodent population, flea population and pathogens in the environment (A). The total human population is divided into six compartments: susceptible human (S_H), exposed human (E_H), bubonic plague infectives (I_{HB}), septicemic plague infectives (I_{HS}), pneumonic plague infective (I_{HP}), Recovered human (R_H) and $N_1 = S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H$. Total rodent population is divided into five compartments: susceptible rodent (S_R); exposed rodent (E_R), bubonic plague infectives (I_{RB}), septicemic plague infectives (I_{RS}), pneumonic plague infective (I_{RP}) and $N_3 = S_R + E_R + I_{RB} + I_{RS} + I_{RP}$. The total flea population is divided into two compartment: susceptible flea (S_F), infectious flea

(I_F) and $N_2 = S_F + I_F$.

Human being gets plague (Bubonic, pneumonic and septicemic) infection after they adequately interact with various infectious agents as follows: infectious human and rodent with pneumonic plague through airborne transmission at the periodic rates $\Gamma_{hph}(t)$ and $\Gamma_{rph}(t)$ respectively; infectious human and rodent with septicemic plague through direct physical contact including sexual contact at the periodic rates $\Gamma_{hsh}(t)$ and $\Gamma_{rsh}(t)$ respectively; infectious flea at a periodic rate $\Gamma_{fh}(t)$ and pathogens in the environment at the periodic rate $\omega_1(t)$ which makes the force of infection to human beings as given in (2)

$$G_1(t) = \frac{\Gamma_{hph}(t)I_{HP} + \Gamma_{hsh}(t)I_{HS}}{N_1} + \Gamma_{fh}(t)\frac{I_F}{N_2} + \frac{\Gamma_{rph}(t)I_{RP} + \Gamma_{rsh}(t)I_{RS}}{N_3} + \omega_1(t)A \quad (2)$$

Rodent also gets plague infection when they adequately contact with various infectious agents as follows: infectious rodent and human with pneumonic plague through airborne transmission at the periodic rates $\Gamma_{rpr}(t)$ and $\Gamma_{hpr}(t)$ respectively; infectious rodent and human with septicemic plague through direct physical contact including sexual contact at the periodic rates $\Gamma_{rsr}(t)$ and $\Gamma_{hsr}(t)$ respectively; infectious flea at aperiodic rate $\Gamma_{fr}(t)$ and pathogens in the environment at the periodic rate $\omega_2(t)$ which makes the force of infection to rodents as given in (3)

$$G_2(t) = \frac{\Gamma_{hpr}(t)I_{HP} + \Gamma_{hsr}(t)I_{HS}}{N_1} + \Gamma_{fr}(t)\frac{I_F}{N_2} + \frac{\Gamma_{rpr}(t)I_{RP} + \Gamma_{rsr}(t)I_{RS}}{N_3} + \omega_2(t)A \quad (3)$$

Susceptible flea may get infection when they bite human beings or rodents with bubonic or septicemic plague at the periodic rated rates $\Gamma_{hbf}(t)$ or $\Gamma_{hsf}(t)$ or $\Gamma_{rbf}(t)$ or $\Gamma_{rsf}(t)$ respectively which makes the force of infection in fleas as given in (4). Human being and rodents with pneumonic plague infest the environment with pathogens causing plague disease at the periodic rates $\eta_1(t)$ and $\eta_2(t)$ respectively.

$$G_3(t) = \frac{\Gamma_{hbf}(t)I_{HB} + \Gamma_{hsf}(t)I_{HS}}{N_1} + \frac{\Gamma_{rbf}(t)I_{RB} + \Gamma_{rsf}(t)I_{RS}}{N_3} \quad (4)$$

7.2.1 Variables and Parameters used in the model

This section presents variables and parameters, their description and their values as used in the model. We obtain the parameters from the literature that relate to this study, the present information on plague disease and through estimation using sensitivity analysis and simulations.

Table 17: Variables and their description for effect of weather on plague.

Variable	Description
S_H	Susceptible Human population
E_H	Exposed human population
I_{HB}	Infectious human population infected with bubonic plague
I_{HS}	Infectious human population with septicemic plague
I_{HP}	Infectious human population with Pneumonic plague
R_H	Recovered Human population
S_R	Susceptible rodents
E_R	Exposed rodents
I_{RB}	Infectious rodents with bubonic plague
I_{RS}	Infectious rodents with septicemic plague
I_{RP}	Infectious rodents with pneumonic plague
S_F	Susceptible fleas
I_F	Infected fleas
A	Pathogens in the soil/environment

Table 18: Parameters and their description for effect of weather on plague.

Parameters	Description	Value	Reference/Source
$\Gamma_{rbf}(t)$	Adequate contact rate: between I_{RB} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{rsf}(t)$	Adequate contact rate: between I_{RS} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{fh}(t)$	Adequate contact rate: between I_F and human	0.0641	Eisen *et al.* (2007)
$\Gamma_{fr}(t)$	Adequate contact rate: between I_F and rodent	0.0641	Eisen *et al.* (2007)
$\Gamma_{hph}(t)$	Adequate contact rate: between I_{HP} and S_H	0.39	Estimated
$\Gamma_{hsh}(t)$	Adequate contact rate: between I_{HS} and S_H	0.12	Estimated
$\Gamma_{rbh}(t)$	Adequate contact rate: between I_{RB} and S_H		
$\Gamma_{rph}(t)$	Adequate contact rate:between I_{RP} and S_H	0.19	Estimated
$\Gamma_{rsh}(t)$	Adequate contact rate: between I_{RS} and S_H	0.21	Estimated
α_1	Probability of progressing from S_H to E_H	0.99	Estimated
α_2	Progression rate out of E_H to infectious state	0.23	Gani and Leach (2004)
$\rho_1\alpha_3$	Progression rate out of I_{HB} to I_{HP}		
$\rho_2\alpha_3$	Progression rate out of I_{HB} to R_H		
$\rho_3\alpha_3$	Progression rate out of I_{HB} to I_{HS}		
δ_{1b}	Disease induced death rate of I_{HB}	0.04	Keeling and Gilligan (2000*a*)
α_4	Progression rate out of I_{HS} to I_{HP} and R_H	0.06	Estimated
δ_{1s}	Disease induced death rate of I_{HS}	0.04	Estimated
α_5	Progression rate out of I_{HP} to R_H	0.4	Gani and Leach (2004)
δ_{1p}	Disease induced death rate of I_{HP}	0.63	Kugeler *et al.* (2015)
γ_1	Probability of progressing from S_R to E_R	0.92	Estimated
$\Gamma_{hbf}(t)$	Adequate contact rate: between I_{HB} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{hsf}(t)$	Adequate contact rate: between I_{HS} and flea	0.1	Eisen *et al.* (2007)
$\Gamma_{rpr}(t)$	Adequate contact rate: between I_{RP} and S_R	0.9	Estimated
$\Gamma_{rsr}(t)$	Adequate contact rate: between I_{RS} and S_R	0.9	Estimated
$\Gamma_{hpr}(t)$	Adequate contact rate: between I_{HP} and S_R	0.00005	Estimated
$\Gamma_{hsr}(t)$	Adequate contact rate: between I_{HS} and S_R	0.00008	Estimated
γ_2	The rate at which rodent become infectious	0.98	Estimated
γ_3	Progression rate out of I_{RB} to I_{RS} and I_{RP}	0.194	Tollenaere *et al.* (2010)
δ_{3b}	Disease induced death rate of I_{RB}	0.1	Estimated

Continued on next page

Table 18 – *Continued from previous page*

Parameters	Description	Value	Reference/Source
γ_4	Progression rate out of I_{RS} to I_{RP}	0.05	Estimated
δ_{3s}	Disease induced death rate of I_{RS}	73	Tollenaere *et al.* (2010)
δ_{3p}	Disease induced death rate of I_{RP}	0.14	Estimated
ϖ	Progression rate of R_H to S_H	0.33	Kugeler *et al.* (2015)
μ_1	Natural death rate for Human being	0.04	Keeling and Gilligan (2000a)
μ_2	Natural death rate for Flea	0.2	Bacot and Martin (1924)
μ_3	Natural death rate for rodent	1	Morand and Harvey (2000)
$\omega_1(t)$	Adequate contact rate: A and Human being		
$\omega_2(t)$	Adequate contact rate: A and rodent		
$\eta_1(t)$	Recruitment rate of A by I_{HP}	0.2	Estimated
$\eta_2(t)$	Recruitment rate of A by I_{RP}	0.4	Estimated
μ_4	Natural death rate for Pathogens	0.1	Estimated
ψ_1	Recruitment rate of human beings	0.09	Estimated
ψ_2	Recruitment rate of fleas		
ψ_3	Recruitment rate of rodents		

Figure 63 shows the dynamics of complex interaction between human beings, rodents, fleas and pathogens in the environment that lead to plague disease transmission from one infectious individual to the susceptible individual.

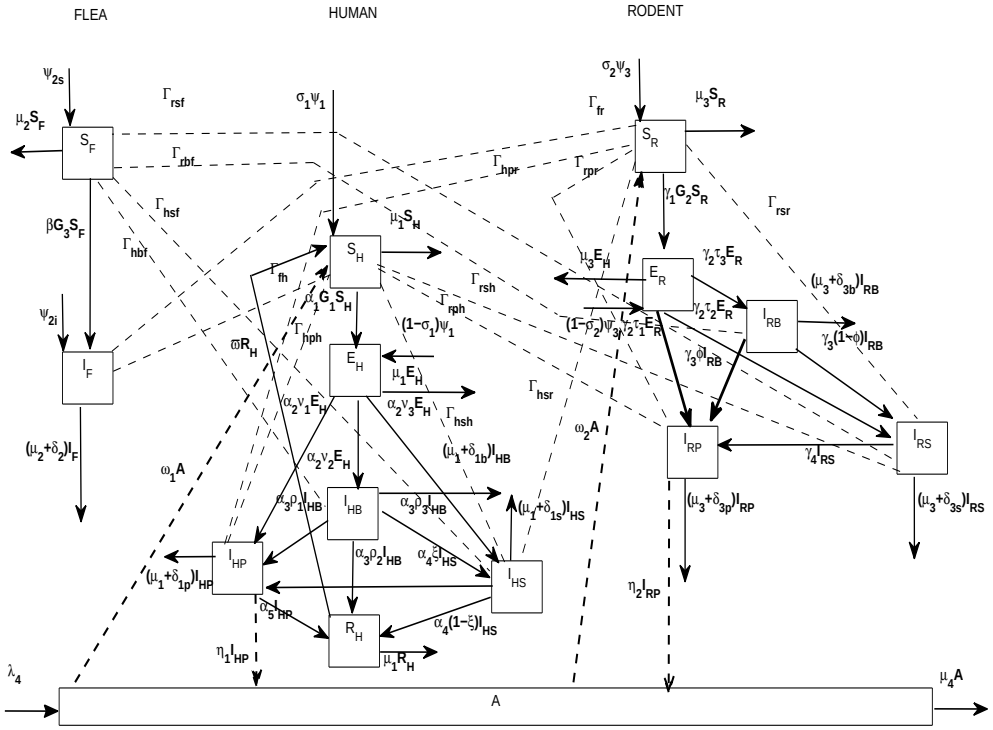


Figure 63: Compartment Model for Plague Disease

Using the description of infection, variables and parameters stated in Tables 17 and 18 and the compartmental diagram in Fig. 63 we derive the system of differential equations that describe plague disease dynamics in human beings, rodents, fleas and pathogens in the environment as given in (5) - (8).

Human beings

$$\frac{dS_H}{dt} = \psi_1 + \varpi R_H - \alpha_1 G_1(t) S_H - \mu_1 S_H, \tag{5a}$$
$$\frac{dE_H}{dt} = \alpha_1 G_1(t) S_H - \alpha_2 E_H - \mu_1 E_H, \tag{5b}$$
$$\frac{dI_{HB}}{dt} = \alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB}, \tag{5c}$$
$$\frac{dI_{HS}}{dt} = \alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS}, \tag{5d}$$
$$\frac{dI_{HP}}{dt} = \alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP}, \tag{5e}$$
$$\frac{dR_H}{dt} = \alpha_3 \rho_2 I_{HB} + \alpha_4 (1 - \xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H. \tag{5f}$$

Rodents

$$\frac{dS_R}{dt} = \psi_3 - \gamma_1 G_2(t) S_R - \mu_3 S_R, \tag{6a}$$
$$\frac{dE_R}{dt} = \gamma_1 G_2(t) S_R - \gamma_2 E_R - \mu_3 E_R, \tag{6b}$$
$$\frac{dI_{RB}}{dt} = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \tag{6c}$$
$$\frac{dI_{RS}}{dt} = \gamma_2 \tau_2 E_R + \gamma_3 (1 - \phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}, \tag{6d}$$
$$\frac{dI_{RP}}{dt} = \gamma_2 \tau_1 E_R + \gamma_3 \phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \tag{6e}$$

Fleas

$$\frac{dS_F}{dt} = \psi_{2s} - \beta G_3(t) S_F - \mu_2 S_F, \tag{7a}$$
$$\frac{dI_F}{dt} = \beta G_3(t) S_F - (\mu_2 + \delta_2) I_F \tag{7b}$$

Pathogens

$$\frac{dA}{dt} = \lambda_4(t) + \frac{\eta_1(t) I_{HP}}{N_1} + \frac{\eta_3(t) I_{RP}}{N_3} - \mu_4(t) A. \tag{8}$$

7.3 Preliminaries

Proposition 3. *The solution (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A) of system (5) - (8) with positive initial condition is positive and ultimately uniformly bounded on* $[0, \infty)$.

Proof. Assume the solution

$$(S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A)$$

with positive initial condition exist and is unique on $[0, b)$ where $0 < b < \infty$. Since

$$S'_H = \psi_1 + \varpi R_H - \alpha G_1(t) S_H - \mu_1 S_H \geq -(\alpha_1 G_1(t) S_H + \mu_1 S_H)$$

$$S_H \geq S_H(0) \text{exp}\left(- \int_0^t \alpha_1 G_1(x) + \mu_1 \right) dx > 0$$

for all $t \in [0, b)$, following the same procedure we ca prove that $E_H > 0$, $I_{HB} > 0$, $I_{HS} > 0$, $I_{HP} > 0$, $R_H > 0$, $S_R > 0$, $E_R > 0$, $I_{RB} > 0$, $I_{RS} > 0$, $I_{RP} > 0$, $S_F > 0$, $I_F > 0$ and $A > 0$

Furthermore Since the system is modeling Human, Rodent, Vector(flea) and pathogens populations, we assume that all state variables and parameters of the model are non-negative $\forall t \geq 0$. We then analyze the model in a suitable feasible region. We are able proved that all forward solutions in $\mathbb{R}^{14}_+$ of the system are feasible if they enter the invariant region Φ for $\Phi = \Omega_H \times \Omega_R \times \Omega_F \times \Omega_A$

where

$$\Omega_H = (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H) \in R^6_+ : S_H + E_H + I_{HB} + I_{HS} + I_{HP} + R_H \leq N_1$$
$$\Omega_R = (S_R, E_R, I_{RB}, I_{RS}, I_{RP}) \in R^5_+ : S_R + E_R + I_{RB} + I_{RS} + I_{RP} \leq N_3$$
$$\Omega_F = (S_F, I_F) \in R^2_+ : S_F + I_F \leq N_2$$
$$\Omega_A = A \in R^1_+$$

and Φ is the positive invariant region of the whole system. □

7.4 Basic reproduction number

In this section, we drive the expression for the basic reproduction number of the plague disease system (5) - (8). The system has disease free equilibrium point given as,

$$\begin{aligned} E^0(S^0_H, E^0_H, I^0_{HB}, I^0_{HS}, I^0_{HP}, R^0_H, S^0_R, E^0_R, I^0_{RB}, I^0_{RS}, I^0_{RP}, S^0_F, I^0_F, A^0) \\ = \left(\tfrac{\psi_1}{\mu_1}, 0, 0, 0, 0, 0, \tfrac{\psi_3}{\mu_3}, 0, 0, 0, 0, \tfrac{\psi_{2s}}{\mu_2}, 0, 0 \right). \end{aligned} \tag{9}$$

Now following the method of finding the basic reproduction number of non-autonomous model systems by Wang and Zhao (2008), we let C_T be the ordered Banach space of all T- periodic function from $\mathbb{R}$ to $\mathbb{R}^n$, which is equipped with the maximum norm $\| \, . \, \|_\infty$ and the positive cone $C^+_T = \{\Phi \in C_T \Phi(t) \geq 0, t \in \mathbb{R}\}$. We define a linear operator $L : C_T \longrightarrow C_T$ by

$$(L\Phi)(t) = \int_0^\infty Y(t, t-a) F(t-a) \Phi(t-a) da, \quad \forall t \in \mathbb{R}, \;\; \Phi \in C_T \tag{10}$$

where L is the next infection operator. Then the basic reproduction number is given by

$$R_T = \rho(L) \tag{11}$$

where $\rho(L)$ is the spectral radius of L.

7.5 Global Stability of DFS

By Zhang and Zhao (2007) [Theorem 2.2] if $R_T > 1$, then DFS is unstable and if $R_T < 1$ then DFS is locally asymptotically stable. Therefore we only need to prove that DSF is globally attractive for $R_T < 1$. Thus we show that independent of the initial population size if the average number of secondary infections is less than one that is $R_T < 1$, then the disease free solution is globally asymptotically stable and then the disease dies out.

Since $S_H(t)$, $E_H(t)$, $I_{HB}(t)$, $I_{HS}(t)$, $I_{HP}(t)$, $R_H(t)$, $S_R(t)$, $E_R(t)$, $I_{RB}(t)$, $I_{RS}(t)$, $I_{RP}(t)$, $S_F(t)$, $I_F(t)$ and $A(t)$ is a non-negative solution for system (5)- (8) in Φ, using Proposition 3 we have:

$$S_H(t) + E_H(t) + I_{HB}(t) + I_{HS}(t) + I_{HP}(t) + R_H(t) \leq \frac{\psi_1}{\mu_1}$$

$$S_R(t) + E_R(t) + I_{RB}(t) + I_{RS}(t) + I_{RP}(t) \leq \frac{\psi_3}{\mu_3}$$

and

$$S_F(t) + I_F(t) \leq \frac{\psi_{2s}}{\mu_2}$$

at disease free we will have,

$$S_H \leq \frac{\psi_1}{\mu_1}, \qquad S_R \leq \frac{\psi_3}{\mu_3}, \qquad S_F \leq \frac{\psi_{2s}}{\mu_2}. \tag{12}$$

Using (12) we can then modify system (5)- (8) for $t \geq 0$. The auxiliary system becomes:

Human beings

$$\frac{dE_H}{dt} \leq \alpha_1 G_1(t)\frac{\psi_1}{\mu_1} - \alpha_2 E_H - \mu_1 E_H, \tag{13a}$$

$$\frac{dI_{HB}}{dt} = \alpha_2\nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b})I_{HB}, \tag{13b}$$

$$\frac{dI_{HS}}{dt} = \alpha_3\rho_3 I_{HB} + \alpha_2\nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s})I_{HS}, \tag{13c}$$

$$\frac{dI_{HP}}{dt} = \alpha_2\nu_1 E_H + \alpha_3\rho_1 I_{HB} + \alpha_4\xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p})I_{HP}, \tag{13d}$$

Rodents

$$\frac{dE_R}{dt} \leq \gamma_1 G_2(t)\frac{\psi_3}{\mu_3} - \gamma_2 E_R - \mu_3 E_R, \tag{14a}$$

$$\frac{dI_{RB}}{dt} = \gamma_2\tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b})I_{RB}, \tag{14b}$$

$$\frac{dI_{RS}}{dt} = \gamma_2\tau_2 E_R + \gamma_3(1-\phi)I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s})I_{RS}, \tag{14c}$$

$$\frac{dI_{RP}}{dt} = \gamma_2\tau_1 E_R + \gamma_3\phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p})I_{RP}, \tag{14d}$$

Fleas

$$\frac{dI_F}{dt} \leq \beta G_3(t)\frac{\psi_{2s}}{\mu_2} - (\mu_2 + \delta_2)I_F \tag{15a}$$

Pathogens

$$\frac{dA}{dt} = \lambda_4(t) + \frac{\eta_1(t)I_{HP}}{N_1} + \frac{\eta_3(t)I_{RP}}{N_3} - \mu_4(t)A. \tag{16}$$

which can be written as:

$$\begin{pmatrix} E_H \\ I_{HB} \\ I_{HS} \\ I_{HP} \\ E_R \\ I_{RB} \\ I_{RS} \\ I_{RP} \\ I_F \\ A \end{pmatrix}' = (F(t) - V(t)) \begin{pmatrix} E_H \\ I_{HB} \\ I_{HS} \\ I_{HP} \\ E_R \\ I_{RB} \\ I_{RS} \\ I_{RP} \\ I_F \\ A \end{pmatrix} \tag{17}$$

Using Zhang and Zhao (2007) [Lemma 2.1] we deduce that there exists a positive T- periodic function $\varrho(t)$ such that $e^{\iota t}\varrho(t)$ is a solution of (17), where $\iota = \frac{1}{T}ln(\rho(\Phi_{(F(t)-V(t))}(T)))$.

We chose $t_1 \geq 0$ and a real number $\varepsilon > 0$ such that

$$\begin{pmatrix} E_H(t_1) \\ I_{HB}(t_1) \\ I_{HS}(t_1) \\ I_{HP}(t_1) \\ E_R(t_1) \\ I_{RB}(t_1) \\ I_{RS}(t_1) \\ I_{RP}(t_1) \\ I_F(t_1) \\ A(t_1) \end{pmatrix} \leq \varepsilon\varrho(0) \tag{18}$$

Using comparison principal, we get

$$\begin{pmatrix} E_H(t) \\ I_{HB}(t) \\ I_{HS}(t) \\ I_{HP}(t) \\ E_R(t) \\ I_{RB}(t) \\ I_{RS}(t) \\ I_{RP}(t) \\ I_F(t) \\ A(t) \end{pmatrix} \leq \varepsilon\varrho(t - t_1)e^{\iota(t-t_1)}, \qquad \forall t \geq t_1 \tag{19}$$

Using Zhang and Zhao (2007) [Theorem 2.2] it is easy to deduce that $R_T < 1$ if and only if $\rho(\Phi_{(F(t)-V(t))}(T)) < 1$, and thus $\iota = \frac{1}{T} ln(\rho(\Phi_{(F(t)-V(t))}(T))) < 0$. Therefore the disease free equilibrium solution is globally and asymptotically stable if $R_T < 1$. It then leads to the following theorem.

Theorem 7.16
The Disease Free solution E^0 of plague disease is globally asymptotically stable if $R_T < 1$and unstable if $R_T > 1$.

7.6 Existence of Positive Periodic Solutions

Define $X_0 = (S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A) \in X : E_H > 0$, $I_{HB} > 0, I_{HS} > 0, I_{HP} > 0, E_R > 0, I_{RB} > 0, I_{RS} > 0, I_{RP} > 0, I_F > 0, A > 0$ and $\partial X_0 = X \backslash X_0$, denote $u(t, x_0)$ as the unique solution of the system (5)- (8) with the initial value $x_0 = (S_H^0, E_H^0, I_{HB}^0, I_{HS}^0, I_{HP}^0, R_H^0, S_R^0, E_R^0, I_{RB}^0, I_{RS}^0, I_{RP}^0, S_F^0, I_F^0, A^0)$. Let $P : X \longrightarrow X$ be the Poincaré map associated with system (5)- (8), that is

$$P(x_0) = u(T, x_0), \ \ \forall x_0 \in X,$$

where T is the period . We then apply the fundamental existence-uniqueness theorem, $u(t, x_0)$ is the unique solution of the system (5)- (8) with $u(0, x_0) = x_0$. This proves that P is uniformly persistent with respect to $(X_0, \partial X_0)$

We have proven that X and X_0 is positively invariant and P is point dissipative and uniformly persistence with respect to $(X_0, \partial X_0)$ from Theorem 4.1. For system (5)- (8), by continuity theorem we have the Proposition 4

Proposition 4. *When $R_T > 1$ there exist a $\ell > 0$ such that when $\parallel (\Xi_0) - P_0 \parallel \leq \ell$ for any $(\Xi_0) \in X_0$ we have $lim_{m \approx \infty} sup d[P^m(\Xi_0), P_0] \geq \ell$.*
where $\Xi_0 = (S_H^0, E_H^0, I_{HB}^0, I_{HS}^0, I_{HP}^0, R_H^0, S_R^0, E_R^0, I_{RB}^0, I_{RS}^0, I_{RP}^0, S_F^0, I_F^0, A^0)$

Proof. By Zhang and Zhao (2007) we know that $R_T > 0$ if and only if $\rho(\Phi_{F(t)-V(t)}(T) > 1$ by continuity of the spectrum for matrices (Kato, 2013) we can choose $\wp > 0$ which is small

enough such that $\Phi_{F(t)-V(t)-M_\wp}(T) > 1$ where

$$M_\wp = \begin{pmatrix} 0 & 0 & \wp & \wp & 0 & 0 & \wp & \wp & \wp & \wp \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \wp & \wp & 0 & 0 & \wp & \wp & \wp & \wp \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \wp & \wp & 0 & 0 & \wp & \wp & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{20}$$

We then prove by contradiction that

$$\limsup_{m \longrightarrow \infty} d(P^m(\Xi_0), P_0) \geq \wp, \quad \forall \Xi \in X_0 \tag{21}$$

If not then

$$\limsup_{m \longrightarrow \infty} d(P^m(\Xi_0), P_0) < \wp \tag{22}$$

for some $\Xi_0 \in X_0$. Without loss of generality we assume that

$$d(P^m(\Xi_0), P_0) < \wp, \quad \forall m \geq 0 \tag{23}$$

By the continuity of the solutions with respect to initial values we obtain

$$\parallel u(t, P^m(\Xi_0)) - u(t, P_0) \parallel \leq \wp \ \ \forall m \geq 0, \forall t \in [0, T] \tag{24}$$

Now for any $t \geq 0$ let $t = mT + t_1$, where $t_1 \in [0, T]$ and $m = \left[\frac{t}{T}\right]$ is the greatest integer less than or equal to $\frac{t}{T}$. We then have

$$\parallel u(t, P^m(\Xi_0)) - u(t, P_0) \parallel = \parallel u(t_1, P^m(\Xi_0)) - u(t_1, P_0) \parallel \leq \ \wp \forall t \geq 0 \tag{25}$$

It then implies that $\hat{S_H} - \wp \leq S_H(t) \leq \hat{S_H} + \wp$, $\hat{S_R} - \wp \leq S_R(t) \leq \hat{S_R} + \wp$, $\hat{S_F} - \wp \leq S_F(t) \leq \hat{S_F} + \wp$, $t \geq 0$. Now for $\parallel (\Xi_0) - P_0 \parallel \leq \wp$ we then have

$$\frac{dE_H}{dt} \geq \alpha_1 G_1(t)(\hat{S_H} - \wp) - \alpha_2 E_H - \mu_1 E_H, \tag{26a}$$

$$\frac{dI_{HB}}{dt} = \alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB}, \tag{26b}$$

$$\frac{dI_{HS}}{dt} = \alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS}, \tag{26c}$$

$$\frac{dI_{HP}}{dt} = \alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP}, \tag{26d}$$

$$\frac{dR_H}{dt} = \alpha_3 \rho_2 I_{HB} + \alpha_4 (1 - \xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H. \tag{26e}$$

$$\frac{dE_R}{dt} \geq \gamma_1 G_2(t)(\hat{S_R} - \wp) - \gamma_2 E_R - \mu_3 E_R, \tag{27a}$$
$$\frac{dI_{RB}}{dt} = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \tag{27b}$$
$$\frac{dI_{RS}}{dt} = \gamma_2 \tau_2 E_R + \gamma_3 (1-\phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}, \tag{27c}$$
$$\frac{dI_{RP}}{dt} = \gamma_2 \tau_1 E_R + \gamma_3 \phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \tag{27d}$$

$$\frac{dI_F}{dt} \geq \beta G_3(t)(\hat{S_F} - \wp) - (\mu_2 + \delta_2) I_F \tag{28a}$$
$$\frac{dA}{dt} = \lambda_4(t) + \frac{\eta_1(t) I_{HP}}{N_1} + \frac{\eta_3(t) I_{RP}}{N_3} - \mu_4(t) A. \tag{29}$$

Next we consider the linear system

$$\frac{dE_H}{dt} = \alpha_1 G_1(t)(\hat{S_H} - \wp) - \alpha_2 E_H - \mu_1 E_H, \tag{30a}$$
$$\frac{dI_{HB}}{dt} = \alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB}, \tag{30b}$$
$$\frac{dI_{HS}}{dt} = \alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS}, \tag{30c}$$
$$\frac{dI_{HP}}{dt} = \alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP}, \tag{30d}$$
$$\frac{dR_H}{dt} = \alpha_3 \rho_2 I_{HB} + \alpha_4 (1-\xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H. \tag{30e}$$

$$\frac{dE_R}{dt} = \gamma_1 G_2(t)(\hat{S_R} - \wp) - \gamma_2 E_R - \mu_3 E_R, \tag{31a}$$
$$\frac{dI_{RB}}{dt} = \gamma_2 \tau_3 E_R - \gamma_3 I_{RB} - (\mu_3 + \delta_{3b}) I_{RB}, \tag{31b}$$
$$\frac{dI_{RS}}{dt} = \gamma_2 \tau_2 E_R + \gamma_3 (1-\phi) I_{RB} - \gamma_4 I_{RS} - (\mu_3 + \delta_{3s}) I_{RS}, \tag{31c}$$
$$\frac{dI_{RP}}{dt} = \gamma_2 \tau_1 E_R + \gamma_3 \phi I_{RB} + \gamma_4 I_{RS} - (\mu_3 + \delta_{3p}) I_{RP}, \tag{31d}$$

$$\frac{dI_F}{dt} = \beta G_3(t)(\hat{S_F} - \wp) - (\mu_2 + \delta_2) I_F \tag{32a}$$
$$\frac{dA}{dt} = \lambda_4(t) + \frac{\eta_1(t) I_{HP}}{N_1} + \frac{\eta_3(t) I_{RP}}{N_3} - \mu_4(t) A. \tag{33}$$

Using Lemma 2.1 in Zhang and Zhao (2007) it follows that there exists a positive T - periodic function $f\hat{(t)}$ such that $f(t) = e^{\iota t} f\hat{(t)}$ is the solution of the linear system (30) - (33) where

$$\iota = \frac{1}{T} ln(\rho(\Phi_{(F(t)-V(t)-M_\wp)}(T)))$$

Now since $\rho(\Phi_{(F(t)-V(t)-M_\varphi)}(T)) > 1$ when $g(0) > 0$, $g(t) \longrightarrow \infty$ as $t \longrightarrow \infty$ when we apply the comparison principal as stated by Smith and Waltman (1995)we have

$E_H(0) \geq 0$, $I_{HB}(0) \geq 0$, $I_{HS}(0) \geq 0$, $I_{HP}(0) \geq 0$, $E_R(0) \geq 0$, $I_{RB}(0) \geq 0$, $I_{RS}(0) \geq 0$, $I_{RP}(0) \geq 0$, $I_F(0) \geq 0$, $A(0) \geq 0$, $E_H \longrightarrow \infty$, $I_{HB} \longrightarrow \infty$, $I_{HS} \longrightarrow \infty$, $I_{HP} \longrightarrow \infty$, $E_R \longrightarrow \infty$, $I_{RB} \longrightarrow \infty$, $I_{RS} \longrightarrow \infty$, $I_{RP} \longrightarrow \infty$, $I_F \longrightarrow \infty$ and $A \longrightarrow \infty$ as $t \longrightarrow \infty$. This lead to a contradiction. □

Now let $M_\partial = \{(\Xi_0) \in \partial X_0 : P^m(\Xi_0) \in \partial X_0, \forall m \geq 0\}$

We claim that

$$M_\partial = \{(S_H, 0, 0, 0, 0, S_R, 0, 0, 0, 0, S_F, 0, 0) : (S_H, S_R, S_F) \geq 0\} \tag{34}$$

Obviously $\{(S_H, 0, 0, 0, 0, 0, S_R, 0, 0, 0, 0, S_F, 0, 0) \in X : (S_H, S_R, S_F) \geq 0\} \subseteq M_\partial$
We therefore need to prove that

$$M_\partial \subseteq \{(S_H, 0, 0, 0, 0, 0, S_R, 0, 0, 0, 0, S_F, 0, 0) \in X : (S_H, S_R, S_F) \geq 0\} \subseteq M_\partial$$

That is for any $(\Xi_0) \in \partial X_0$ we have
$E_H(mT) = I_{HB}(mT) = I_{HS}(mT) = I_{HP}(mT) = R_H(mT) = E_R(mT) = I_{RB}(mT) = I_{RS}(mT) = I_{RP}(mT) = I_F(mT) = A(mT) \ \forall m \geq 0$

If there exists an $m_1 \geq 0$ such that:
$(E_H(m_1T), I_{HB}(m_1T), I_{HS}(m_1T), I_{HP}(m_1T), R_H(m_1T), E_R(m_1T), I_{RB}(m_1T), I_{RS}(m_1T), I_{RP}(m_1T), I_F(m_1T), A(m_1T))^T > 0,$

We replace the initial time 0 with m_1T following the same process as in Dumont *et al.* (2008) we can prove that $S_H > 0, S_R > 0, S_F > 0$. Analogously we also have $(E_H(mT), I_{HB}(mT), I_{HS}(mT), I_{HP}(mT), R_H(mT), E_R(mT), I_{RB}(mT), I_{RS}(mT), I_{RP}(mT), I_F(mT), A(mT))^T > 0, \forall t > m_1T$. Thus we have

$$(\Xi(t)) \in X_0 \forall t > m_1T$$

where $\Xi(t) = (S_H(t), E_H(t), I_{HB}(t), I_{HS}(t), I_{HP}(t), R_H(t), S_R(t), E_R(t), I_{RB}(t), I_{RS}(t), I_{RP}(t), S_F(t), I_F(t), A(t))$ which contradicts that $(\Xi_0) \in \partial X_0$ that requires $P^m(\Xi_0) \in \partial X_0, \ \forall m \geq 0$. So the equality (34) holds, which implies that E_0 is the only fixed point of P and acyclic in ∂X_0.

$P_0 = (S_H, 0, 0, 0, 0, 0, S_R, 0, 0, 0, 0, S_F, 0, 0)$ is an isolated invariant set in X and $W^S(P_0) \cap X_0 = \emptyset$. By the acyclicity theorem on uniform persistence for map (see Zhao (2013)) it follows that P is uniformly persistent with respect to $(X_0, \partial X_0)$.

Using the study by Zhao (2013) (Theorem 1.3.6) implies the P has a fixed point $(S_H^*(0), E_H^*(0), I_{HB}^*(0), I_{HS}^*(0), I_{HP}^*(0), R_H^*(0), S_R^*(0), E_R^*(0), I_{RB}^*(0), I_{RS}^*(0), I_{RP}^*(0), S_F^*(0), I_F^*(0), A^*(0)) \in X_0$.

Now from the first equation of the system (5) - (8) we have

$$S_H^* = e^{-\int_0^t(\alpha_1 G_1(s)+\mu_1)ds}[S_{H0} + \int_0^t (\psi_1 + \varpi R_H)e^{\int_0^t(\alpha_1 G_1(s)+\mu_1)ds}ds]$$

$$\geq \psi_1 e^{-\int_0^t(\alpha_1 G_1(s)+\mu_1)ds} \int_0^t e^{\int_0^t(\alpha_1 G_1(s)+\mu_1)ds}ds > 0 \quad \forall t \in [0,T]$$

The seasonality of S_H^* implies that $S_H^*(t) > 0$ for all $t > 0$. Following the same process as in Lemma 5.1, we get $E_H^*(t) > 0$, $I_{HB}^*(t) > 0$, $I_{HS}^*(t) > 0$, $I_{HP}^*(t) > 0$, $R_H^*(t) > 0$, $S_R^*(t) > 0$, $E_R^*(t) > 0$, $I_{RB}^*(t) > 0$,$I_{RS}^*(t) > 0$, $I_{RP}^*(t) > 0$ $S_F^*(t) > 0$, $I_F^*(t) > 0$ and $A^*(t) > 0$ $\forall t \geq 0$. Therefore ,

($S_H^*(t)$, $E_H^*(t)$, $I_{HB}^*(t)$, $I_{HS}^*(t)$, $I_{HP}^*(t)$, $R_H^*(t)$, $S_R^*(t)$, $E_R^*(t)$, $I_{RB}^*(t)$,$I_{RS}^*(t)$, $I_{RP}^*(t)$ $S_F^*(t)$, $I_F^*(t)$ $A^*(t)$) is a positive T-periodic solution of system (5)- (8). Thus lead to Theorem 7.17 below

Theorem 7.17

System (5)- (8) has at least one positive periodic solution.

7.6.1 Global stability of the positive periodic solution

Here we establish the sufficient condition for the global stability of positive periodic solution. A system (5)- (8) is said to be globally attractive if there exist a positive periodic solution

$soln1(t)$ =($S_{H1}(t)$, $E_{H1}(t)$, $I_{HB1}(t)$, $I_{HS1}(t)$, $I_{HP1}(t)$, $R_{H1}(t)$, $S_{R1}(t)$, $E_{R1}(t)$, $I_{RB1}(t)$,$I_{RS1}(t)$, $I_{RP1}(t)$ $S_{F1}(t)$, $I_{F1}(t)$ $A_1(t)$) for a system (5)- (8) and any other solution

$soln2(t)$ =($S_{H2}(t)$, $E_{H2}(t)$, $I_{HB2}(t)$, $I_{HS2}(t)$, $I_{HP2}(t)$, $R_{H2}(t)$, $S_{R2}(t)$, $E_{R2}(t)$, $I_{RB2}(t)$,$I_{RS2}(t)$, $I_{RP2}(t)$ $S_{F2}(t)$, $I_{F2}(t)$ $A_2(t)$) with positive initial values such that

$$\lim_{t\longrightarrow\infty} \mid soln1_i(t) - soln2_i(t) \mid = 0$$

where $soln1_i$ and $soln2_i$ are the two solutions of the system (5)- (8).

We prove the global stability of the positive periodic solution using Korobeinikov approach. We first formulate a suitable Lyapunov function for plague disease model (Korobeinikov, 2004,

2007)

The Lyapunov function is as given in the form below;

$$V = \sum a_i(y_i - y_i^* \ln y_i)$$

where a_i is defined as a properly selected positive constant, y_i defines the population of the i^{th} compartment at time t, and y_i^* is the periodic solution for model system (5)- (8) at time t.
Now the Lyapunov function is,

$$\begin{aligned} V = \; & W_1(S_H - S_H^* \ln S_H) + W_2(E_H - E_H^* \ln E_H) + W_3(I_{HB} - I_{HB}^* \ln I_{HB}) \\ & + W_4(I_{HS} - I_{HS}^* \ln I_{HS}) + W_5(I_{HP} - I_{HP}^* \ln I_{HP}) + W_6(R_H - R_H^* \ln R_H) \\ & + W_7(S_R - S_R^* \ln S_R) + W_8(E_R - E_R^* \ln E_R) + W_9(I_{RB} - I_{RB}^* \ln I_{RB}) \\ & + W_{10}(I_{RS} - I_{RS}^* \ln I_{RS}) + W_{11}(I_{RP} - I_{RP}^* \ln I_{RP}) + W_{12}(S_F - S_F^* \ln S_F) \\ & + W_{13}(I_F - I_F^* \ln I_F) + W_{14}(A - A^* \ln A) \end{aligned}$$

The constants W_i are non negative in Φ for $i = 1, 2, 3...12$, V is Lyapunov function. The function V together with its constants $W_1, W_2...W_{14}$ are chosen such that V is continuous and differentiable in a space

We compute the time derivative of V this yields;

$$\begin{aligned} \frac{dV}{dt} = \; & W_1(1 - \tfrac{S_H^*}{S_H})\tfrac{dS_H}{dt} + W_2(1 - \tfrac{E_H^*}{E_H})\tfrac{dE_H}{dt} + W_3(1 - \tfrac{I_{HB}^*}{I_{HB}})\tfrac{dI_{HB}}{dt} + W_4(1 - \tfrac{I_{HS}^*}{I_{HS}})\tfrac{dI_{HS}}{dt} \\ & + W_5(1 - \tfrac{I_{HP}^*}{I_{HP}})\tfrac{dI_{HP}}{dt} + W_6(1 - \tfrac{R_H^*}{R_H})\tfrac{dR_H}{dt} + W_7(1 - \tfrac{S_R^*}{S_R})\tfrac{dS_R}{dt} + W_8(1 - \tfrac{E_R^*}{E_R})\tfrac{dE_R}{dt} \\ & + W_9(1 - \frac{I_{RB}^*}{I_{RB}})\frac{dI_{RB}}{dt} + W_{10}(1 - \frac{I_{RS}^*}{I_{RS}})\frac{dI_{RS}}{dt} + W_{11}(1 - \frac{I_{RP}^*}{I_{RP}})\frac{dI_{RP}}{dt} \\ & + W_{12}(1 - \frac{S_F^*}{S_F})\frac{dS_F}{dt} + W_{13}(1 - \frac{I_F^*}{I_F})\frac{dI_F}{dt} + W_{14}(1 - \frac{A^*}{A})\frac{dA}{dt} \end{aligned}$$

Using system (5)- (8) we will have

$$\begin{aligned} \frac{dV}{dt} = \; & W_1(1 - \tfrac{S_H^*}{S_H})[\psi_1 + \varpi R_H - \alpha_1 G_1(t) S_H - \mu_1 S_H,] \\ & + W_2(1 - \tfrac{E_H^*}{E_H})[\alpha_1 G_1(t) S_H - \alpha_2 E_H - \mu_1 E_H,] \\ & + W_3(1 - \frac{I_{HB}^*}{I_{HB}})[\alpha_2 \nu_2 E_H - \alpha_3 I_{HB} - (\mu_1 + \delta_{1b}) I_{HB},] \\ & + W_4(1 - \tfrac{I_{HS}^*}{I_{HS}})[\alpha_3 \rho_3 I_{HB} + \alpha_2 \nu_3 E_H - \alpha_4 I_{HS} - (\mu_1 + \delta_{1s}) I_{HS},] \\ & + W_5(1 - \tfrac{I_{HP}^*}{I_{HP}})[\alpha_2 \nu_1 E_H + \alpha_3 \rho_1 I_{HB} + \alpha_4 \xi I_{HS} - \alpha_5 I_{HP} - (\mu_1 + \delta_{1p}) I_{HP},] \\ & + W_6(1 - \tfrac{R_H^*}{R_H})[\alpha_3 \rho_2 I_{HB} + \alpha_4 (1 - \xi) I_{HS} + \alpha_5 I_{HP} - \varpi R_H - \mu_1 R_H,] \\ & + W_7(1 - \tfrac{S_R^*}{S_R})[\psi_3 - \gamma_1 G_2(t) S_R - \mu_3 S_R,] \\ & + W_8(1 - \tfrac{E_R^*}{E_R})[\gamma_1 G_2(t) S_R - \gamma_2 E_R - \mu_3 E_R,] \end{aligned}$$

$$
\begin{aligned}
&+W_9(1-\tfrac{I^*_{RB}}{I_{RB}})[\gamma_2\tau_3E_R-\gamma_3I_{RB}-(\mu_3+\delta_{3b})I_{RB},]\\
&+W_{10}(1-\tfrac{I^*_{RS}}{I_{RS}})[\gamma_2\tau_2E_R+\gamma_3(1-\phi)I_{RB}-\gamma_4I_{RS}-(\mu_3+\delta_{3s})I_{RS},]\\
&+W_{11}(1-\tfrac{I^*_{RP}}{I_{RP}})[\gamma_2\tau_1E_R+\gamma_3\phi I_{RB}+\gamma_4I_{RS}-(\mu_3+\delta_{3p})I_{RP},]\\
&+W_{12}(1-\tfrac{S^*_F}{S_F})[\psi_{2s}-\beta G_3(t)S_F-\mu_2S_F,]\\
&+W_{13}(1-\tfrac{I^*_F}{I_F})[\beta G_3(t)S_F-(\mu_2+\delta_2)I_F]\\
&+W_{14}(1-\tfrac{A^*}{A})[\lambda_4+\tfrac{\eta_1(t)I_{HP}}{N_1}+\tfrac{\eta_2(t)I_{RP}}{N_3}-\mu_4A.]
\end{aligned}
$$

Using system (5) - (8) at endemic equilibrium we can after simplification we get the following;

$$
\begin{aligned}
\frac{dV}{dt} =& -W_1(1-\frac{S^*_H}{S_H})^2-W_2(1-\frac{E^*_H}{E_H})^2-W_3(1-\frac{I^*_{HB}}{I_{HB}})^2-W_4(1-\frac{I^*_{HS}}{I_{HS}})^2\\
&-W_5(1-\frac{I^*_{HP}}{I_{HP}})^2-W_6(1-\frac{R^*_H}{R_H})^2-W_7(1-\frac{S^*_R}{S_R})^2-W_8(1-\frac{E^*_R}{E_R})^2\\
&-W_9(1-\frac{I^*_{RB}}{I_{RB}})^2-W_{10}(1-\frac{I^*_{RS}}{I_{RS}})^2-W_{11}(1-\frac{I^*_{RP}}{I_{RP}})^2-W_{12}(1-\frac{S^*_F}{S_F})^2\\
&-W_{13}(1-\frac{I^*_F}{I_F})^2-W_{14}(1-\frac{A^*}{A})^2\\
&+F(S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A)
\end{aligned}
\tag{35}
$$

where the function $F(S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A)$ is non positive. We follow the procedures by McCluskey (2006); Korobeinikov and Wake (2002). We take:

$$F(S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A)\geq 0$$

for all

$$S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A$$

. Then $\frac{dV}{dt}\leq 0$ for all $S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A$ and it is zero when $S_H=S^*_H,E_H=E^*_H,I_{HB}=I^*_{HB},I_{HS}=I^*_{HS},I_{HP}=I^*_{HP},R_H=R^*_H,S_R=S^*_R,E_R=E^*_R,I_{RB}=I^*_{RB},I_{RS}=I^*_{RS},I_{RP}=I^*_{RP},S_F=S^*_F,I_F=I^*_F,A=A^*$. Hence the largest compact invariant set in $S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A$ such that $\frac{dV}{dt}=0$ is the singleton E^* which is periodic solution of the plague disease system (5)-(8). Using LaSalles's invariant principle by La Salle (1976), it entails that the periodic solution of plague disease system (E^*) is globally asymptotically stable in the interior of the region of $S_H,E_H,I_{HB},I_{HS},I_{HP},R_H,S_R,E_R,I_{RB},I_{RS},I_{RP},S_F,I_F,A$ and thus leads to Theorem 7.18.

Theorem 7.18

If $R_T>1$ then the model system (5) and (8) of plague disease has a unique periodic solution E^* which is globally asymptotically stable in S_H, E_H, I_{HB}, I_{HS}, I_{HP}, R_H, S_R, E_R, I_{RB}, I_{RS}, I_{RP}, S_F, I_F, A .

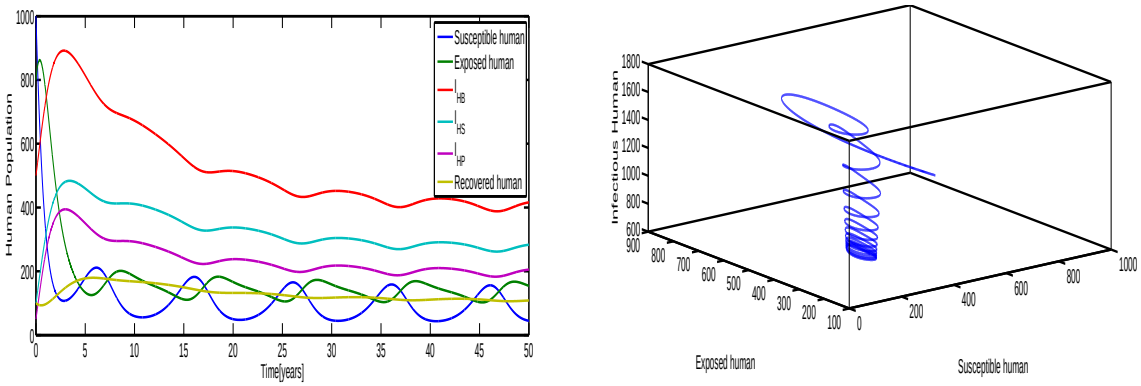
7.7 Numerical Results and Discussion

We use the parameter values given in Table 18 to study the behavior of the model system (5) - (8) through numerical simulation. Sub-Fig. 4b shows the dynamics in human population and the solution trajectory in (S_H, E_H, I_{HB}, I_{HS}, I_{HP})-Space. We can see that, there is a periodic decrease of the susceptible and exposed populations to its periodic solution. This behavior is caused by the presence of all three main forms of plague disease, which consequently lead to mammoth increase of the force of infection. Number of human beings who recover from the disease somewhat periodically increase and then drops off to its periodic solution. Human population experiences a very little recovery rate due to the assumption that there is no effort invested in treating the infected individuals, which is also justified by Gani and Leach (2004). As the disease become endemic the number of susceptible individuals will decrease and become exposed to the disease and then infected in any of the three forms of plague depending on the kind of transmission and individual got into.

Figure 65a shows the dynamics of rodent population, We can see that the infected rodent population (I_{RB}, I_{RB} and I_{RB}) experience the periodic increase before it lingers to its periodic solution. The number of susceptible and exposed rodent periodically decreases due to endemicity of the disease to their periodic solutions.

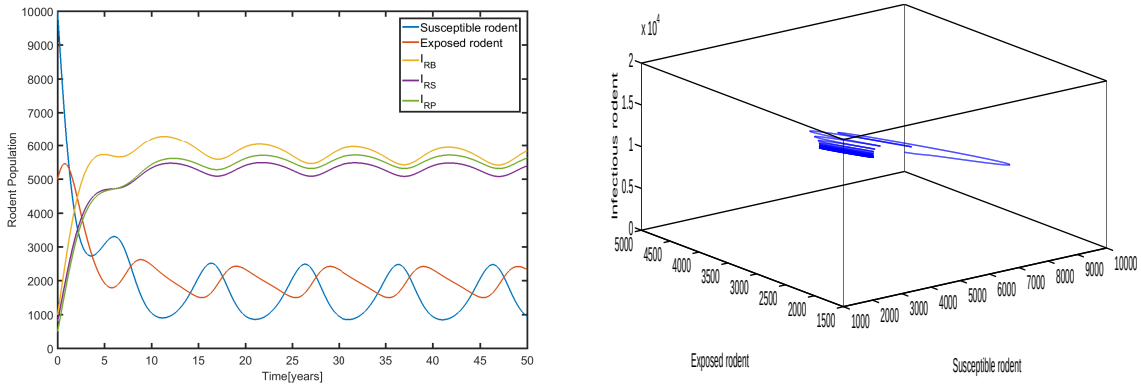
When there is an increase in human beings and rodents infected with plague disease, the rate of transmission of the disease from Human being and rodents to flea also increases. Figure 66a shows the dynamics in flea population, it shows a significant increase of I_F which is mostly contributed by the increase in number of I_{HB}, I_{HS}, I_{RB} and I_{RS}. The pathogens in the environment also shows a periodic increase to its periodic solution as in Fig. 67. The behavior shown by the pathogens in the environment is mostly contributed by the increase in number of individuals (Human beings and Rodents) with pneumonic plague.

Figures 5, 65b and 66b shows the orbits in (S_H, E_H, $I = I_{HB} + I_{HS} + I_{HP}$) phase-space, ($S_R$, E_R, $I = I_{RB} + I_{RS} + I_{RP}$) phase-space and ($S_H$, I_F) phase-space for Human beings, rodents and flea populations. These orbits shows the magnitude of periodic solutions which is determined by the strength of seasonal forcing (σ). The repeated oval shapes illustrated by these Figures also represent the existence and global stability of the periodic solution in these populations.



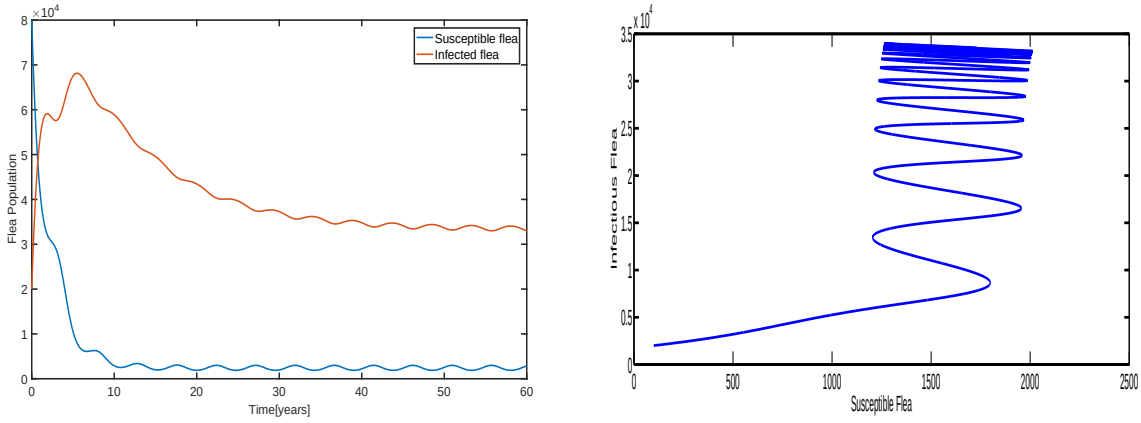
(a) **(b)**

Figure 64: Figure 64a gives the dynamics of Human with baseline parameter values given in Table 18. Figure 64b gives the (S_H, E_H, $I = I_{HB} + I_{HS} + I_{HP}$) phase-space plot of system 5



(a) **(b)**

Figure 65: Figure 65a gives the dynamics of Rodent with baseline parameter values given in Table 18. Figure 65b gives the (S_R, E_R, $I = I_{RB} + I_{RS} + I_{RP}$) phase-space plot of system 6



(a) **(b)**

Figure 66: Figure 66a gives the dynamics of Flea with baseline parameter values given in Table 18. Figure 66b gives the (S_H, I_F) phase-space plot of system 7

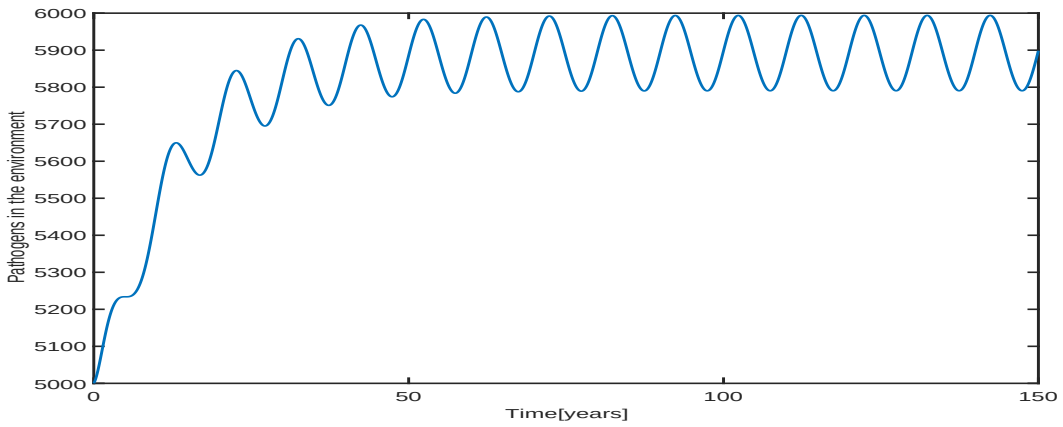


Figure 67: The dynamics of Pathogens in the environment with baseline parameter values given in Table 18

Weather variation affects the dynamics of plague disease in deferent magnitudes depending on the intensity and the duration it stays supportive or not supportive to the transmission of plague disease (Chiyaka *et al.*, 2010). Figure 68, Fig. 69 and Fig. 70, Fig. 71, Fig. 72 and Fig. 73, Fig. 74 and Fig. 75 shows that the increase of the amplitude of seasonality periodically increases the number of infectives in Human beings, Rodents, Fleas and Pathogens in the environment respectively.

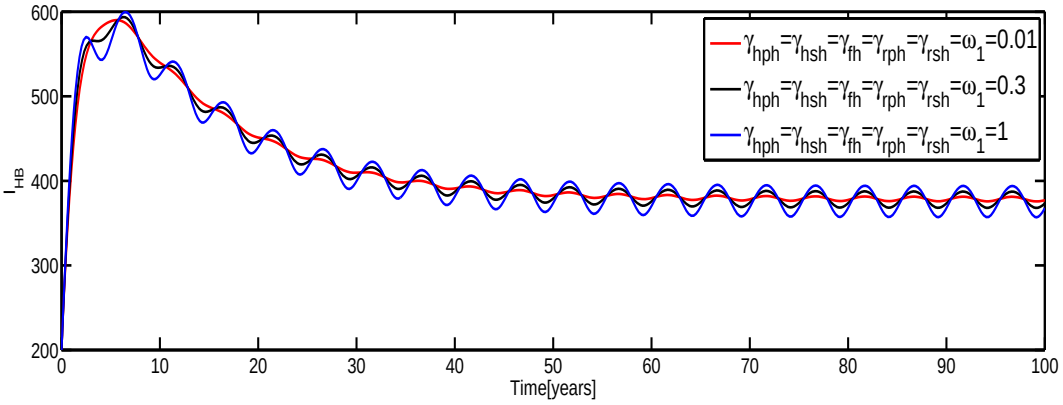


Figure 68: The Effect of the Amplitude of Seasonality in the dynamics of I_{HB}.

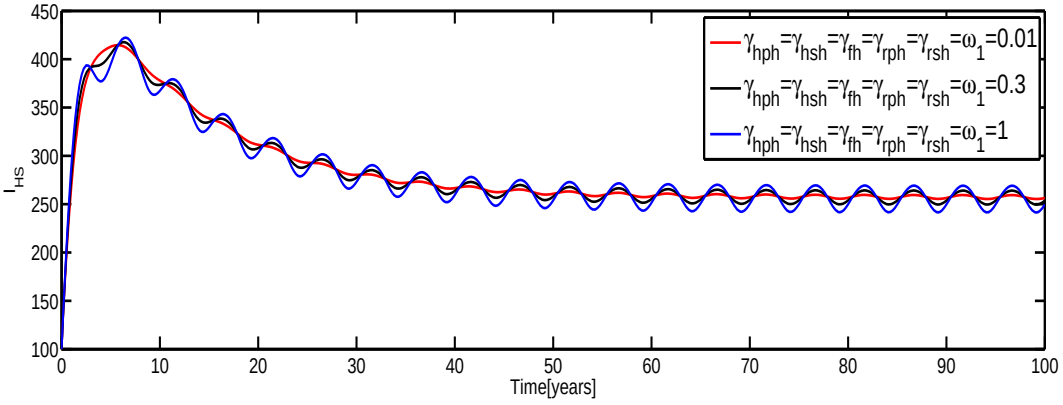


Figure 69: The Effect of the Amplitude of Seasonality in the dynamics of I_{HS}.

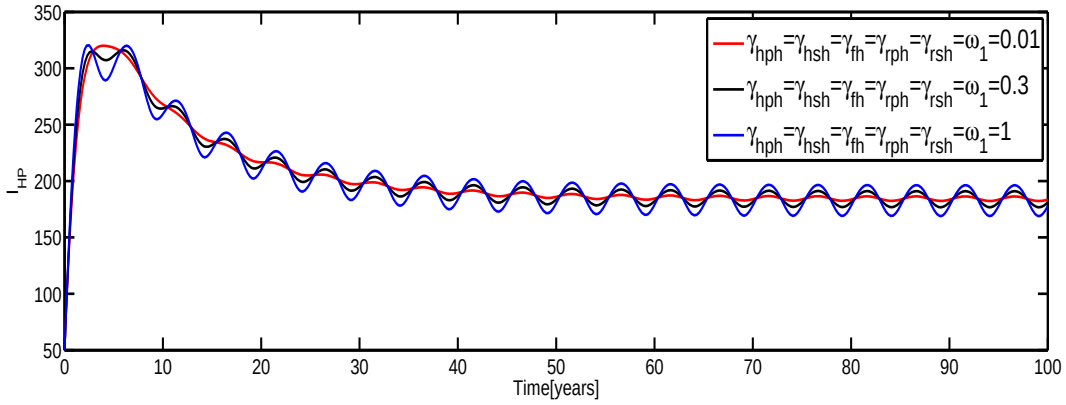


Figure 70: The Effect of the Amplitude of Seasonality in the dynamics of I_{HP}.

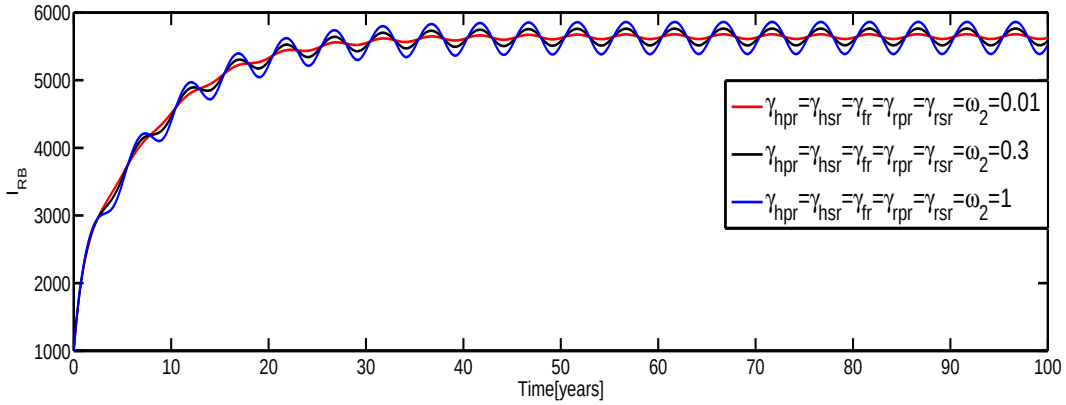


Figure 71: The Effect of the Amplitude of Seasonality in the dynamics of I_{RB}.

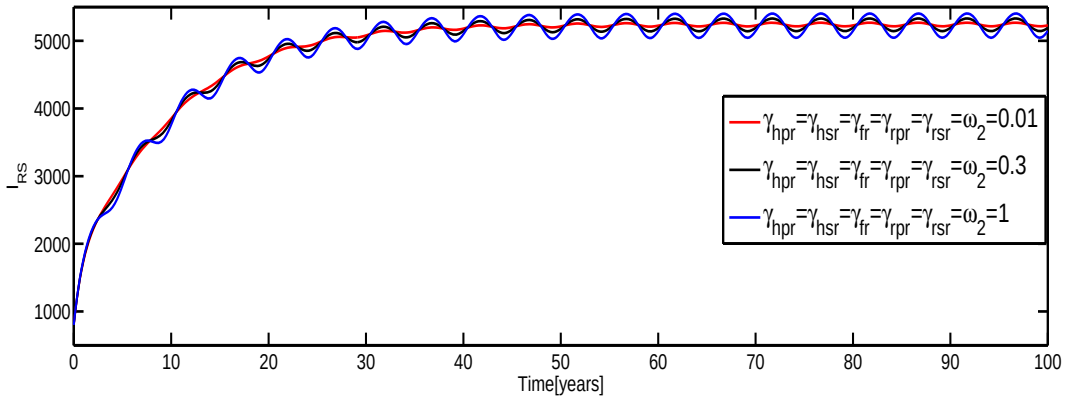


Figure 72: The Effect of the Amplitude of Seasonality in the dynamics of I_{RS}.

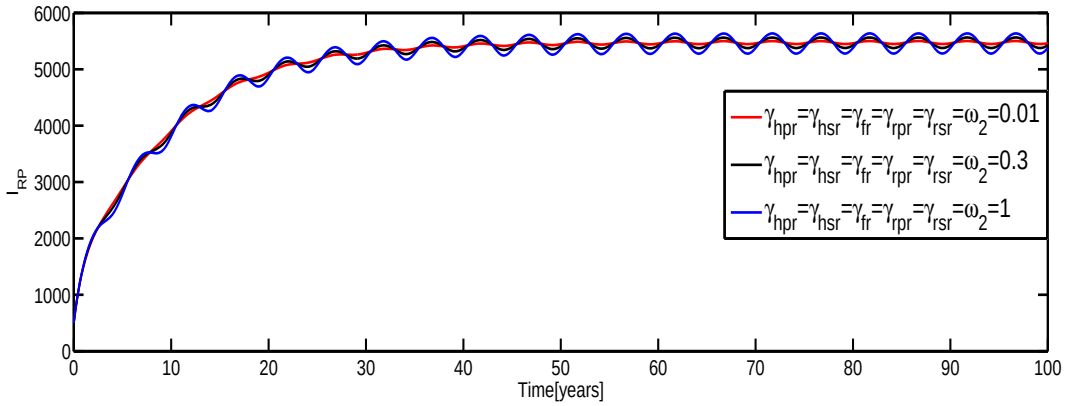


Figure 73: The Effect of the Amplitude of Seasonality in the dynamics of I_{RP}.

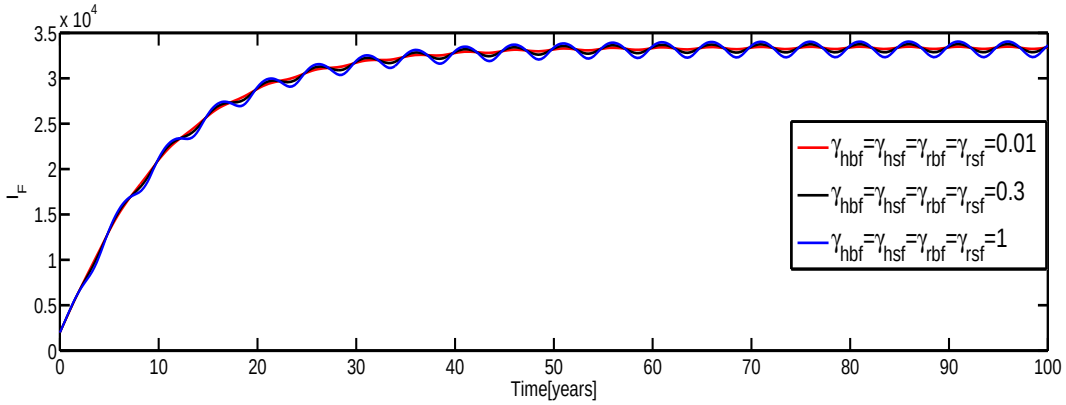


Figure 74: The Effect of the Amplitude of Seasonality in the dynamics of I_F.

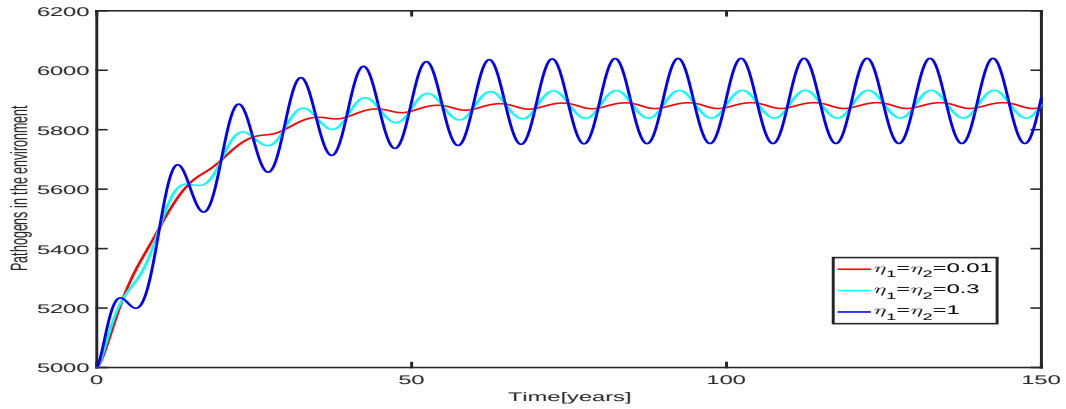
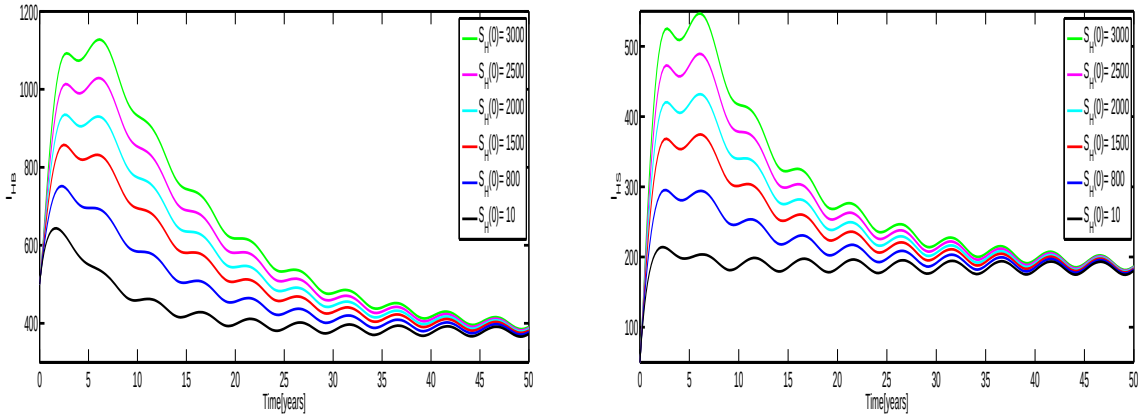


Figure 75: The Effect of the Amplitude of Seasonality in the dynamics of Pathogens in the Environment.

These results suggest that, when the weather condition fevers the increase of transmission rates of plague disease in Human beings, Rodents, Fleas and Pathogens in the environment the prevalence of the disease increases significantly. The effect posed by weather variation on the rate of transmission of plague disease, is mainly based on how long and to what extent the weather

condition favors or hinders the plague disease transmission. This implies that for effective control results the control measures should be put in place to reduce infection in accordance of the fluctuation of the plague disease transmission due to seasonality.

The initial conditions used in this model are partly from related literature and others are estimated. In most cases initial values are observed to have stronger influence on the infectious classes. However in other cases the influence may be little or almost of no effect on the infectious classes (Zhang *et al.*, 2012). It is then important to study the effects that the initial condition within the particular population has on the dynamics of the plague disease infection in human beings, rodents, fleas and pathogens in the environment. From Fig. 76 and Fig. 77 we can see that the changes of initial conditions in susceptible human beings $S_H(0)$ shows the significant effect on the human infectious classes I_{HB}, I_{HS} and I_{HP}. We can also see the same behavior in infectious rodent and flea as the initial values for $S_R(0)$ and $S_F(0)$ changes as in Fig. 78, 79 and 80 respectively.



(a) **(b)**

Figure 76: The Effect of initial conditions of S_H on the number of I_{HB} and I_{HS}

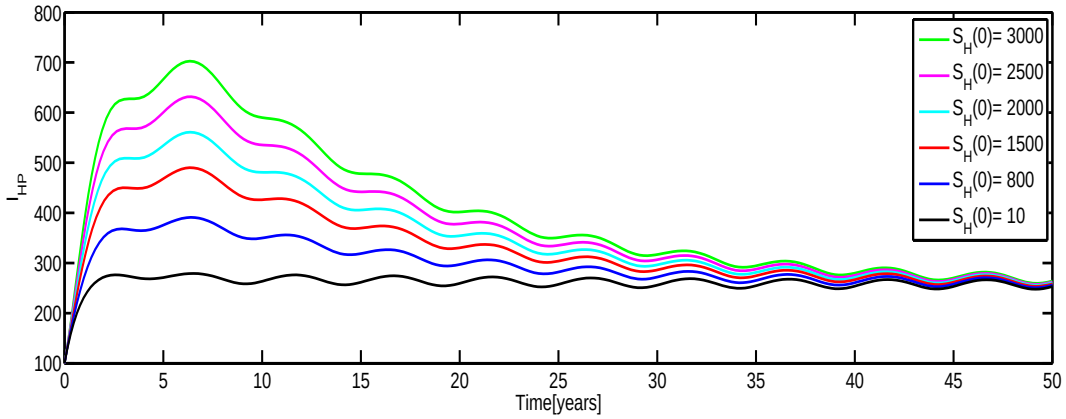
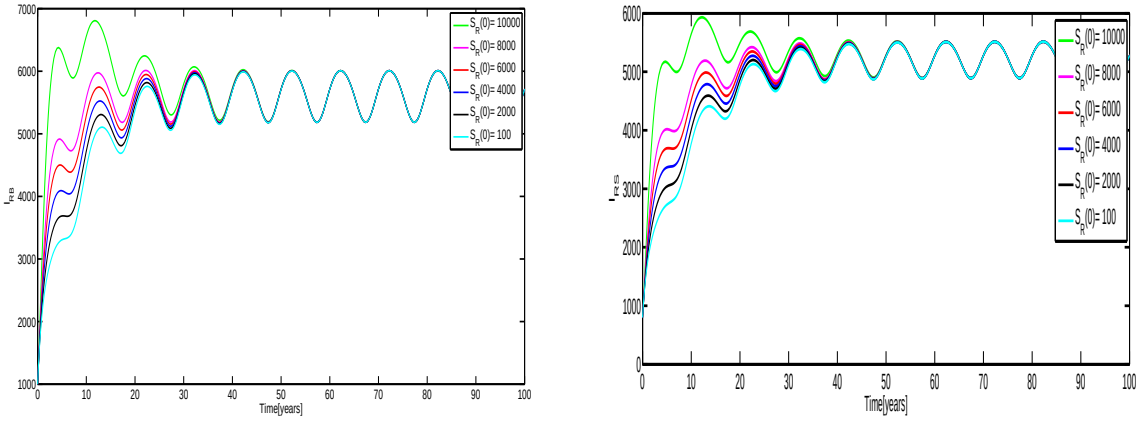
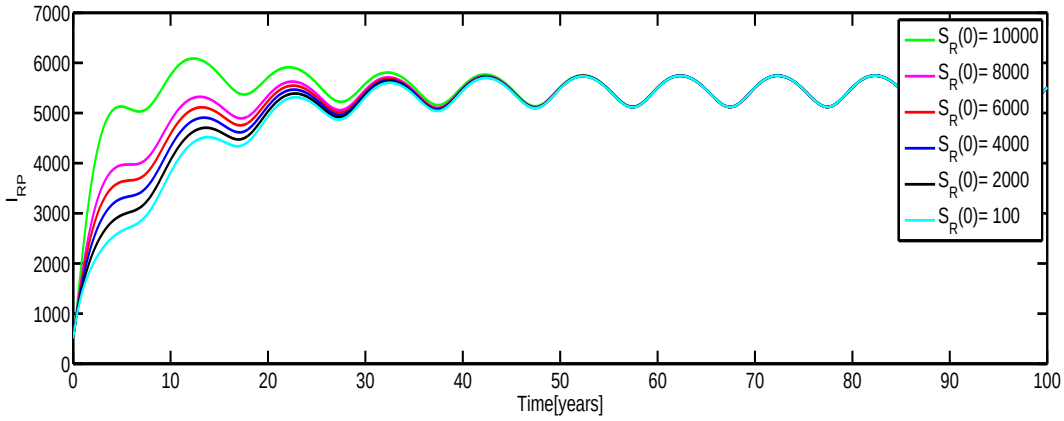


Figure 77: The Effect of initial conditions of S_H on the number of I_{HP}



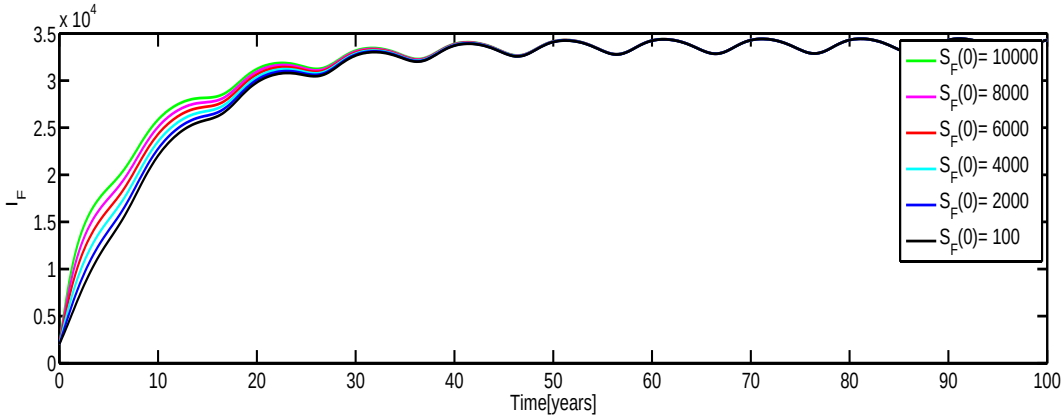
(a) **(b)**

Figure 78: The Effect of initial conditions of S_H on the number of I_{RB} and I_{RS}



(a)

Figure 79: The Effect of initial conditions of S_H on the number of I_{RP}



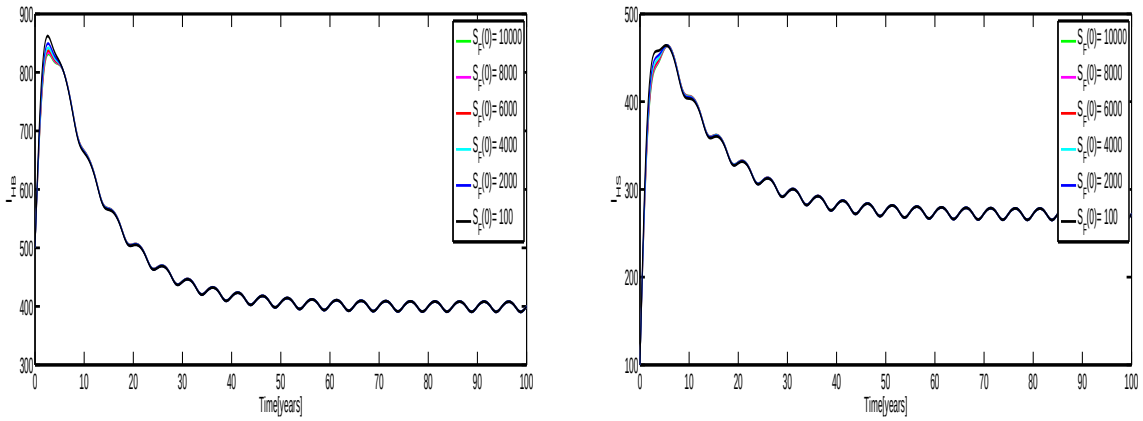
(a)

Figure 80: The Effect of initial conditions of S_F on the number of I_F.

This entails that the increase (decrease) of the initial values will result to the increase (decrease) of the adequate interaction which lead to the disease within the particular population. It thus

shows that, reducing the interaction between the susceptible individuals and the infectious hinders the spread of the disease from one individual to the other. This then concludes that an outbreak of the disease that occur in areas with dense population spreads faster compared to the one in area of low population.

The effect of changes of initial conditions may also be extended between two different populations in which the change of initial values in one population affects the dynamics in another population. Figure 81, Fig. 83, Fig. 84, Fig. 82 and Fig. 85 shows that, the changes in the initial values of $S_F(0)$ and $S_R(0)$ has the marginal effect to the infectious human beings and pathogens in the environment respectively.



(a) **(b)**

Figure 81: The Effect of initial conditions of S_F on the number of I_{HB} and I_{HS}

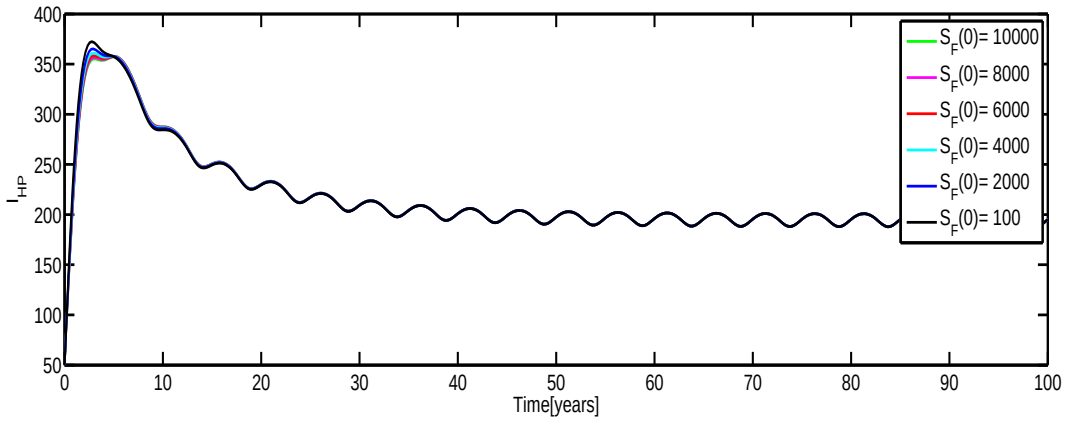
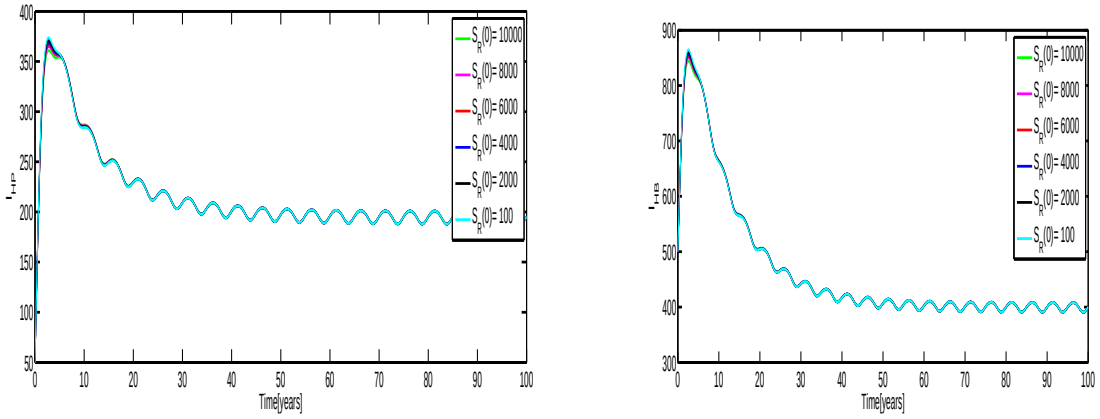


Figure 82: The Effect of initial conditions of S_F on the number of I_{HP}



(a) **(b)**

Figure 83: The Effect of initial conditions of S_R on the number of I_{HP} and I_{HB}

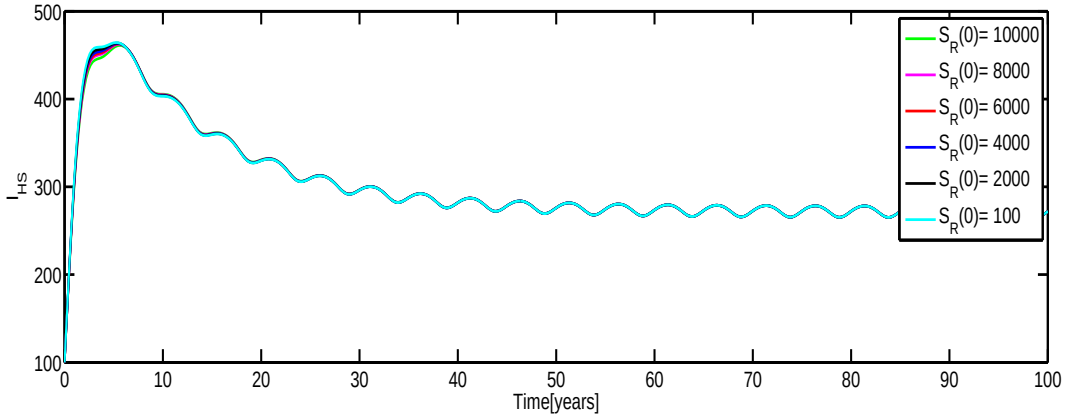
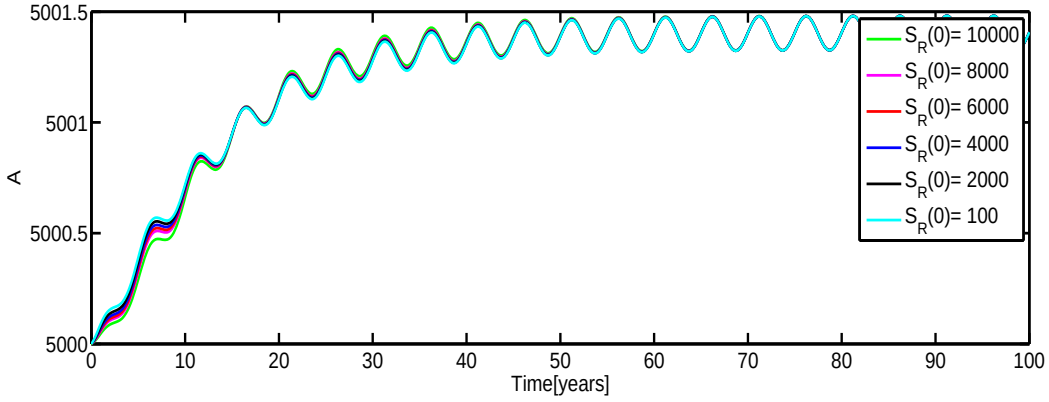


Figure 84: The Effect of initial conditions of S_R on the number of I_{HS}



(a)

Figure 85: The Effect of initial conditions of S_R on the number of A

Not all changes of initial conditions have significant effects to the dynamics of plague infection in another population. Some have a minor effect to other population and the reason may be due

to the nature of interaction of the respective populations. Figure 86 and Fig. 87 shows that the changes in initial conditions in $S_H(0)$ has a negligible effect in the dynamics of the disease in rodents, fleas and pathogens in the environment. The same result can also be seen in Fig. 88 which shows that the changes in initial conditions of susceptible flea $S_F(0)$ do not affect the incidences of infection in rodents and the pathogens in the environment. Moreover we can also see the that the changes of initial conditions in susceptible rodents $S_R(0)$ have no effect on the pervasiveness of infection in fleas and pathogens in the environment as in Fig. 89.

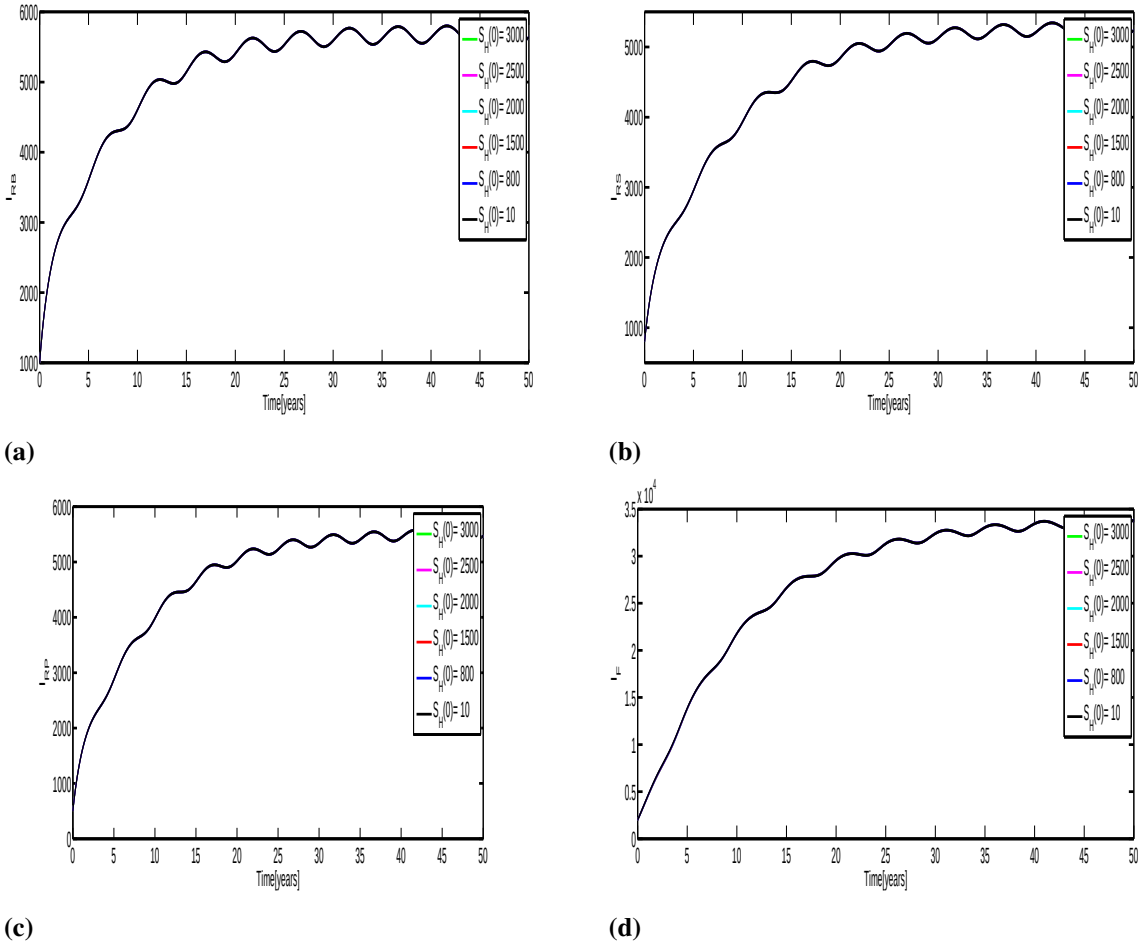
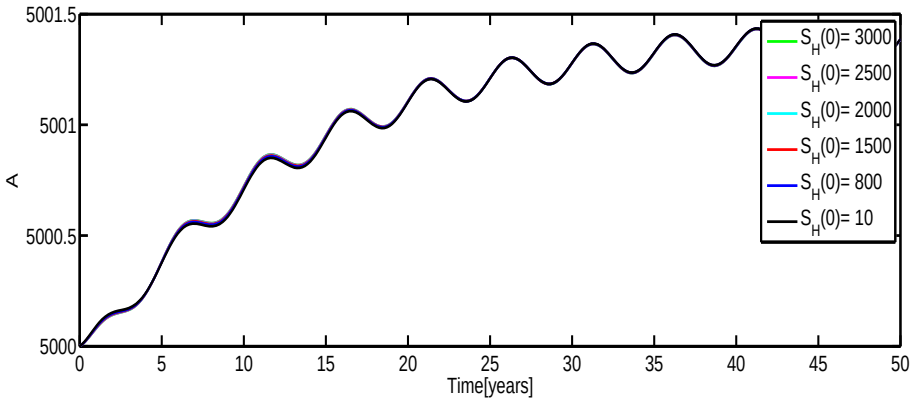
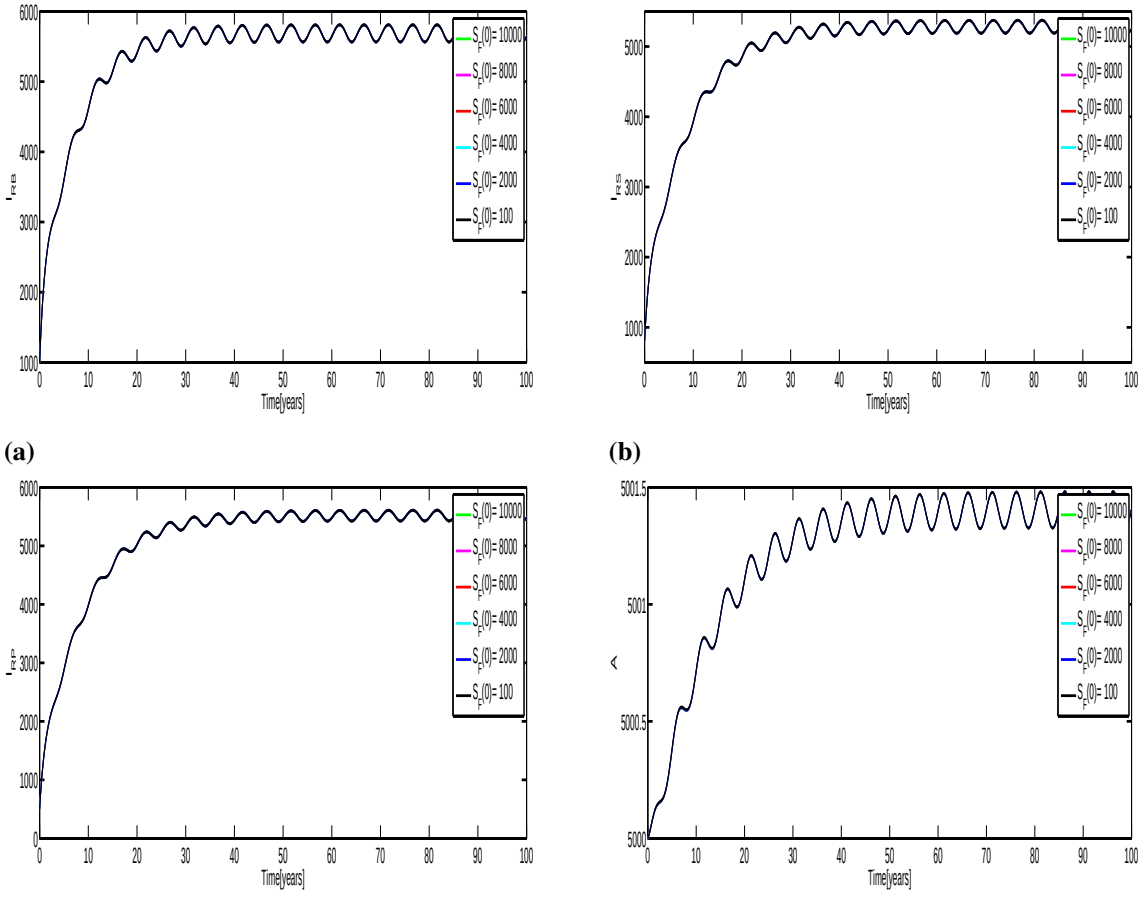


Figure 86: The Effect of initial conditions of $S_H(0)$ on the number of infectious rodent and flea.



(a)

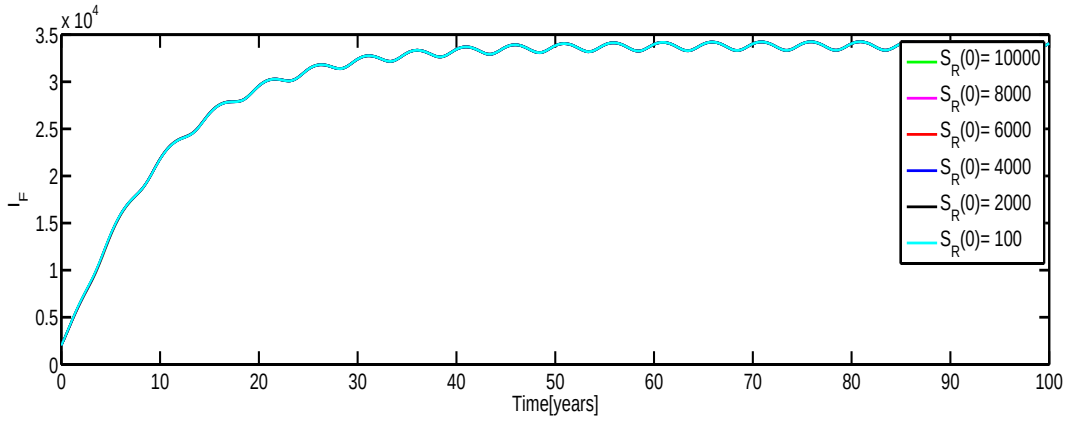
Figure 87: The Effect of initial conditions of $S_H(0)$ on the number of pathogens in the environment.



(a) **(b)**

(c) **(d)**

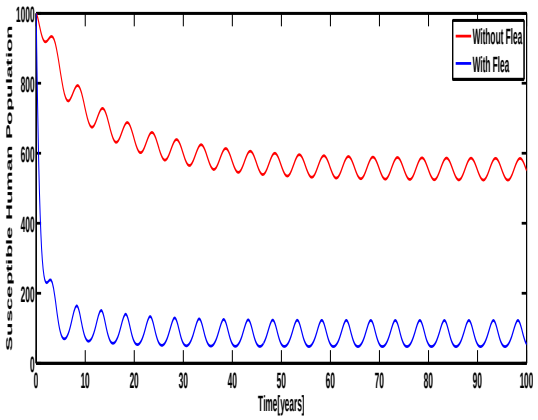
Figure 88: The Effect of initial conditions of $S_F(0)$ on the number of infectious rodent and pathogens in the environment.



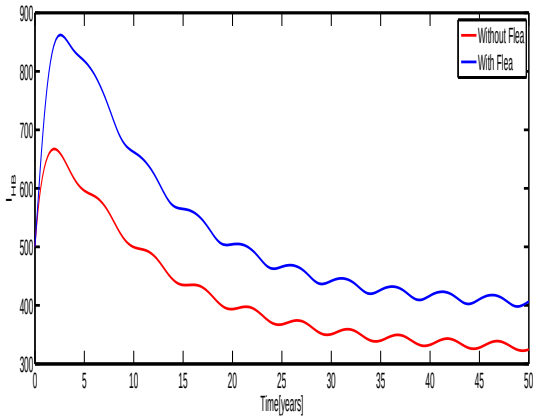
(a)

Figure 89: The Effect of initial conditions of $S_R(0)$ on the number of infectious flea.

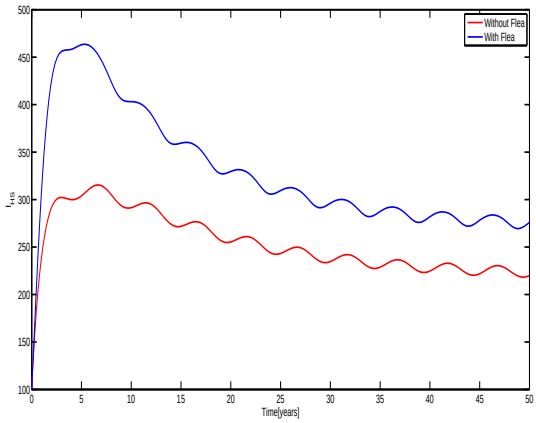
Infectious flea plays a vital role in the transmission of the primary forms of plague disease in Human beings and Rodents. This gives it an ability to change the dynamics of plague disease by significantly increase the number of infectious individuals with bubonic and/or septicemic plague. Figure 90 Fig. 91 and Fig. 92 show the effect of infectious flea in the dynamics of plague disease in Human beings and Rodents respectively. We can see that in both Human beings and Rodents, presence of flea lead to the increase in the number of infectious classes of all three forms of plague disease. The graphs shows that Human beings and Rodents with bubonic plague are mostly affected followed by those with septicemic plague and lastly the pneumonic plague infectives. In both populations, bubonic and septicemic plague infectious classes are highly affected by flea in light of the fact that they are directly transmitted through flea bite. Thus the increase of infectious flea proportionally increase the bubonic and septicemic plague infection rates.



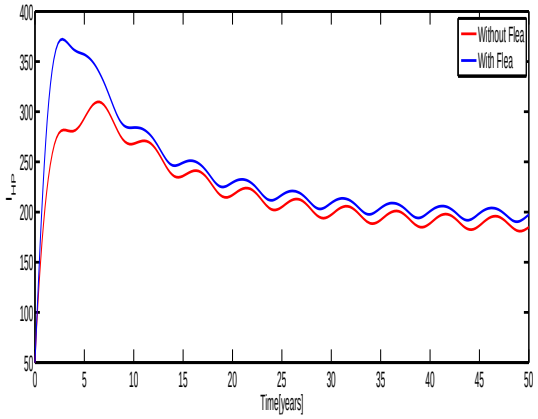
(a)



(b)

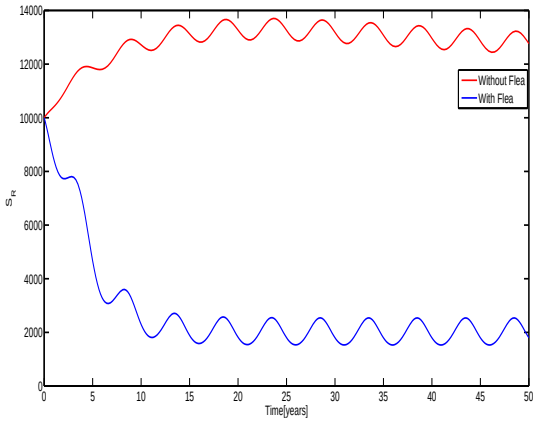


(c)

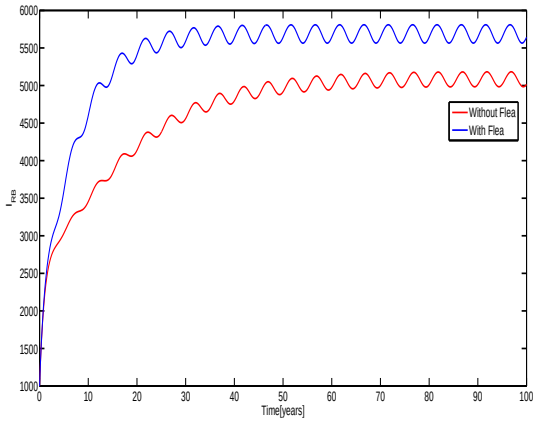


(d)

Figure 90: The effect of flea in the dynamics of plague in Human population.

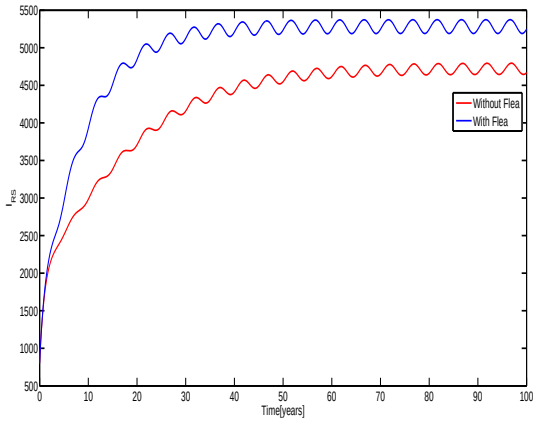


(a)

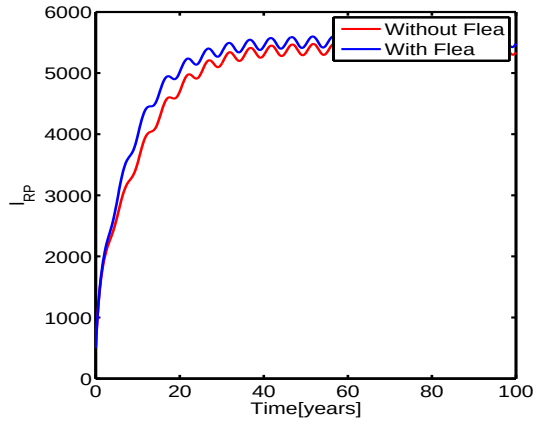


(b)

Figure 91: The effect of flea in the dynamics of S_R and I_{RB}.



(a)

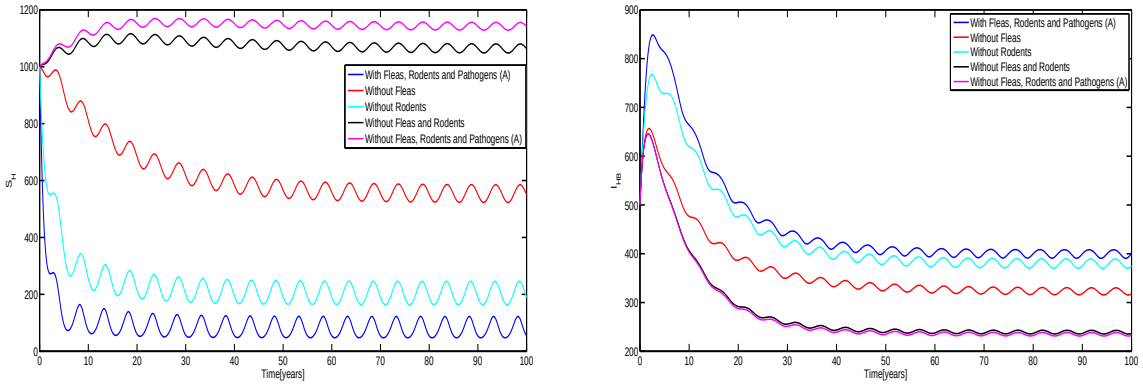


(b)

Figure 92: The effect of flea in the dynamics of I_{RS} and I_{RP}.

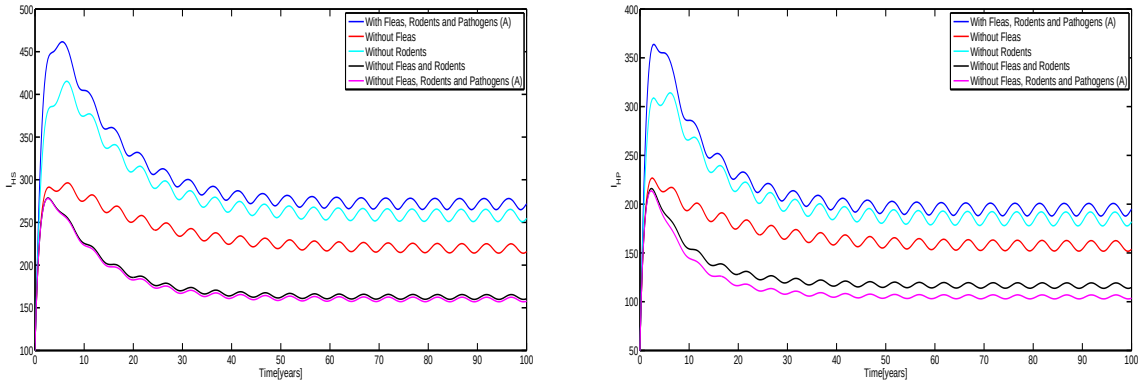
The dynamics and transmission of plague disease in Human population is mainly sustained by the presence of infectious fleas, rodents and the pathogens in the environment. Each of these

agents plays different role in the transmission and spread of plague disease. Figure 93 and Fig. 94 shows the contribution of each agent in the dynamics of plague disease in human population. It shows the dynamics of human population when these plague disease transmission agents in different levels are assumed not to contribute to the transmission of plague disease. The results shows that, the absence of flea alone lead to a very significant decrease of the infectious human beings compared to the absence of rodent alone. However the decrease of infection appear to be of much significance when both flea and rodent are removed from the human dynamics of plague disease. Moreover, since the pathogens in the environment mostly affect the Human lungs causing pneumonia, it is the reason why we see that the removal of pathogens in the environment affect more the human being with pneumonic plague than those with bubonic and septicemic plague.



(a) **(b)**

Figure 93: The effect of non-human plague agents in the dynamics of plague in S_H and I_{HB}.



(a) **(b)**

Figure 94: The effect of non-human plague agents in the dynamics of plague in I_{HS} and I_{HP}.

The substantial decrease of infectious classes shown in Fig. 94 justifies the tangible role played by flea, rodents and pathogens in the environment in the transmission and spread of plague

disease in Human population. This confirms that controlling flea's and rodent population will reduce the interaction between Human being and non human agents of plague disease and as a result reduce the transmission and spread of plague disease. It also suggests that maintaining the good environmental hygiene mostly to the people living in rural areas should be encouraged in order to reduce multiplication and growth of pathogens in the environment which will in-turn reduce the probability of being affected by the pathogens in the environment.

These results suggest that, when the weather condition favours the increase of transmission rates of plague disease in Human beings, Rodents, Fleas and Pathogens in the environment the prevalence of the disease increases significantly. The effect posed by weather variation on the rate of transmission of plague disease, is mainly based on how long and to what extent the weather condition favours or hinders the plague disease transmission. This implies that the control measures should be put in place to reduce infection in accordance of the fluctuation of the plague disease transmission due to seasonal weather variation.

7.8 Conclusion

Seasonality continues to be a the great challenge for effective planning and control of infectious diseases. In most cases, these fluctuations are unpredictable in terms of time they occur and scope, which extremely harden the proper and effective control plans. In this paper we have formulated and analyzed the plague disease model with periodic infection rate. We defined the basic reproduction number R_T for the proposed model. We have shown that under some appropriate biological assumption the disease free equilibrium of the plague disease model is globally asymptotically stable if $R_T < 1$. If $R_T > 1$ then the proposed model has at least one periodic solution which is globally asymptotically stable. Also using numerical simulation we have shown the global behavior of the model. From our simulation result we can deduce that the periodic solution of the plague disease model exists and is globally asymptotically stable.

CHAPTER EIGHT

General Discussion, Conclusion and Recommendations

8.1 General Discussion

In this study, the mathematical models for the dynamics of plague disease have been developed and analyzed. The models include four populations which are human, rodent, flea and pathogens in the environment. The plague disease model is developed in three stages in which the first stage is the development of bubonic plague model which in our case is considered as the primary form of plague disease. We then develop the pneumonic plague disease model while incorporating the features and characteristics that link it with bubonic plague. Third stage is the development of the combined model of all three forms of plague disease (Bubonic, Pneumonic and septicemic plague). We finally modify and analyze the general model by incorporating variations in the parameters due to seasonal weather variation.

In Chapter Two, we developed a bubonic plague disease model that considered two major modes of transmission which are through infected flea bites and the interaction with the infected materials in the environment. We used the next generation matrix methods to compute the basic reproduction number R_0. We then performed the sensitivity analysis of R_0 to determine the effects of various parameters. We are able to deduce that the number of secondary cases of individuals with bubonic plague depends on: flea's infective period, probability that a rodent survive the infected class, the adequate contact rate flea to human, rodent infectious period, the probability that flea gets the disease from the rodent or human, human infectious period, probability that human survive the infected class, the rate at which fleas get infected, the adequate contact rate between flea and rodent, and the rate at which human and rodent become exposed to the disease.

In Chapter Three, we worked on the existence of equilibrium points and established the conditions for their local and global stability. The analysis shows that both endemic equilibrium and disease free equilibrium points exist. Using the basic reproduction number R_0 computed in Chapter Two we established the condition for persistence and extinction of the disease. We were able to deduce that the disease free equilibrium point is locally and globally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$ while the endemic equilibrium point was found to be locally and globally asymptotically stable when $R_0 > 1$ and unstable when $R_0 < 1$.

In Chapter Four, we developed a pneumonic plague disease model to assess the dynamics of plague disease when the bacteria are in lungs. In this model we considered the community with individuals with both bubonic plague and pneumonic plague in light of the fact that after

three to seven days of bubonic infection, infected individuals with bubonic plague progresses to become pneumonic plague infectives. We thus have two infective classes, the individuals with pneumonic plague and the other with bubonic plague. The analytical result in this model shows that the disease free equilibrium and the endemic equilibrium are locally and globally asymptotically stable whenever they exist. We also show that the transmission and spread of pneumonic plague depends on the favorable condition of the environment as it is mainly transmitted through aerosol droplets. The results further postulate that the adequate contact rate between the infected individual and the susceptible, the incubation period and the infectious period of an individual are the main factor that drive occurrences and the dynamics of pneumonic plague epidemic whenever it occurs. These three factors also define the number of secondary cases of infection any infected individual can produce when introduced in any completely susceptible population.

In Chapter Five, we formulated the mathematical model that includes the bubonic plague infectives, pneumonic plague infectives and the individuals that are affected by the bacteria causing plague in their blood system (Septicemic plague infectives). This gave us the combined plague disease model that has all three forms of plague disease considered in our study. In here we consider three infectious classes which are the individuals with Bubonic plague, Septicemic plague and Pneumonic plague. In the combined plague disease model we still found that the number of secondary cases is the function of the adequate contact rate between the infected individual and the susceptible, the incubation period and the infectious period of the infected individual. We are able to show that the model is well posed and found the disease free equilibrium point and the endemic equilibrium point to be locally and globally asymptotically stable whenever they exist. The result shows the compact relationship between the increase of the number of individuals with pneumonic plague and the increase of the secondary cases of pneumonic plague infectives. This proves that even in the absence a vector flea and the adequate interaction between individuals from different populations plague can still prevail within human population and may lead to a significant number of deaths.

We also observed the a significant relationship between the increase of primary forms of plague disease to the secondary forms. This result is due to the fact that there is high possibility of individual with a primary form of plague disease to progress and become secondary forms of plague disease infectives. For example the increase in the number of individuals with bubonic plague eventually lead to the increase in the number of individuals with pneumonic plague and septicemic plague. Also the increase of the number of individual with septicemic plague proportionally increase the number of individual with pneumonic plague. This result calls for attention to the importance of early treatment to control the spread of plague disease. The result may be the reason why plague disease still affect mostly african countries as most of her people

do not have access to drugs for treating or preventing plague disease.

The environment also appear to be the potential agent in the spread and transmission of plague disease. We noted that, upon favorable condition pathogens survive in the environment and remain infectious for the long period of time. Then the environment may act as an agent of transmission and spread of plague disease and the adequate contact with a susceptible individual leads to infection. The results show the compact relationship between the increase in number of individuals with pneumonic plague and the increase in the number of pathogens in the environment. We are able to show how and to what extent each individual in each possible disease transmission in a pair of one susceptible and one infected individual (k_{ij}) contribute to the number of secondary cases of plague disease. Due to these results we were able to deduce that the best, effective and sustainable way to determine the actual number of secondary cases of plague disease is to find out how and to what extent each individual from each population of each form of plague disease has contributed to the basic reproduction number.

In Chapter Six and Chapter Seven, we modeled the plague disease that incorporate the parameters that are affected by seasonal weather variation. The study considers three element of weather which are Temperature, Humidity and Precipitation. To asses the impact of these elements of weather we assume all weather affected parameters ultimately affect the transmission rates of the plague disease. We then modified the transmission rates to be the function of time, and for mathematical convenience we assume disease transmission rates to be sinusoidal. In here we are able to show that the positive periodic solution exist and it is locally and globally asymptotically stable when the average number of secondary infections (R_T) is greater than 1 and unstable when $R_T < 1$. The results show that, the seasonal weather variation dictate the longevity, lifestyle, death rates, immigration rates, multiplication rates and reproduction rate of individuals. This in-turn affect the transmission, spread and ultimately the whole dynamic of the plague disease. It is seen that seasonal weather variation makes the dynamic of the disease to be suicidal in which the rate of infection increases or decreases when the weather condition favors or hinder the disease transmission respectively.

We found that the effect posed by the seasonal weather variation to the dynamics of plague disease depends on two major factors: one is the extent to which the condition favors components and factors that positively or negatively affect the spread and transmission of plague disease, two is the duration at which the weather condition remain favorable or unfavorable to the transmission and spread of plague disease. The result shows that the little twist of the amplitude of seasonality bring about the significant change in the dynamics of plague disease. Awareness of the capacity to shift the dynamic of plague disease that the change of seasonality amplitude has is very important as it helps to know when and what control measure should be applied when the

amplitude is high, moderate or low to effectively control the disease. However we should also put into consideration the factors that leads to the increase or decrease of the baseline quantity of the infection rate from one individual to the other for better results.

8.2 Conclusion

Generally we have formulated the mathematical models that show the dynamics of plague disease covering all possible ways in which plague disease can be transmitted. We have also explored the effect of seasonal weather variation in the dynamics of plague disease. The models formulated in this study represent the behavior of Human beings, Rodents(and other domestic animals), Fleas and pathogens in the environment that give a very complex interaction that may lead to transmission and spread of Plague disease. All model formulations and analysis are based on the assumptions and the values of the parameter that are presented in this study. Although this work doest exhaust all forms of plague disease but it is the milestone of the studies on the dynamics of other forms of plague disease. It also paves a way on the further analysis on the effects of seasonal weather variation on the dynamics of plague disease.

8.2.1 Significance of the Research

The significances of this study include the following:

(i) The study will improve the current knowledge about the disease especially on the transmission capacity and the dynamics of the disease with accordance to seasonal weather variation. This will save life of a lot of people especially from rural areas, as they will take precautions.

(ii) The study will inform policy makers on the threat that may be caused by an outbreak of plague disease; this will enable them to decide on the best ways of combating the disease or even preparing the conditions that narrow the possibility of its occurrence.

(iii) Due to the extraordinarily ability of plague disease to cross borders this study will encourage and promote international collaborations in health sectors for easy monitoring of the disease and for security purposes.

(iv) The study will also serve as a milestone to other researchers and pave a way to a even more exhaustive studies on plague disease.

(v) The study will influence the behavior change in most of the pastoralists societies whose culture increases the chance of contracting and spreading plague disease.

(vi) The study will serve as an alert to the national security stakeholders and help them to plan for the effective way to combat the disease when plague bacterium are used as bio-weapon by terrorists or enemies.

8.3 Recommendations from the study

The ability of Plague disease to reemerge even after years of silence, the complex transmission network it has, its ability to spread fast to large population and cross borders, its potential for being used as a biological weapon and the way in which it can easily be affected by seasonal weather variation makes plague disease a unique challenge that should be given attention by the health and national security stakeholders for effective planning of control strategies. Now the results of this study point to the following recommendations:

(i) There should be a serious and effective provision of education to the people especially those living in rural areas. This may be done through various education campaign that should reach out large population in order to raise people's awareness on: The general understanding of all forms of plague disease and the way they can be transmitted and spread. The risk of contracting plague disease when human beings live close to domestic and wild animals. Risk hobbies such as camping and hunting, occupation like veterinarians that may lead to plague infection. The precautions that one should take to avoid getting the disease when there is an outbreak. The complications that may be caused by plague disease, like the massive number of deaths it has caused, possibility that plague disease can lead to gangrene which is the death of tissue that is caused by disruption of the blood flow due to blood clots in the tiny blood vessels of an individual's fingers and toes and may also result in an inflammation of the membranes surrounding ones brain and spinal cord known as meningitis.

(ii) There should be a plan for emergence and effective strategies to combat the disease when it occur whether naturally or as an outbreak.

(iii) The government should give special attention to high risk areas, especially areas where plague disease has ever occurred and areas with the weather condition that foster rapid plague disease occurrence, transmission and spread.

(iv) There should be a continuous monitoring of flea, rodents and pathogens abundances in the environment especially those which are close to residential areas.

(v) Instigate a special plague disease committee in every region that will monitor plague occurrence in the entire region and help to keep records of plague cases and their consequences in human life. These records are important for further studies on plague disease and for effective planning of control strategies.

(vi) Ensure the availability of special health practitioners in every hospital, and making sure that there is an easy access to drugs for treating or preventing plague disease for all. This will foster early treatment and help to prevent primary forms of plague from progressing to severe and fatal secondary forms.

(vii) As it is easy for plague disease to cross borders there should be a stable collaboration between the neighbouring countries in areas like plague disease awareness campaign, warnings and the strategies to control the disease.

8.4 Future work

This study does not exhaust 100% of a study of plague disease, it may be adjusted in many ways and analyzed to produce different results to enable the broad understanding of the dynamics of the plague disease. The study can be extended and adjusted in various ways as given below:

(i) Model optimal control of plague disease under the interventions of vaccination and treatment.

(ii) This study assumes that seasonal weather variation ultimately affect the transmission rate but one may also analyze the effect of seasonal weather variation by looking at each individual parameter that is affected by weather variation and include it in the model.

(iii) Include other rare forms of the plague disease like pharyngeal plague and meningeal plague in the dynamics of plague disease.

(iv) Include the effect of drug resistance in the model.

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APPENDICES

Appendix 1: Matlab Code for Chapters Two and Three

```
function dy = m11(t,y)
dy=zeros(size(y))
beta = 0.99; mu2 = 0.07; delta2= 0.03; lambda2 = 0.3; lambda1 = 0.1; theta1 = 0.6; theta2 = 0.78;
mu3 = 0.2; delta3 = 0.05; alpha2 = 0.04; alpha1 = 0.9; theta4 = 0.5; theta3 = 0.5;
mu1 = 0.04; delta1 = 0.04; alpha3 = 0.1; rho = 0.2;pi1=0.5;pi2=0.4;pi3=0.1; psi1=0.09;varpi=0.1;Gamma1=0.09;omega1=0.001;kappa1=0.5;psi3=300;gamma1 =0.9;Gamma2=4.7;
omega2=0.0073;kappa3=0.2;kappa2=0.3;gamma2=0.05;psi22=0.7;Gamma3=0.28; Gamma4=0.6;psi21=0.99;lambda4=0.89;mu4=0.1;
S1=y(1);
E1=y(2);
I1=y(3);
R1=y(4);
S3=y(5);
E3=y(6);
I3=y(7);
S2=y(8);
I2=y(9);
A=y(10);
N1=S1+E1+I1+R1;
N2=S2+I2;
N3=S3+E3+I3;
dy(1)=pi1*psi1+ varpi*R1 - alpha1*S1*(Gamma1*((I2)/(N2))+omega1*A)- mu1*S1;
dy(2)=pi2*psi1+alpha1*S1*(Gamma1*(I2/N2)+omega1*A)-alpha2*E1-mu1*E1;
dy(3)=alpha2*E1-alpha3*I1-I1*(mu1+delta1);
dy(4)=pi3*psi1+alpha3*I1-varpi*R1-mu1*R1;
dy(5)=kappa1*psi3-gamma1*S3*(Gamma2*((I2)/(N2))+omega2*A)-mu3*S3;
dy(6)=kappa2*psi3+gamma1*S3*(Gamma2*((I2)/(N2))+omega2*A)-gamma2*E3-mu3*E3;
dy(7)=kappa3*psi3+gamma2*E3-I3*(mu3+delta3);
dy(8)=psi22-beta*S2*(rho*Gamma3*((I1)/(N1))+(1-rho)*Gamma4*((I3)/(N3)))-mu2 *S2;
dy(9)=psi21+beta*S2*(rho*Gamma3*((I1)/(N1))+(1-rho)*Gamma4*((I3)/(N3)))- I2 *(mu2+delta2);
dy(10)=lambda4-omega1*A*S1-omega2*A*S3-mu4*A;
```

```
clear
tspan=[0 50]
```

```
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1), t,y(:,2), t,y(:,3),t,y(:,4))
legend('Susceptible human','Exposed human','Infected human','Recovered
    human')
xlabel('Time[years]')
ylabel('Human Population')
```

```
clear
tspan=[0 30]
y0=[2000, 1500, 500, 300 ,2500,2000,200,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(2)
plot(t,y(:,5), t,y(:,6), t,y(:,7))
legend('Susceptible rodent','Exposed rodent','Infectious rodent')
xlabel('Time[years]')
ylabel('Rodent Population')
```

```
clear
tspan=[0 100]
y0=[2000, 1500, 500, 300 ,2500,2000,200,8000,1000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(3)
plot(t,y(:,8),t,y(:,9))
legend('Susceptible flea ','Infectious flea')
xlabel('Time[years]')
ylabel('Flea Population')
```

```
clear
tspan=[0 100]
y0=[2000, 1500, 500, 300 ,5000,3000,2000,8000,5000,5000]
[t,y]=ode45(@m11,tspan,y0)
figure(4)
plot(t,y(:,10))
legend('Pathogens')
xlabel('Time[years]')
ylabel('Pathogens Population')
```

```
clear
```

```
tspan=[0 10]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,5]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,10),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
tspan=[0 10]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,200]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,10),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 10]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,400]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,10),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 10]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,600]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,10),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 10]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,800]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,10),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 10]
```

```
y0=[1800, 1500, 100, 300 ,5000,3000,2000,8000,5000,1000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,10),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold off
legend('A(0)= 5','A(0)= 200','A(0)= 400', 'A(0)= 600','A(0)= 800','A(0)=
    1000')
```

```
clear
tspan=[0 30]
y0=[1800, 1800, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,2),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed human')
hold on
tspan=[0 30]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,2),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed human')
hold on
tspan=[0 30]
y0=[1800, 1000, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,2),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed human')
hold on
tspan=[0 30]
y0=[1800, 800, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,2),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed human')
hold on
tspan=[0 30]
```

```
y0=[1800, 500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,2),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed human')
hold on
tspan=[0 30]
y0=[1800, 10, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,2),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed human')
hold off
legend('E_H(0)= 1800','E_H(0)= 1500','E_H(0)= 1000','E_H(0)= 800', 'E_H(0)=
    500','E_H(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,5000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,4000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
```

```
y0=[1800, 1500, 500, 300 ,5000,2000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,1000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'b','linewidth',2)
%legend('Susceptible human')
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,10,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'k','linewidth',2)
%legend('Susceptible human')
xlabel('Time[years]')
ylabel('Exposed rodent')
hold off
legend('E_R(0)= 5000','E_R(0)= 4000','E_R(0)= 3000', 'E_R(0)= 2000','E_R(0)
    = 1000','E_R(0)= 10')
```

```
clear
tspan=[0 100]
y0=[2800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1))
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
```

```
clear
tspan=[0 100]
y0=[100, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
```

```
plot(t,y(:,1))
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
```

```
clear
tspan=[0 100]
y0=[0, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1))
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
```

```
clear
tspan=[0 100]
y0=[3800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1))
xlabel('Time[years]')
ylabel('Susceptible human')
hold off
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,4000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
```

```
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,3000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,2000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,1000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,10,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold off
legend('I_F(0)= 5000','I_F(0)= 4000','I_F(0)= 3000', 'I_F(0)= 2000','I_F(0)
    = 1000','I_F(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 2800, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
```

```
tspan=[0 100]
y0=[1800, 1500, 1800, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 1200, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 800, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 400, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 10, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold off
legend('I_H(0)= 2800','I_H(0)= 1800','I_H(0)= 1200', 'I_H(0)= 800','I_H(0)=
    400','I_H(0)= 10')
```

```
clear
```

```
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,5000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,4000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,3000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,1000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,10,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'k','linewidth',2)
```

```
xlabel('Time[years]')
ylabel('Infected rodent')
hold off
legend('I_R(0)= 5000','I_R(0)= 4000','I_R(0)= 3000', 'I_R(0)= 2000','I_R(0)
    = 1000','I_R(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 2300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 1800 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 1300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 800 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'b','linewidth',2)
```

```
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 0 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold off
legend('R_H(0)= 2300','R_H(0)= 1800','R_H(0)= 1300','R_H(0)= 800', 'R_H(0)=
    300','R_H(0)= 5')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,6000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,8),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,5000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,8),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,4000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,8),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,3000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,8),'y','linewidth',2)
```

```
xlabel('Time[years]')
ylabel('Susceptible flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,1500,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,8),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,10,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,8),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible flea')
hold off
legend('S_F(0)= 6000','S_F(0)= 5000','S_F(0)= 4000', 'S_F(0)= 3000','S_F(0)
    = 1500','S_F(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
tspan=[0 100]
y0=[2800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
tspan=[0 100]
y0=[500, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1),'y','linewidth',2)
```

```
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
tspan=[0 100]
y0=[100, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
tspan=[0 100]
y0=[0, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible human')
hold on
tspan=[0 100]
y0=[3800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,1),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible human')
hold off
legend('S_H(0)= 1800','S_H(0)= 2800','S_H(0)= 500','S_H(0)= 100', 'S_H(0)=
    10','S_H(0)= 3800')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,6000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,5),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Susceptible rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,5),'m','linewidth',2)
```

```
15 xlabel('Time[years]')
16 ylabel('Susceptible rodent')
17 hold on
18 tspan=[0 100]
19 y0=[1800, 1500, 500, 300 ,4000,3000,2000,8000,5000,10000]
20 [t,y]=ode45(@m11,tspan,y0)
21 figure(1)
22 plot(t,y(:,5),'r','linewidth',2)
23 xlabel('Time[years]')
24 ylabel('Susceptible rodent')
25 hold on
26 tspan=[0 100]
27 y0=[1800, 1500, 500, 300 ,3000,3000,2000,8000,5000,10000]
28 [t,y]=ode45(@m11,tspan,y0)
29 figure(1)
30 plot(t,y(:,5),'b','linewidth',2)
31 xlabel('Time[years]')
32 ylabel('Susceptible rodent')
33 hold on
34 tspan=[0 100]
35 y0=[1800, 1500, 500, 300 ,1000,3000,2000,8000,5000,10000]
36 [t,y]=ode45(@m11,tspan,y0)
37 figure(1)
38 plot(t,y(:,5),'k','linewidth',2)
39 xlabel('Time[years]')
40 ylabel('Susceptible rodent')
41 hold on
42 tspan=[0 100]
43 y0=[1800, 1500, 500, 300 ,10,3000,2000,8000,5000,10000]
44 [t,y]=ode45(@m11,tspan,y0)
45 figure(1)
46 plot(t,y(:,5),'y','linewidth',2)
47 xlabel('Time[years]')
48 ylabel('Susceptible rodent')
49 hold off
50 legend('S_R(0)= 6000','S_R(0)= 5000','S_R(0)= 4000', 'S_R(0)= 3000','S_R(0)
      = 1000','S_R(0)= 10')
```

Appendix 2: Matlab Code for Chapter Four

```
function dy = m11(t,y)
dy=zeros(size(y))
beta = 0.99; mu2 = 0.1; delta2= 0.03; lambda2 = 0.3; lambda1 = 0.1; theta1 = 0.6; theta2 = 0.78;
mu3 = 0.08; delta3 = 0.05; alpha2 = 0.96; alpha1 = 0.3; theta4 = 0.5; theta3 = 0.5;
mu1 = 0.04; delta1 = 0.09; alpha3 = 0.3; rho = 0.2;pi1=0.5;pi2=0.4;pi3=0.1; psi1=50;varpi=0.8;Gamma1=0.5;omega1=0.00061;kappa1=0.5;psi3=200;gamma1 =0.1;Gamma2=0.78;
omega2=0.0009;kappa3=0.2;kappa2=0.3;gamma2=0.2;psi22=200;Gamma3=0.5;Gamma4 =0.5;psi21=250;lambda4=150;mu4=0.1;
S1=y(1);
E1=y(2);
I1=y(3);
I2=y(4);
R1=y(5);
S2=y(6);
I3=y(7);
S3=y(8);
E3=y(9);
I4=y(10);
I5=y(11);
A=y(12);
N1=S1+E1+I1+I2+R1;
N2=S2+I3;
N3=S3+E3+I4+I5;
dy(1)=pi1*psi1+ varpi*R1 - alpha1*S1*(Gamma1*((I2)/(N1))+Gamma2*((I3)/(N2)) +Gamma3*((I5)/(N3))+omega1*A)- mu1*S1;
dy(2)=pi2*psi1+alpha1*S1*(Gamma1*((I2)/(N1))+Gamma2*((I3)/(N2))+Gamma3*((I5 )/(N3))+omega1*A)-alpha2*E1-mu1*E1;
dy(3)=pi3*psi1+tau1*alpha2*E1-alpha3*I1-I1*(mu1+kappa1);
dy(4)=(1-tau1)*alpha2*E1+rho*alpha3*I1-alpha4*I2-I2*(mu1+delta1);
dy(5)=pi4*psi1+alpha4*I2+(1-rho)*alpha3*I1-varpi*R1-mu1*R1;
dy(6)=psi22-beta*S2*(Gamma7*((rho1*I1+rho2*I2)/(N1))+ (Gamma8*((rho3*I4+ rho4*I5)/(N3))))-mu2*S2;
dy(7)=psi21+beta*S2*(Gamma7*((rho1*I1+rho2*I2)/(N1))+ Gamma8*((rho3*I4+rho4 *I5)/(N3)))- I3*(mu2+delta2);
```

```
dy(8)=k1*psi3-gamma1*S2*(Gamma4*((I5)/(N3))+Gamma5*((I3)/(N2))+Gamma6*((I2)
    /(N1))+omega2*A)-mu3*S3;
dy(9)=k2*psi3+gamma1*S2*(Gamma4*((I5)/(N3))+Gamma5*((I3)/(N2))+Gamma6*((I2)
    /(N1))+omega2*A)-gamma2*E3-mu3*E3;
dy(10)=k3*psi3+tau2*gamma2*E3-gamma3*I4-I3*(mu3+kappa2);
dy(11)=(1-tau2)*gamma2*E3+gamma3*I4-I5*(mu3+delta3);
dy(12)=lambda4+eta1*((I2)/(N1))+eta2*((I5)/(N3))-mu4*A;
```

```
function dy = m11_CHAP2(~,y)
dy=zeros(size(y))
beta = 0.99; mu2 = 0.07; delta2= 0.03; lambda2 = 0.3; lambda1 = 0.1; theta1
     = 0.6; theta2 = 0.78;
mu3 = 0.2; delta3 = 0.05; alpha2 = 0.95; alpha1 = 0.9; theta4 = 0.5; theta3
     = 0.5;
mu1 = 0.04; delta1 = 0.04; alpha3 = 0.6; rho = 0.7;pi1=0.7;pi2=0.2;pi3=0.1;
    psi1=0.09;varpi=0.1;Gamma1=0.019;omega1=0.8;kappa1=0.5;psi3=0.03;gamma1
    =0.9;Gamma2=0.09;
omega2=0.04;kappa3=0.2;kappa2=0.013;gamma2=0.9;psi22=0.08;Gamma3=0.09;
    Gamma4=0.029;psi21=0.008;lambda4=0.89;mu4=0.1;
tau1=0.6;alpha4 = 0.006;pi4=0.05;Gamma7=0.28; rho1=0.5;rho2=0.1;rho3=0.31;
    rho4=0.09;Gamma8=0.6;k1=0.4;k2=0.4; k3=0.2;Gamma5=4.7;Gamma6=0.005;tau2
    =0.4;gamma3=0.015;
eta1=0.37; eta2=0.89;
S1=y(1);
E1=y(2);
I1=y(3);
I2=y(4);
R1=y(5);
S2=y(6);
I3=y(7);
S3=y(8);
E3=y(9);
I4=y(10);
I5=y(11);
A=y(12);
N1=S1+E1+I1+I2+R1;
N2=S2+I3;
N3=S3+E3+I4+I5;
dy(1)=pi1*psi1+varpi*R1 - alpha1*S1*(Gamma1*((I2)/(N1))+Gamma2*((I3)/(N2))+
    Gamma3*((I5)/(N3))+omega1*A)- mu1*S1;
dy(2)=pi2*psi1+alpha1*S1*(Gamma1*((I2)/(N1))+Gamma2*((I3)/(N2))+Gamma3*((I5
    )/(N3))+omega1*A)-alpha2*E1-mu1*E1;
dy(3)=pi3*psi1+tau1*alpha2*E1-alpha3*I1-I1*(mu1+kappa1);
dy(4)=(1-tau1)*alpha2*E1+rho*alpha3*I1-alpha4*I2-I2*(mu1+delta1);
```

```
dy(5)=pi4*psi1+alpha4*I2+(1-rho)*alpha3*I1-varpi*R1-mu1*R1;
dy(6)=psi22-beta.*S2*(Gamma7*((rho1*I1+rho2*I2)/(N1))+ Gamma8*((rho3*I4+
    rho4*I5)/(N3)))-mu2*S2;
dy(7)=psi21+beta.*S2*(Gamma7*((rho1*I1+rho2*I2)/(N1))+ Gamma8*((rho3*I4+
    rho4*I5)/(N3)))- I3*(mu2+delta2);
dy(8)=k1*psi3-gamma1*S3*(Gamma4*((I5)/(N3))+Gamma5*((I3)/(N2))+Gamma6*((I2)
    /(N1))+omega2*A)-mu3*S3;
dy(9)=k2*psi3+gamma1*S3*(Gamma4*((I5)/(N3))+Gamma5*((I3)/(N2))+Gamma6*((I2)
    /(N1))+omega2*A)-gamma2*E3-mu3*E3;
dy(10)=k3*psi3+tau2*gamma2*E3-gamma3*I4-I3*(mu3+kappa2);
dy(11)=(1-tau2)*gamma2*E3+gamma3*I4-I5*(mu3+delta3);
dy(12)=lambda4+eta1*((I2)/(N1))+eta2*((I5)/(N3))-mu4*A;
```

```
clear
tspan=[0 250]
y0=[1000, 800, 500, 100 ,50,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@END_CHAP2,tspan,y0)
figure(1)
plot(t,y(:,1), t,y(:,2), t,y(:,3),t,y(:,4),t,y(:,5))
legend('Susceptible human','Exposed human','I_{HA}','I_{HB}','Recovered
    human')
xlabel('Time[years]')
ylabel('Human Population')
```

```
clear all
tspan=[0 30]
y0=[2000, 1500, 500, 300 ,2500,2000,200,8000,1000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(5)
plot(t,y(:,1), t,y(:,2), t,y(:,3),t,y(:,4),t,y(:,5), t,y(:,6), t,y(:,7),t,y
    (:,8),t,y(:,9),t,y(:,10))
legend('S_H','E_H','I_H','R_H','S_R','E_R','I_R','S_F','I_F','A')
xlabel('Time[years]')
ylabel('Population')
```

```
clear
tspan=[0 500]
y0=[1000, 800, 500, 100 ,50,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@END_CHAP2,tspan,y0)
figure(2)
plot(t,y(:,8),t,y(:,9),t,y(:,10),t,y(:,11))
legend('Susceptible rodent','Exposed rodent','I_{RA}','I_{RB}')
```

```
xlabel('Time[years]')
ylabel('Rodent Population')
```

```
clear
tspan=[0 250]
y0=[1000, 800, 500, 100 ,50,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@END_CHAP2,tspan,y0)
figure(3)
plot(t,y(:,6),t,y(:,7))
ylim([0 10000])
legend('Susceptible flea ','Infectious flea')
xlabel('Time[years]')
ylabel('Flea Population')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1500,500,1000,500,200, 100, 2000]
[t,y]=ode45(@m11_CHAP2,tspan,y0)
figure(4)
plot(t,y(:,12))
legend('Pathogens')
xlabel('Time[years]')
ylabel('Pathogens Population')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1500,500,1000,500,200, 100, 2000]
[t,y]=ode45(@m11_CHAP2,tspan,y0)
figure(4)
plot(t,y(:,12))
legend('Pathogens')
xlabel('Time[years]')
ylabel('Pathogens Population')
hold on
figure(5)
plot( y(:,7),y(:,3))
xlabel('Infected fleas')
ylabel('Infected Human with Bubonic Plague')
title('Effect of Encreased flea population to Human with Bubonic Plague ')
hold on
figure(6)
plot( y(:,7),y(:,10))
```

```
xlabel('Infected fleas')
ylabel('Infected Rodent with Bubonic Plague')
title('Effect of Encreased flea population to Rodent with Bubonic Plague ')
figure(7)
plot( y(:,12),y(:,4))
xlabel('Pathogens Population')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of Pathogens in the environment to Human with Pneumonic
    Plague ')
figure(8)
plot( y(:,12),y(:,11))
xlabel('Pathogens Population')
ylabel('Infected Rodent with Pneumonic Plague')
title('Effect of Pathogens in the environment to Rodent with Pneumonic
    Plague ')
figure(9)
plot( y(:,11),y(:,4))
xlabel('Infected Rodent with Pneumonic Plague')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of rodent with pneumonic plague to human with Pneumonic
    plague ')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1500,500,1000,500,200, 100, 2000]
[t,y]=ode45(@m11_CHAP2,tspan,y0)
figure(1)
plot( y(:,7),y(:,3))
xlabel('Infected fleas')
ylabel('Infected Human with Bubonic Plague')
title('Effect of Encreased flea population to Human with Bubonic Plague ')

figure(2)
plot( y(:,7),y(:,10))
xlabel('Infected fleas')
ylabel('Infected Rodent with Bubonic Plague')
title('Effect of Encreased flea population to Rodent with Bubonic Plague ')
figure(3)
plot( y(:,12),y(:,4))
xlabel('Pathogens Population')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of Pathogens in the environment to Human with Pneumonic
    Plague ')
figure(4)
```

```
22 plot( y(:,12),y(:,11))
23 xlabel('Pathogens Population')
24 ylabel('Infected Rodent with Pneumonic Plague')
25 title('Effect of Pathogens in the environment to Rodent with Pneumonic
       Plague ')
26 figure(5)
27 plot( y(:,11),y(:,4))
28 xlabel('Infected Rodent with Pneumonic Plague')
29 ylabel('Infected Human with Pneumonic Plague')
30 title('Effect of rodent with pneumonic plague to human with Pneumonic
       plague ')
31 figure(6)
32 plot( y(:,3),y(:,4))
33 xlabel('Infected Human with Bubonic Plague')
34 ylabel('Infected Human with Pneumonic Plague')
35 title('Effect of Human with Bubonic plague to Human with Pneumonic plague '
       )
36 figure(7)
37 plot( y(:,10),y(:,11))
38 xlabel('Infected Rodent with Bubonic Plague')
39 ylabel('Infected Rodent with Pneumonic Plague')
40 title('Effect of Rodent with Bubonic plague to Rodent with Pneumonic plague
        ')
41 figure(8)
42 plot( y(:,4),y(:,12))
43 xlabel('Infected Human with Pneumonic Plague')
44 ylabel('Pathogens in the Environment')
45 title('Effect of Human with Pneumonic Plague to the number of Pathogens in
       the Enviroment')
46 figure(9)
47 plot( y(:,11),y(:,12))
48 xlabel('Infected Rodent with Pneumonic Plague')
49 ylabel('Pathogens in the Environment')
50 title('Effect of Rodent with Pneumonic Plague to the number of Pathogens in
        the Enviroment')
51
52 figure(10)
53 plot( y(:,12),y(:,3), y(:,12),y(:,4), y(:,12),y(:,7), y(:,12),y(:,10),y
       (:,12),y(:,11))
54 xlabel('Pathogens in the Environment')
55 ylabel('Population')
56 title('Effect of Rodent with Pneumonic Plague to the number of Pathogens in
        the Enviroment')
```

Appendix 3: Matlab Code for Chapter Five

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot(y(:,8), y(:,3),y(:,8),y(:,4),y(:,8),y(:,5),y(:,8),y(:,11),y(:,8),y
    (:,12),y(:,8),y(:,13))
legend('I_{HB}','I_{HS}','I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Flea')
ylabel('Infected Individual')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 0]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
N_1=y(:,3)+y(:,4)+y(:,5);
N_3=y(:,11)+y(:,12)+y(:,13);
plot( y(:,14),N_1,y(:,14),N_3)%,y(:,14),y(:,5),y(:,14),y(:,11),y(:,14),y
    (:,12),y(:,14),y(:,13))
legend('Infected Human','Infected Rodent')%,'I_{HP}','I_{RB}','I_{RS}','I_{
    RP}')
xlabel('Pathogens in soil/environment ')
ylabel('Infected Individuals')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,5),y(:,3),y(:,5),y(:,4))%,y(:,8),y(:,5),y(:,8),y(:,11),y(:,8),y
    (:,12),y(:,8),y(:,13))
legend('I_{HB}','I_{HS}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
ylabel('Infected Human with I_{HB} or I_{HS} ')
xlabel('Infected Human with Pneumonic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,5),y(:,5),y(:,5),y(:,13))%,y(:,8),y(:,5),y(:,8),y(:,11),y(:,8),y
    (:,12),y(:,8),y(:,13))
legend('I_{HP}','I_{RP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
ylabel('Individuals with Pneumonic plague')
xlabel('Infected Human with Pneumonic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,13),y(:,13),y(:,13),y(:,5))%,y(:,8),y(:,5),y(:,8),y(:,11),y(:,8),
    y(:,12),y(:,8),y(:,13))
legend('I_{RP}','I_{HP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
ylabel('Individuals with Pneumonic plague ')
xlabel('Infected Rodent with Pneumonic Plague')
```

```
function dy =m11(t,y)
dy=zeros(size(y))
re=1000;c=3;rho=0.02;g=0,25;u=0.02;k=0.4;si=0.5;tau=0.3;v=0.5;de=0.45;B
    =0.15;n1=0.2;n2=0.12;n3=0.15;r=0.3;
S=y(1);
I=y(2);
P=y(3);
T=y(4);
A=y(5);
L=c*B*(I+n1*P+n2*T+n3*A)/(1+r*(I+n1*P+n2*T+n3*A));
dy(1)=re-(1-rho)*L*S-u*S;
dy(2)=(1-rho)*L*S-(g+u)*I;
dy(3)=g*I-(k+si+u)*P;
dy(4)=k*P-(tau*(1-v)+u)*T;
dy(5)=si*P+tau*(1-v)*T-(de+u)*A
```

```
function dy = m11_CHAP3_new(~,y)
dy=zeros(size(y))
beta = 0.99; mu2 = 0.07; delta2= 0.03; lambda2 = 0.3; lambda1 = 0.1; theta1
     = 0.6; theta2 = 0.78; mu3 = 1; delta3 = 0.05; alpha2 = 0.95;
```

```
alpha1 = 0.99; theta4 = 0.5; theta3 = 0.5; mu1 = 0.04; delta1 = 0.5; alpha3 = 0.038; rho = 0.2;pi2=0.2;pi3=0.1;psi1=100.9500;varpi=0.33;
omega1=0.58;kappa1=0.5;psi3=0.03;gamma1=0.925;omega2=0.004;kappa3=0.2; kappa2=0.013;gamma2=0.982;psi22=1000;psi21=2500;
lambda4=50,000;mu4=0.1;alpha4 = 0.23;pi4=0.05; rho3=0.5;rho4=0.09;k2=0.4; k3=0.2;gamma3=0.194; eta1=0.2; eta2=0.4;
sigma1=0.5;sigma2=0.5;delta1b=0.04;delta1s=0.06911;delta1p=0.63; delta3b =0.1;delta3s=0.09;delta3p=0.14;Gamma1=0.5;Gamma2=0.85;Gamma3=0.0641; Gamma4=0.805;
Gamma5=0.805;Gamma6=0.00005;Gamma7=0.00008;Gamma8=0.0641;Gamma9=0.9;Gamma10 =0.9;Gamma11=0.1;Gamma12=0.1;Gamma13=0.99;Gamma14=0.1;nu1=0.3; nu2=0.4;
nu3=0.3;xi=0.71; alpha5=0.4;tau3=0.4;tau2=0.3;tau1=0.3;phi=0.5;gamma4=0.05; rho1=0.3;rho2=0.2;

S1=y(1);E1=y(2);I1=y(3);I2=y(4);I3=y(5);R1=y(6);S2=y(7);I4=y(8);S3=y(9);E3= y(10);I5=y(11);I6=y(12);I7=y(13);A=y(14);N1=S1+E1+I1+I2+I3+R1; N2=S2+I4;
N3=S3+E3+I5+I6+I7;
G1=(Gamma1.*I3+Gamma2.*I2)./N1+(Gamma3.*I4)./N2+(Gamma4.*I7+Gamma5.*I6)./N3 +omega1.*A;
G2=(Gamma6*I3+Gamma7*I2)/N1+(Gamma8*I4)/N2+(Gamma9*I7+Gamma10*I6)/N3+omega2 .*A;
G3=(Gamma11*I1+Gamma12*I2)/N1+(Gamma13*I5+Gamma14*I6)/N3;
dy(1)=sigma1*psi1+varpi*R1 - alpha1*S1*(G1)- mu1*S1;
dy(2)=(1-sigma1)*psi1+alpha1*S1*(G1)-alpha2*E1-mu1*E1;
dy(3)=nu2*alpha2*E1-alpha3*I1-I1*(mu1+delta1b);
dy(4)=nu3*alpha2*E1+rho3*alpha3*I1-alpha4*I2-I2*(mu1+delta1s);
dy(5)=nu1*alpha2*E1+rho1*alpha3*I1+alpha4*xi*I2 -alpha5*I3-I3*(mu1+delta1p) ;
dy(6)=alpha3*rho2*I2+alpha4*(1-xi)*I2+alpha5*I3-(varpi+mu1)*R1;
dy(7)=psi22-beta*S2*(G3)-mu2*S2;
dy(8)=psi21+beta*S2*(G3)- I4*(mu2+delta2);
dy(9)=sigma2*psi3-gamma1*S3*(G2)-mu3*S3;
dy(10)=(1-sigma2)*psi3+gamma1*S3*(G2)-gamma2*E3-mu3*E3;
dy(11)=gamma2*tau3*E3-gamma3*I5-I5*(mu3+delta3b);
dy(12)=tau2*gamma2*E3+gamma3*(1-phi)*I5-gamma4*I6-I6*(mu3+delta3s);
dy(13)=tau1*gamma2*E3+gamma3*phi*I5+gamma4*I6-I7*(mu3+delta3p);
dy(14)=lambda4+eta1*((I3)/(N1))+eta2*((I7)/(N3))-mu4*A;
```

```
clear
tspan=[0 50]
y0=[1000, 900, 200, 100 ,50,100,300000,2000,7000,500,1000,800, 500,300, 5000]
[t,y]=ode45(@m11_CHAP3_new,tspan,y0)
figure(1)
```

```
plot(y(:,1), y(:,2));%, t,y(:,3),t,y(:,4),t,y(:,5),t,y(:,6))
legend('Susceptible human','Exposed human','I_{HB}','I_{HS}','I_{HP}','
    Recovered human')
xlabel('Time[years]')
ylabel('Human Population')
```

```
clear all
tspan=[0 30]
y0=[2000, 1500, 500, 300 ,2500,2000,200,8000,1000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(5)
plot(t,y(:,1), t,y(:,2), t,y(:,3),t,y(:,4),t,y(:,5), t,y(:,6), t,y(:,7),t,y
    (:,8),t,y(:,9),t,y(:,10))
legend('S_H','E_H','I_H','R_H','S_R','E_R','I_R','S_F','I_F','A')
xlabel('Time[years]')
ylabel('Population')
```

```
clear
tspan=[0 50]
y0=[800, 600, 500, 100 ,50,100,300000,2000,7000,500,1000,800, 500,300,
    5000]
[t,y]=ode45(@m11_CHAP3_new,tspan,y0)
figure(2)
plot(t,y(:,9),t,y(:,10),t,y(:,11),t,y(:,12),t,y(:,13))
legend('Susceptible rodent','Exposed rodent','I_{RB}','I_{RS}','I_{RP}')
xlabel('Time[years]')
ylabel('Rodent Population')
```

```
clear
tspan=[0 50]
y0=[800, 600, 500, 100 ,50,100,80000,20000,7000,500,1000,800, 500,300, 50]
[t,y]=ode45(@m11_CHAP3_new,tspan,y0)
figure(3)
plot(t,y(:,7),t,y(:,8))
legend('Susceptible flea ','Infectious flea')
xlabel('Time[years]')
ylabel('Flea Population')
```

```
clear
tspan=[0 100]
```

```
y0=[800, 600, 500, 100 ,50,100,300000,2000,7000,500,1000,800, 500,300,
    5000]
[t,y]=ode45(@m11_CHAP3_new,tspan,y0)
figure(4)
plot(t,y(:,12))
legend('Pathogens')
xlabel('Time[years]')
ylabel('Pathogens Population')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1500,500,1000,500,200, 100, 2000]
[t,y]=ode45(@m11_CHAP2,tspan,y0)
figure(4)
plot(t,y(:,12))
legend('Pathogens')
xlabel('Time[years]')
ylabel('Pathogens Population')
hold on
figure(5)
plot( y(:,7),y(:,3))
xlabel('Infected fleas')
ylabel('Infected Human with Bubonic Plague')
title('Effect of Encreased flea population to Human with Bubonic Plague ')
hold on
figure(6)
plot( y(:,7),y(:,10))
xlabel('Infected fleas')
ylabel('Infected Rodent with Bubonic Plague')
title('Effect of Encreased flea population to Rodent with Bubonic Plague ')
figure(7)
plot( y(:,12),y(:,4))
xlabel('Pathogens Population')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of Pathogens in the environment to Human with Pneumonic
    Plague ')
figure(8)
plot( y(:,12),y(:,11))
xlabel('Pathogens Population')
ylabel('Infected Rodent with Pneumonic Plague')
title('Effect of Pathogens in the environment to Rodent with Pneumonic
    Plague ')
figure(9)
plot( y(:,11),y(:,4))
```

```
xlabel('Infected Rodent with Pneumonic Plague')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of rodent with pneumonic plague to human with Pneumonic
    plague ')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1500,500,1000,500,200, 100, 2000]
[t,y]=ode45(@m11_CHAP2,tspan,y0)
figure(1)
plot( y(:,7),y(:,3))
xlabel('Infected fleas')
ylabel('Infected Human with Bubonic Plague')
title('Effect of Encreased flea population to Human with Bubonic Plague ')

figure(2)
plot( y(:,7),y(:,10))
xlabel('Infected fleas')
ylabel('Infected Rodent with Bubonic Plague')
title('Effect of Encreased flea population to Rodent with Bubonic Plague ')
figure(3)
plot( y(:,12),y(:,4))
xlabel('Pathogens Population')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of Pathogens in the environment to Human with Pneumonic
    Plague ')
figure(4)
plot( y(:,12),y(:,11))
xlabel('Pathogens Population')
ylabel('Infected Rodent with Pneumonic Plague')
title('Effect of Pathogens in the environment to Rodent with Pneumonic
    Plague ')
figure(5)
plot( y(:,11),y(:,4))
xlabel('Infected Rodent with Pneumonic Plague')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of rodent with pneumonic plague to human with Pneumonic
    plague ')
figure(6)
plot( y(:,3),y(:,4))
xlabel('Infected Human with Bubonic Plague')
ylabel('Infected Human with Pneumonic Plague')
title('Effect of Human with Bubonic plague to Human with Pneumonic plague '
    )
```

```
figure(7)
plot( y(:,10),y(:,11))
xlabel('Infected Rodent with Bubonic Plague')
ylabel('Infected Rodent with Pneumonic Plague')
title('Effect of Rodent with Bubonic plague to Rodent with Pneumonic plague
    ')
figure(8)
plot( y(:,4),y(:,12))
xlabel('Infected Human with Pneumonic Plague')
ylabel('Pathogens in the Environment')
title('Effect of Human with Pneumonic Plague to the number of Pathogens in
   the Enviroment')
figure(9)
plot( y(:,11),y(:,12))
xlabel('Infected Rodent with Pneumonic Plague')
ylabel('Pathogens in the Environment')
title('Effect of Rodent with Pneumonic Plague to the number of Pathogens in
    the Enviroment')
figure(10)
plot( y(:,12),y(:,3), y(:,12),y(:,4), y(:,12),y(:,7), y(:,12),y(:,10),y
   (:,12),y(:,11))
xlabel('Pathogens in the Environment')
ylabel('Population')
title('Effect of Rodent with Pneumonic Plague to the number of Pathogens in
    the Enviroment')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,13),y(:,11),y(:,13),y(:,12))%,y(:,8),y(:,5),y(:,8),y(:,11),y(:,8)
   ,y(:,12),y(:,8),y(:,13))
legend('I_{RB}','I_{RS}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
ylabel('Infected Rodent with I_{HB} or I_{HS} ')
xlabel('Infected Rodent with Pneumonic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,11),y(:,3),y(:,12),y(:,3),y(:,13),y(:,3))%,y(:,8),y(:,5),y(:,8),y
```

```
    (:,11),y(:,8),y(:,12),y(:,8),y(:,13))
legend('I_{RB}','I_{RS}','I_{RP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Rodent ')
ylabel('Infected Human with Bubonic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,11),y(:,4),y(:,12),y(:,4),y(:,13),y(:,4))%,y(:,8),y(:,5),y(:,8),y
    (:,11),y(:,8),y(:,12),y(:,8),y(:,13))
legend('I_{RB}','I_{RS}','I_{RP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Rodent ')
ylabel('Infected Human with Septicemic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 0]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
N_1=y(:,3)+y(:,4)+y(:,5);
N_3=y(:,11)+y(:,12)+y(:,13);
plot( y(:,14),N_1,y(:,14),N_3)%,y(:,14),y(:,5),y(:,14),y(:,11),y(:,14),y
    (:,12),y(:,14),y(:,13))
legend('Infected Human','Infected Rodent')%,'I_{HP}','I_{RB}','I_{RS}','I_{
    RP}')
xlabel('Pathogens in soil/environment ')
ylabel('Infected Individuals')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,3),y(:,11),y(:,4),y(:,11),y(:,5),y(:,11))%,y(:,8),y(:,5),y(:,8),y
    (:,11),y(:,8),y(:,12),y(:,8),y(:,13))
legend('I_{HB}','I_{HS}','I_{HP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Human ')
ylabel('Infected Rodent with Bubonic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,3),y(:,12),y(:,4),y(:,12),y(:,5),y(:,12))%,y(:,8),y(:,5),y(:,8),y
    (:,11),y(:,8),y(:,12),y(:,8),y(:,13))
legend('I_{HB}','I_{HS}','I_{HP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Human ')
ylabel('Infected Rodent with Septicemic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
plot( y(:,3),y(:,13),y(:,4),y(:,13),y(:,5),y(:,13))%,y(:,8),y(:,5),y(:,8),y
    (:,11),y(:,8),y(:,12),y(:,8),y(:,13))
legend('I_{HB}','I_{HS}','I_{HP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Human ')
ylabel('Infected Rodent with Pneumonic Plague')
```

```
clear
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000]
[t,y]=ode45(@m11_CHAP3,tspan,y0)
figure(1)
N_1=y(:,3)+y(:,4)+y(:,5);
N_3=y(:,11)+y(:,12)+y(:,13);
plot( N_1,N_3)%,y(:,8),y(:,5),y(:,8),y(:,11),y(:,8),y(:,12),y(:,8),y(:,13))
%legend('I_{HB}','I_{HS}','I_{HP}')%,'I_{HP}','I_{RB}','I_{RS}','I_{RP}')
xlabel('Infected Human')
ylabel('Infected Rodent')
```

Appendix 4: Matlab Code for Chapters Six & Seven

```
1
2  function dy = chap4(t,y)
3  global alpha2_1 alpha3_1 alpha4_1 alpha5_1 alpha2 Gamma1_0 Gamma1_1
       Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0 Gamma4_1 Gamma5_0 Gamma5_1
       Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0 Gamma8_1 Gamma9_0 Gamma9_1
       Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1  Gamma12_0 Gamma12_1 Gamma13_0
       Gamma13_1 Gamma14_0 Gamma14_1 eta1_0  eta1_1 eta2_0 eta2_1 omega1_0
       omega1_1 omega2_0 omega2_1 alpha3 alpha4 alpha5
4
5  beta = 0.99; mu2 = 0.07; delta2= 0.03; lambda2 = 0.3; lambda1 = 0.1; theta1
        = 0.6; theta2 = 0.78; mu3 = 1; delta3 = 0.05; alpha2 = 0.95;
6  alpha1 = 0.99; theta4 = 0.5; theta3 = 0.5; mu1 = 0.04; delta1 = 0.5; alpha3
        = 0.038; rho = 0.2;pi2=0.2;pi3=0.1;psi1=100.9500;varpi=0.33;
7  kappa1=0.5;psi3=0.03;gamma1=0.925;kappa3=0.2;kappa2=0.013;gamma2=0.982;
       psi22=1000;psi21=2500;
8  lambda4=50,000;mu4=0.1;alpha4 = 0.23;pi4=0.05; rho3=0.5;rho4=0.09;k2=0.4;
       k3=0.2;gamma3=0.194;
9  sigma1=0.5;sigma2=0.5;delta1b=0.04;delta1s=0.06911;delta1p=0.63; delta3b
       =0.1;delta3s=0.09;delta3p=0.14;
10 nu1=0.3; nu2=0.4; nu3=0.3;xi=0.71; alpha5=0.4;tau3=0.4;tau2=0.3;tau1=0.3;
       phi=0.5;gamma4=0.05;rho1=0.3;rho2=0.2;
11
12 sigma1=0.5;sigma2=0.5;delta1b=0.05;delta1s=0.06911;delta1p=0.07; delta3b
       =0.1;delta3s=0.0471;
13 delta3p=0.14;nu1=0.3; nu2=0.4; nu3=0.3;
14 xi=0.71; alpha5=0.17;tau3=0.4;tau2=0.3;tau1=0.3;phi=0.5;gamma4=0.05;rho1
       =0.3;rho2=0.2;
15 %baseline value (Time avaraged value)
16 Gamma1_0=0.5;Gamma2_0=0.85;Gamma3_0=0.0641;Gamma4_0=0.805;Gamma5_0=0.805;
       Gamma6_0=0.00005;
17 Gamma7_0=0.00008;Gamma8_0=0.0641;Gamma9_0=0.9;Gamma10_0=0.9;Gamma11_0=0.1;
       Gamma12_0=0.1;
18 Gamma13_0=0.99;Gamma14_0=0.1;omega1_0=0.58;omega2_0=0.004;eta1_0=0.2;
       eta2_0=0.4;
19 %Relative amplitude of the seasonal oscillator it ranges between 0 and 1
20 Gamma1_1=0.7;Gamma2_1=0.7;Gamma3_1=0.7;Gamma4_1=0.7;Gamma5_1=0.7;Gamma6_1
       =0.7;Gamma7_1=0.7;
```

```
Gamma8_1=0.7;Gamma9_1=0.7;alpha3_1=0.7;alpha4_1=0.7;alpha5_1=0.7;
Gamma10_1=0.7;Gamma11_1=0.7;Gamma12_1=0.7;Gamma13_1=0.7;Gamma14_1=0.7;
    omega1_1=0.7;omega2_1=0.7;
eta1_1=0.7; eta2_1=0.7;alpha2_1 = 0.5;

S1=y(1);E1=y(2);I1=y(3);I2=y(4);I3=y(5);R1=y(6);S2=y(7);I4=y(8);S3=y(9);E3=
    y(10);I5=y(11);I6=y(12);
I7=y(13);A=y(14);tt=y(15);N1=S1+E1+I1+I2+I3+R1; N2=S2+I4; N3=S3+E3+I5+I6+I7
    ;
k22= ((alpha3.*rho3)./(alpha3.*rho3+mu1)+(alpha2.*nu3)./(alpha2.*nu3)./(
    alpha2.*nu3+mu1)).*(Gamma2(tt))./(alpha4+mu1+delta1s);
G1=(Gamma1(tt).*I3+Gamma2(tt).*I2)./N1+(Gamma3(tt).*I4)./N2+(Gamma4(tt).*I7
    +Gamma5(tt).*I6)./N3+omega1(tt).*A;
G2=(Gamma6(tt).*I3+Gamma7(tt).*I2)./N1+(Gamma8(tt).*I4)./N2+(Gamma9(tt).*I7
    +Gamma10(tt)*I6)./N3+omega2(tt).*A;
G3=(Gamma11(tt).*I1+Gamma12(tt).*I2)/N1+(Gamma13(tt).*I5 + Gamma14(tt).*I6)
    ./N3;
dS1=sigma1*psi1+varpi*R1 - alpha1*S1.*(G1)- mu1*S1;
dE1=(1-sigma1)*psi1+alpha1*S1.*(G1)-alpha2*E1-mu1*E1;
dI1=nu2*alpha2*E1-alpha3*I1-I1*(mu1+delta1b);
dI2=nu3*alpha2*E1+rho3*alpha3*I1-alpha4*I2-I2*(mu1+delta1s);
dI3=nu1*alpha2*E1+rho1*alpha3*I1+alpha4*xi*I2 -alpha5*I3-I3*(mu1+delta1p);
dR1=alpha3.*rho2.*I2+alpha4.*(1-xi).*I2+alpha5.*I3-(varpi+mu1).*R1;
dS2=psi22-beta.*S2.*(G3)-mu2*S2;
dI4=psi21+beta.*S2.*(G3)- I4*(mu2+delta2);
dS3=sigma2*psi3-gamma1*S3*(G2)-mu3*S3;
dE3=(1-sigma2)*psi3+gamma1*S3*(G2)-gamma2*E3-mu3*E3;
dI5=gamma2*tau3*E3-gamma3*I5-I5*(mu3+delta3b);
dI6=tau2*gamma2*E3+gamma3*(1-phi)*I5-gamma4*I6-I6*(mu3+delta3s);
dI7=tau1*gamma2*E3+gamma3*phi*I5+gamma4*I6-I7*(mu3+delta3p);
dA=lambda4+eta1(tt).*((I3)/(N1))+eta2(tt).*((I7)/(N3))-mu4*A;
ds=0.2;
dy = [dS1;dE1;dI1;dI2;dI3;dR1;dS2;dI4;dS3;dE3;dI5;dI6;dI7;dA;ds];
```

```
global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
    Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
    Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
    Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
    eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
options = odeset('MaxStep',0.01);
[t,y] = ode45('chap4',[0 50],[1000, 800, 500, 100, 50, 100, 100, 2000,
    1000, 5000,1000,800, 500, 5000,0],options);
figure(1)
plot(t,y(:,1), t,y(:,2), t,y(:,3),t,y(:,4),t,y(:,5),t,y(:,6));
```

```
6 legend('Susceptible human','Exposed human','I_{HB}','I_{HS}','I_{HP}','
      Recovered human')
7 xlabel('Time[years]')
8 ylabel('Human Population')
```

```
1 global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
      Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
      Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
      Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
      eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
2 options = odeset('MaxStep',0.01);
3 [t,y] = ode45('chap4',[0 50],[1000, 800, 500, 100
      ,50,100,40000,2000,1000,5000,1000,800, 500, 5000,0],options);
4 figure(1)
5 plot(t,k22)
```

```
1 global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
      Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
      Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
      Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
      eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
2
3 options = odeset('MaxStep',0.01);
4 [t,y] = ode45('chap4',[0 50],[1000, 800, 500, 100
      ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0],options);
5 figure(1)
6 plot(t,y(:,14));
7 xlabel('Time[years]')
8 ylabel('Pathodens in the environment')
```

```
1 global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
      Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
      Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
      Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
      eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
2 options = odeset('MaxStep',0.01);
3 [t,y] = ode45('chap4',[0 50],[1000, 800, 500, 100
      ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0],options);
4 figure(1)
5 plot(t,y(:,9), t,y(:,10), t,y(:,11),t,y(:,12),t,y(:,13));
6 legend('Susceptible rodent','Exposed rodent','I_{RB}','I_{RS}','I_{RP}')
7 xlabel('Time[years]')
```

```
ylabel('Rodent Population')
```

```
global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
    Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
    Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
    Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
    eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
options = odeset('MaxStep',0.01);
[t,y] = ode45('chap4',[0 50],[1000, 800, 500, 100
    ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0],options);
figure(1)
plot(y(:,7),y(:,8));
xlabel('Susceptible Flea')
ylabel('Infectious Flea')
```

```
global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
    Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
    Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
    Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
    eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
options = odeset('MaxStep',0.01);
[t,y] = ode45('chap4_try',[0 50],[1000, 800, 500, 100
    ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0],options);
sss1=y(:,3)+y(:,4)+y(:,5);
figure(1)
plot3(y(:,1), y(:,2), sss1);
xlabel('Susceptible human')
ylabel('Exposed human')
zlabel('Infectious Human')
```

```
global Gamma1_0 Gamma1_1 Gamma2_0 Gamma2_1 Gamma3_0 Gamma3_1 Gamma4_0
    Gamma4_1 Gamma5_0 Gamma5_1 Gamma6_0 Gamma6_1 Gamma7_0 Gamma7_1 Gamma8_0
    Gamma8_1 Gamma9_0 Gamma9_1 Gamma10_0 Gamma10_1 Gamma11_0 Gamma11_1
    Gamma12_0 Gamma12_1 Gamma13_0 Gamma13_1 Gamma14_0 Gamma14_1 eta1_0
    eta1_1 eta2_0 eta2_1 omega1_0 omega1_1 omega2_0 omega2_1
options = odeset('MaxStep',0.01);
[t,y] = ode45('chap4',[0 50],[1000, 800, 500, 100
    ,50,100,100,2000,10000,5000,1000,800, 500, 5000,0],options);
sss2=y(:,11)+y(:,12)+y(:,13);
figure(1)
plot3(y(:,9), y(:,10), sss2);
xlabel('Susceptible rodent')
```

```
ylabel('Exposed rodent')
zlabel('Infectious rodent')
```

4.1 Varying Initials

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 4000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 3000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 2000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 1000,0]
```

```
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold on
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 10,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Pathogens in the Environment')
hold off
legend('A(0)= 5000','A(0)= 4000','A(0)= 3000', 'A(0)= 2000','A(0)= 1000','A
    (0)= 10')
```

```
clear
tspan=[0 50]
y0=[1000, 1800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'g','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 50]
y0=[1000, 1500, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'c','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 50]
y0=[1000, 1000, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'m','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 50]
```

```
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'r','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 50]
y0=[1000, 400, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'b','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 50]
y0=[1000, 10, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'k','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold off
legend('E_H(0)= 1800','E_H(0)= 1500','E_H(0)= 1000','E_H(0)= 800', 'E_H(0)=
    500','E_H(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,5000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,4000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
```

```
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,2000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,1000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,10,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,6),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Exposed rodent')
hold off
legend('E_R(0)= 5000','E_R(0)= 4000','E_R(0)= 3000', 'E_R(0)= 2000','E_R(0)
    = 1000','E_R(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
```

```
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,4000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,3000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,2000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,1000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,10,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,9),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Infected flea')
hold off
legend('I_F(0)= 5000','I_F(0)= 4000','I_F(0)= 3000', 'I_F(0)= 2000','I_F(0)
    = 1000','I_F(0)= 10')
```

```
clear
tspan=[0 100]
```

```
y0=[1800, 1500, 2800, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 1800, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 1200, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 800, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 400, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Infected human')
hold on
tspan=[0 100]
y0=[1800, 1500, 10, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,3),'k','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('Infected human')
hold off
legend('I_H(0)= 2800','I_H(0)= 1800','I_H(0)= 1200', 'I_H(0)= 800','I_H(0)=
    400','I_H(0)= 10')
```

```
clear
tspan=[0 50]
y0=[1000, 800, 140, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,3),'g','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HB}')
hold on
tspan=[0 50]
y0=[1000, 800, 110, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,3),'m','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HB}')
hold on
tspan=[0 50]
y0=[1000, 800, 80, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,3),'C','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HB}')
hold on
tspan=[0 50]
y0=[1000, 800, 70, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,3),'r','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HB}')
hold on
tspan=[0 50]
y0=[1000, 800, 40, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,3),'b','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('I_{HB}')
hold on
tspan=[0 50]
y0=[1000, 800, 10, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,3),'k','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HB}')
hold off
legend('I_{HB}(0)= 2500','I_{HB}(0)= 2000','I_{HB}(0)= 1500','I_{HB}(0)=
    1000', 'I_{HB}(0)= 500','I_{HB}(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,1200,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'g','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,1000,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'m','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 100]
y0=[2000, 800, 500, 100 ,800,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'y','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 100]
y0=[1500, 800, 500, 100 ,600,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'r','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('I_{HP}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,400,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'b','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold on
tspan=[0 100]
y0=[100, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'k','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HP}')
hold off
legend('I_{HP}(0)= 1500','I_{HP}(0)= 1000','I_{HP}(0)= 800','I_{HP}(0)= 600
    ', 'I_{HP}(0)= 200','I_{HP}(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 260 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,4),'g','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 210 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,4),'m','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 160 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,4),'y','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 110 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,4),'r','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 60 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,4),'b','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 10 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,4),'k','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold off
legend('I_{HS}(0)= 1500','I_{HS}(0)= 1000','I_{HS}(0)= 800','I_{HS}(0)= 600
    ', 'I_{HS}(0)= 200','I_{HS}(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,5000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'g','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,4000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'y','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,3000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,1000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,10,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,7),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Infected rodent')
hold off
legend('I_R(0)= 5000','I_R(0)= 4000','I_R(0)= 3000', 'I_R(0)= 2000','I_R(0)
    = 1000','I_R(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1800, 1500, 500, 2300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'g','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 1800 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'y','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 1300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'m','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 800 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'r','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 300 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'b','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold on
tspan=[0 100]
y0=[1800, 1500, 500, 0 ,5000,3000,2000,8000,5000,10000]
[t,y]=ode45(@m11,tspan,y0)
figure(1)
plot(t,y(:,4),'k','linewidth',2)
xlabel('Time[years]')
ylabel('Recovered human')
hold off
legend('R_H(0)= 2300','R_H(0)= 1800','R_H(0)= 1300','R_H(0)= 800', 'R_H(0)=
    300','R_H(0)= 5')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1500,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'g','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,1000,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'m','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[2000, 800, 500, 100 ,50,800,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'c','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1500, 800, 500, 100 ,50,500,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'r','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,300,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,5),'b','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold on
tspan=[0 100]
y0=[100, 800, 500, 100 ,50,50,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
```

```
plot(t,y(:,5),'k','linewidth',2)
xlabel('Time[years]')
ylabel('I_{HS}')
hold off
legend('R_H(0)= 1500','R_H(0)= 1000','R_H(0)= 800','R_H(0)= 500', 'R_H(0)=
    300','R_H(0)= 50')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,10000,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'g','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,8000,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'m','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,6000,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'r','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,4000,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,2000,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'b','linewidth',2)
```

```
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'k','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold off
legend('S_F(0)= 10000','S_F(0)= 8000','S_F(0)= 6000', 'S_F(0)= 4000','S_F
    (0)= 2000','S_F(0)= 100')
```

```
clear
tspan=[0 50]
y0=[3000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'g','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 50]
y0=[2500, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'m','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 50]
y0=[2000, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'c','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 50]
y0=[1500, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'r','linewidth',2)
```

```
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 50]
y0=[800, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'b','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 50]
y0=[10, 800, 500, 100 ,50,100,100,2000,1000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
xlabel('Time[years]')
ylabel('A')
hold off
legend('S_H(0)= 3000','S_H(0)= 2500','S_H(0)= 2000','S_H(0)= 1500', 'S_H(0)
    = 800','S_H(0)= 10')
```

```
clear
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,15000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'g','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,8000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'m','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,6000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'r','linewidth',2)
xlabel('Time[years]')
```

```
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,4000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'b','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,2000,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'k','linewidth',2)
xlabel('Time[years]')
ylabel('A')
hold on
tspan=[0 100]
y0=[1000, 800, 500, 100 ,50,100,100,2000,100,5000,1000,800, 500, 5000,0]
[t,y]=ode45(@chap4,tspan,y0)
figure(1)
plot(t,y(:,14),'c','linewidth',2))
xlabel('Time[years]')
ylabel('A')
hold off
legend('S_R(0)= 10000','S_R(0)= 8000','S_R(0)= 6000', 'S_R(0)= 4000','S_R
    (0)= 2000','S_R(0)= 100')
```

4.2 Sinusoidal functions for parameters that are affected by weather variation

```
function r1 = Gamma1(t)
global Gamma1_0 Gamma1_1
r1 = Gamma1_0.*(1+Gamma1_1.*cos(2.*pi.*t));
```

```
function r2 = Gamma2(t)
global Gamma2_0 Gamma2_1
r2 = Gamma2_0*(1+Gamma2_1*cos(2*pi*t));
```

```
function r3 = Gamma3(t)
global Gamma3_0 Gamma3_1
```

```
3 r3 = Gamma3_0*(1+Gamma3_1*cos(2*pi*t));
```

```
1 function r4 = Gamma4(t)
2 global Gamma4_0 Gamma4_1
3 r4 = Gamma4_0*(1+Gamma4_1*cos(2*pi*t));
```

```
1 function r5 = Gamma5(t)
2 global Gamma5_0 Gamma5_1
3 r5 = Gamma5_0*(1+Gamma5_1*cos(2*pi*t));
```

```
1 function r6 = Gamma6(t)
2 global Gamma6_0 Gamma6_1
3 r6 = Gamma6_0*(1+Gamma6_1*cos(2*pi*t));
```

```
1 function r7 = Gamma7(t)
2 global Gamma7_0 Gamma7_1
3 r7 = Gamma7_0*(1+Gamma7_1*cos(2*pi*t));
```

```
1 function r8 = Gamma8(t)
2 global Gamma8_0 Gamma8_1
3 r8 = Gamma8_0*(1+Gamma8_1*cos(2*pi*t));
```

```
1 function r9 = Gamma9(t)
2 global Gamma9_0 Gamma9_1
3 r9 = Gamma9_0*(1+Gamma9_1*cos(2*pi*t));
```

```
1 function r10 = Gamma10(t)
2 global Gamma10_0 Gamma10_1
3 r10 = Gamma10_0*(1+Gamma10_1*cos(2*pi*t));
```

```
1 function r11 = Gamma11(t)
2 global Gamma11_0 Gamma11_1
3 r11 = Gamma11_0*(1+Gamma11_1*cos(2*pi*t));
```

```
1 function r12 = Gamma12(t)
```

```
2 global Gamma12_0 Gamma12_1
3 r12 = Gamma12_0*(1+Gamma12_1*cos(2*pi*t));
```

```
1 function r13 = Gamma13(t)
2 global Gamma13_0 Gamma13_1
3 r13 = Gamma13_0*(1+Gamma13_1*cos(2*pi*t));
```

```
1 function r14 = Gamma14(t)
2 global Gamma14_0 Gamma14_1
3 r14 = Gamma14_0*(1+Gamma14_1*cos(2*pi*t));
```

```
1 function r17 = omega1(t)
2 global omega1_0 omega1_1
3 r17 = omega1_0*(1+omega1_1*cos(2*pi*t));
```

```
1 function r18 = omega2(t)
2 global omega2_0 omega2_1
3 r18 = omega2_0*(1+omega2_1*cos(2*pi*t));
```

```
1 function r15 = eta1(t)
2 global eta1_0 eta1_1
3 r15 = eta1_0*(1+eta1_1*cos(2*pi*t));
```

```
1 function r16 = eta2(t)
2 global eta2_0 eta2_1
3 r16 = eta2_0*(1+eta2_1*cos(2*pi*t));
```