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# A mathematical model to inform on desirable dog-rabies control methods in an urban setting: a case study of Arusha-Tanzania

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**A MATHEMATICAL MODEL TO INFORM ON DESIRABLE  
DOG-RABIES CONTROL METHODS IN AN URBAN SETTING: A  
CASE STUDY OF ARUSHA-TANZANIA**

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**Dissertation Submitted in Partial Fulfillment of the Requirements for the Degree of  
Master's in Mathematical and Computer Science and Engineering of the Nelson  
Mandela African Institution of Science and Technology**

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## ABSTRACT

Rabies is a zoonotic, viral disease that causes an acute brain inflammation in mammals. It is transmitted through the saliva of infected animals via bites, scratches or contact with infectious tissue. In this study, we formulate a deterministic model which measures the effects of culling and vaccination on dog mediated transmission of rabies for urban areas near wildlife, using the Arusha region as an example. Various parameter values were deduced from five years worth of survey data on Arusha's dog population and dog vaccination coverage from the Mbwa wa Africa group, a Non Governmental Organisation and from records of dog bite incidence and deaths cases from the Ministry of Livestock and Fisheries, Tanzania. Three distinct dog populations were assumed: domestic dogs, stray dogs and Pastoralist dogs. The basic reproduction number  $R_0$  and effective reproduction number  $R_e$  for rabies were computed to estimate transmission and found to be 1.9 and 1.2 respectively. The disease free equilibrium  $\varepsilon_0$  was also computed. When  $R_e < 1$  it implies that it is globally asymptotically stable in the feasible region  $\Phi$ . When  $R_e > 1$ , it implies that, there is an equilibrium point which is endemic and locally asymptotically stable. According to the sensitivity indices, infection rate of stray dogs  $\beta_s$  is the most positive sensitive parameter and natural death rate of stray dogs  $\mu_s$  is the most negative sensitive parameter. This study proposes putting much emphasis on the most positive and most negative sensitive parameters when fighting against dog-rabies transmission in urban areas near wildlife reservoirs. Under the assumption that a dog is immune to rabies for 3 years once vaccinated, the numerical simulations of the formulated model predict that the number of infected stray dogs will increase to its highest in 2020. However, the number of infected domestic dogs is expected to decline to its minimum in 2020, while the number of infected Pastoralist dogs will stay similar the same as the previous years in 2020. These results show that, rabies incidence for the infected stray dogs is the highest followed by the incidence for infected Pastoralist dogs and lastly for the infected domestic dogs. The numerical simulation of the reproduction number shows that dog mass vaccination is the most appropriate method in the long term to control rabies transmission among dog sub-populations for urban areas near wildlife reservoirs such as Arusha. Culling on the other hand, is effective at the moment in time when it is practiced, but its protective effect quickly decreases after just 6 to 8 months when all culled dogs will have been replaced by un-vaccinated new born puppies.

## DECLARATION

I, **Edwiga K. Renald** declare that this research report is my own original work and that it has not been presented and will not be presented to any other University for a similar or any other degree award.

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**Candidate's Signature**

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**Date**

The above declaration is confirmed by:

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**Prof. Dmitry Kuznetsov**

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**Dr. Katharina Kreppel**

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**Date**

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## CERTIFICATION

The undersigned certify that they have read and found the dissertation titled “*A Mathematical Model to Inform on Desirable Dog-Rabies Control Methods in an Urban Setting: A Case Study of Arusha-Tanzania*” acceptable by the Nelson Mandela African Institution of Science and Technology.

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## LIST OF PUBLICATIONS

### Articles Published from this Dissertation

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## LIST OF ABBREVIATIONS AND SYMBOLS

<b>ACRONYM</b>	<b>DEFINITION</b>
DFE	Disease Free Equilibrium
LGDs	Livestock Guardian Dogs
LMIC	Low and Middle Income Countries
MWECAU	Mwenge Catholic University
NGO	Non Governmental Organisation
NM-AIST	Nelson Mandela African Institution of Science and Technology
ORV	Oral Rabies Vaccination
PEP	Post Exposure Prophylaxis
SEI	Susceptible Exposed Infectious
SEIV	Susceptible Exposed Infectious Vaccinated
SEIR	Susceptible Exposed Infectious Removed
SIR	Susceptible Infectious Removed
SIS	Susceptible Infectious Susceptible
SPSS	Statistical Package for Social Sciences
TVR	Trap Vaccinate Release
URT	United Republic of Tanzania
US	United States



# CHAPTER ONE

## INTRODUCTION

### 1.1 Background of the Problem

Rabies is a zoonotic, viral disease that causes an acute inflammation of the brain in humans and other mammals (Tulu & Koya, 2017). Rabies transmission occur through the saliva of an infected animal by being bitten or scratched, with dogs being the primary source of transmission to humans (Gongal & Wright, 2011). Rabies is 100% fatal if not treated early enough before onset of symptoms. People with violently intense rabies exhibit signs of hyperactivity, excitable behaviour, hydrophobia (fear of water) and sometimes aerophobia (fear of drafts or of fresh air). Death occurs after a few days due to cardio-respiratory arrest.

Rabies is still a worldwide one of the important health problems since it has become a re-emergent infection especially for the developing countries (Wunner & Jackson, 2010). Over 150 countries in the world including territories, suffer from rabies disease, with Asia and developing countries in Africa being the most affected (Ega *et al.*, 2015). Especially poor communities are mostly in the risk of being attacked with rabies due to increased interactions with domestic mammals such as dogs (Ega *et al.*, 2015).

Globally, rabies claims an estimated 60 000 human lives annually (Léchenne *et al.*, 2016). This is the highest number of deaths caused by any zoonotic disease (Hampson *et al.*, 2009; Lembo *et al.*, 2010). In Tanzania, it claims the lives of around 1500 people yearly and those victims who receive Post-Exposure Prophylaxis (PEP) after a bite, incur high costs (Mpolya *et al.*, 2017).

There are two main ways that are used to control dog-mediated-rabies transmission, mass-dog vaccination and culling, whereby the culling method is perceived to be easier and cheaper than vaccination, especially in the presence of free-roaming and poorly socialized animals and in areas where veterinarians and animal health workers have relatively little experience or confidence in handling dogs (Morters *et al.*, 2013).

However, despite control efforts, rabies remains a problem and more than 99% of all human deaths from rabies occur in the low and middle income countries (LMIC) (Knobel *et al.*, 2005). In Tanzania, wildlife diseases are monitored, but not controlled and dogs are frequently in contact with wild animals due to the fact that all the 17 national parks have no fences. Pastoralists, such as the Maasai tribe, Sukuma tribe, Barbaig (Mang'ati) tribe, Taturu tribe and others, have

access to grazing land in and around the national parks and they often have dogs helping to protect their livestock which travel long distances with them. These dogs therefore can roam far and encounter wildlife and other dogs, both of which can transmit rabies, in and around villages and urban areas. Spill over of infectious diseases such as rabies is therefore a constant threat in these areas.

For public health policy, it is therefore paramount to find the best control method to reduce transmission and evaluate the impact of mass dog vaccination and culling respectively.

With regard to culling, according to Mbwa wa Africa, an animal welfare organization in Arusha conducting research, every killed dog is replaced within 6 to 8 months by a new young dog as resources such as food and shelter are freed-up. Another effect of culling on disease transmission arises from the fact that dogs are territorial and defend their resting and feeding grounds in packs, killed members of a pack affect its ability to hold a territory, leading to more fighting and mixing of the overall dog population. Killing a neutered, vaccinated dog, therefore leads to having it replaced by an unvaccinated unneutered dog, increasing the number of potential hosts and thus the risk for rabies outbreaks (Fissenebert, personal communication 2018).

Mass-dog vaccination on the other hand requires resources, trained personnel and time to ensure up to 70% of the dog population is vaccinated in an area to break rabies transmission (Kaare *et al.*, 2009). Also, currently, vaccination is not free of charge, which leads to some dog owners to object (poor awareness) (Kaare *et al.*, 2009).

The best intervention method to control rabies in resource-poor countries and particularly in areas such as Arusha remains debatable.

To shed light on the impact of the two control methods on rabies transmission and inform public health policies, Mathematical modeling has been chosen as the best course of action.

Hence, Mathematical modeling can assist with coming up with a strategy to control a disease and to decrease its incidence. The first epidemic model on rabies was formulated and solved by Daniel Bernoulli in 1760 (Abta *et al.*, 2014).

Various models have since been used to study different aspects of rabies transmission and control (Abta *et al.*, 2014; Zhang *et al.*, 2011). However, in the region of Arusha, with unique factors influencing the decisions of officials, the best strategy to disrupt rabies transmission has not been presented yet and human rabies incidence remains high. This is most likely due to unique factors such as close contact to wildlife reservoirs by dogs. This is exacerbated by the presence of 3 distinct dog populations, with Pastoralist dogs moving into National Parks with

the livestock they are guarding and covering large distances and with a large population of stray dogs present.

In the Arusha region, livestock travels from wildlife parks, where they graze, to suburban areas and cities and also to market. The pastoralists and their animals travel always with many dogs used for guarding the livestock against wild animals. These dogs can be classed as a specific dog population and is here labelled as “Pastoralist dogs”.

In the Arusha region, there is a strong interest in keeping human rabies cases low, not only out of humanitarian reasons, but also due to the importance of tourism in the area. This study has come up with a model which will best describe the dynamics of rabies here and help decide on the best technique to fight against the transmission of the disease in urban areas near wildlife reservoirs, whereby Arusha region has been used as an example.

## **1.2 Statement of the Problem**

In Africa, nearly 24 000 people die due to the rabies disease and this make it the continent most affected by the disease (Tulu & Koya, 2017). However, this estimate is still considered to be conservative. Thirty per cent (30%) to sixty per cent (60%) of dog bite victims in dog-endemic areas are children less than 15 years of age. Unfortunately, the majority of these cases go unreported to parents or health services (Addo, 2012).

Statistics in Tanzania show that rabies claims the life of around 1500 people annually and those victims who receive PEP after a bite, incur high costs. Every year several rabies cases and deaths are reported from the Arusha-Moshi area.

Although various Mathematical models describing the dynamics of rabies disease have been developed, there is no model which best describes the dynamics of rabies disease based on the sub-populations of dogs present in this area: domestic dogs, stray dogs and Pastoralist dogs in urban areas near wildlife reservoirs. To be able to advise on the best strategy to control rabies in a city like Arusha, an appropriate model has been developed. Here, dog mass vaccination has been compared to dog culling as a disease control method in terms of its effects on rabies transmission risk.

### **1.3 Justification of the Study**

This study has come up with a model which best describes the dynamics of rabies and it has helped to decide on the best technique to fight against the disease transmission in urban areas near wildlife reservoirs using Arusha region as an example. The model includes three dog sub-populations: domestic dogs, stray dogs and Pastoralist dogs. This study will be beneficial to the health officials, government officials and society at large. Here is a list of a few ways in which the study will make a significant contribution to society.

- (i) The findings of this study will help to suggest the best intervention for rabies control in urban areas near wildlife reservoirs.
- (ii) It will produce a model that can be used by authorities, to decide on the best practice on studying the dynamics and controlling rabies transmission risks to humans by free-roaming dogs.
- (iii) The developed model can be applied to similar settings all over the world.

### **1.4 Objectives of the Study**

#### **1.4.1 General Objective**

The main objective of this study is to develop a Mathematical model for the transmission and control of rabies disease in dogs for urban areas near wildlife reservoirs, using the Arusha region as an example to inform control policies.

#### **1.4.2 Specific Objectives**

- (i) To develop the appropriate Mathematical model based on the specificity of the Tanzania case.
- (ii) To use the available secondary data on rabies cases, number of bites, vaccinations and culling numbers to test the model and to estimate optimal values of parameters of the model that give the best accuracy of the model regarding real statistical data.
- (iii) To carry out theoretical and numerical analyses of the formulated model, such as stability analysis, sensitivity analysis and numerical simulation.

- (iv) To analyse the response of the dynamic system to applications of different control strategies such as vaccination and culling through numerical simulation.

## **1.5 Research Questions**

- (i) Based on the specificity of the Arusha-Tanzania case, what is the most appropriate Mathematical model describing the transmission of dog rabies in the most adequate way in accordance with the given statistical data?
- (ii) What are the analysis and simulation results of the formulated model?
- (iii) What are the optimal values of parameters of the derived model?
- (iv) Based on culling and mass vaccination control methods, what is the dynamic system response?

## **1.6 Significance of the Study**

The findings of this study will redound to the benefit of society considering that, dog-rabies disease has remained to be a burden over years. This justifies a need for the best strategy to combat rabies transmission. Thus, if the government officials and health policy makers for urban areas near wildlife reservoirs that will will apply the strategy proposed in this study as per analysis results, dog-rabies transmission will be controlled and if the strategy will be implemented over years, the disease shall get eliminated. For researchers, this research can be used as a backup for referencing.

## **1.7 Delineation of the Study**

Mathematical modeling of dog rabies transmission is very broad. This research did not intend to cover all settings and all mammal sub-populations. Rather, it was very specific to urban areas near wildlife reservoirs with Arusha region taken as example. This study focused on the dogs only and more specifically to dog sub-populations namely: domestic dogs, stray dogs and Pastoralist dogs. This study intended to develop a Mathematical model which so far has helped to best understand the disease dynamics and hence come up with the best strategy to

control the disease transmission among the specified dog sub-populations by comparing the most commonly used strategies which are: dog mass vaccination and dog mass culling.

## CHAPTER TWO

### LITERATURE REVIEW

#### 2.1 Introduction

This chapter explores and summarises various studies on the dynamics and control of rabies disease transmission and developed disease transmission models.

#### 2.2 Review of Previous Studies

For Tanzania, to start with, Hampson *et al.* (2009) conducted a study to assess whether global elimination of canine rabies is possible. In this case, researchers relied on quantitative understanding of transmission dynamics in domestic dog populations, whereby they gathered data on rabies exposures, PEP delivered and deaths in two rural districts in northwestern Tanzania from 2002 to 2006. Interestingly, the results of the study showed that global elimination of canine rabies can be achieved through appropriately designed and sustained domestic dog vaccination campaigns including areas near wildlife with a large number of carnivores. This study was limited as no Mathematical model was formulated to study the disease dynamics. The endemicity of the rabies disease was determined with the help of the basic reproduction number. The strategy suggested by this study can be applied specifically to areas near wildlife with large carnivores. Transmission between dog populations with accordance to the specificity of Tanzania case was not considered.

Lembo *et al.* (2010) conducted a study on the feasibility of canine rabies elimination in Africa. In this study, the researcher used a probability decision tree framework and the available data on animal bites and human rabies deaths to estimate the burden of rabies in Africa and Asia. The results of this study showed that rabies is an important disease whereby domestic dogs are the main source of infection to humans. Very interesting information from this study is that, vaccinating a large enough proportion will not only protect the vaccinated individuals but will reduce transmission such that, on average, less than one secondary infection will result from every 6 primary cases. From this the researcher suggested the domestic mass dog vaccination as the most feasible way of combating rabies. This study considered transmission between domestic dogs and humans. Mathematical modeling techniques were not incorporated. Also, the method of fighting against transmission of dog rabies as suggested by the researchers, is

specific for humans. The study did not suggest a strategy for combating rabies transmission among dog sub populations for areas near wildlife reservoirs.

Zhang *et al.* (2011) conducted a study on analysing rabies disease in China. This study proposed a deterministic model to study the transmission dynamics of rabies in China. The model consisted of Susceptible, Exposed, Infectious and Recovered (SEIR) dogs and humans. It describes the spread of rabies among dogs and from infectious dogs to humans. Data reported by the Chinese Ministry of Health were used to test the model. The basic reproduction number ( $R_0$ ) was approximated to 2 and this predicted that the number of human rabies in China was decreasing but may reach another peak around 2030. This study was limited to generally dogs and humans. One might be interested to deal with dog sub groups of a particular setting and study the model dynamics among dog sub populations. Also, one can be interested in lengthening the time limit application of the model, by incorporating the vaccination class due to the fact that once an individual become infected, what follows is death because of the incurability of the rabies disease.

Hou *et al.* (2012) proposed a Susceptible-Exposed-Infectious-Vaccinated (SEIV) model for the dog-human transmission of rabies taking both domestic and stray dogs into consideration. The results of their study showed that cases of rabies in Guangdong province in China would decrease gradually in the next few years and increase slightly afterward, which indicates that rabies cannot be controlled or eradicated by using the often used culling method. Based on their study results, the authors suggested that rabies control and prevention strategies should include public education and awareness about rabies, increase of the domestic dog vaccination rate and reduction of the stray dog population. Results of this study cannot be directly applied to Arusha, as it lacks one of the very important group of dogs present in Tanzania. As a limitation to this study, one of the very important group of dogs was not incorporated. That is the Livestock Guardian Dogs (LGDs). With specificity to Tanzania case in Arusha region, these are the Pastoralist dogs (Cleaveland *et al.*, 2007). Pastoralist dogs move in two major aspects. That is when they escort livestock to the market and also for grazing. This study did not consider this very important aspect which influence rabies transmission among Pastoralist dogs (LGDs used by Pastoralist tribe in Arusha region) and livestock.

In the United States (US), Keller *et al.* (2013) conducted a study to model the spread of rabies in raccoons across a heterogeneous and continuous landscape as a complex geographical setting in New York State. The heterogeneities included in this study are lakes, mountains and main



waterways. Numerical simulation of a Susceptible-Exposed-Infectious (SEI) space-continuous model for the spread of rabies with the inclusion of the diffusion term was used. In this study, the researchers found that in areas with a setting similar to this setting and also with high human population density, infectious animals are easily identified and hence can be removed. So researchers suggested that one of the possibilities to control rabies could be to reduce the infection rate in these areas as a consequence of a high level of surveillance. In this study, the researchers did not consider the situation that when an exposed animal gets vaccinated before it develops symptoms, it is considered as vaccinated and after a time when symptoms could be observed if it did not get vaccinated, it shifts to the susceptible class. Also, the study considered raccoons in their general aspect and not in terms of their subgroups.

Townsend *et al.* (2013) conducted a study on modeling dog rabies in poorly resourced countries using a stochastic simulation model with inclusion of proper and effective surveillance and detection probabilities. The researchers found that, rabies disease will be eliminated through a proactive strategy of continued mass vaccination over a 2-year period if that is followed by 6 consecutive months without any detected cases. Further, the researchers in this study recommended minimum requirements for surveillance capacity including detection of at least 5% and preferably 10% of all cases. In this study, the researchers were interested in dealing with poorly resourced countries setting. Conversely, one can be interested in considering a setting such as areas near wildlife reservoirs whereby rabies infections are largely persisting.

Abta *et al.* (2014) conducted a study to analyse the dynamics and control of rabies disease transmission. Researchers proposed a Susceptible-Infectious-Recovered (SIR) model with delay as a bifurcation parameter, to assess the impact of some control measures by reformulating the model as an optimal control problem with vaccination and treatment. The results of the study revealed that the optimal strategy becomes more effective when vaccination and other treatment strategies are combined. One of the shortcoming to this model is that, it does not incorporate the exposed class of dogs. When a susceptible animal is bitten or scratched by a rabies infected animal, it become exposed and after developing symptoms it become infected.

Ega *et al.* (2015) in their study on modeling the dynamics rabies transmission among dogs, livestock and humans found that transmission of rabies shall increase in Addis Ababa in Ethiopia including nearby areas and will max out in 2024 and 2026 for both human and livestock respectively. This setting is very similar to the Arusha region. The researcher suggested the use of combination of dog mass vaccination and culling interventions to be able to eradicate rabies

in Ethiopia. The model in study did not consider the dynamics of rabies disease among dogs. Rather, it did not consider rabies transmission in urban areas near wildlife reservoirs. Another limitation observed in this study is that, the researchers did not consider vaccinated group of dogs as a different class.

In other places such as US, other mammals than dogs are the main rabies reservoirs. For example, Elmore *et al.* (2017) conducted a study on management and modeling approaches for controlling raccoon rabies in wildlife areas in the US. The study identified Oral Rabies Vaccination (ORV) programs as one of the methods for managing rabies. Also, the study reveals that since 1978 it has been used to eliminate the virus from red foxes in Western Europe and reduced the disease incidence in central Europe. Other rabies management methods identified by this study include; Trap Vaccine Release (TVR) (for boosting population immunity), population reduction and fertility control. Modeling approaches to understanding wildlife rabies identified by this paper include; simple epidemic models such as SIR, SIS and SEIR, host heterogeneity models, multi-host/multi-pathogen models, seasonal models and spatial models. A detailed discussion up on which model best fits a particular setting is missing in this study. The researchers intended to give out the techniques to be used when fighting against rabies transmission but rather they were not specific to which model that best fits in areas similar the stated setting and give out the theoretical and numerical analyses results of the model. Additionally, it is unfortunate that ORV cannot be recommended because the exactly amount a dog consumes cannot be assured, because dogs share their food. No universal bait containing oral vaccination has been identified to date (Cliquet *et al.*, 2018). What is exciting in this study is that, the researchers acknowledged the contribution of Mathematical modeling in understanding of disease dynamics.

Ruan (2017) reviewed some spatiotemporal epidemic models for rabies among animals. The study provided a diminutive review on some reaction-diffusion models describing the spatial spread of rabies among animals. The researcher specifically introduced the SEI model for the spatial transmission of rabies among foxes and spatiotemporal epidemic model for rabies among raccoons. Results showed that the spatial spread of rabies is due to the result of the dispersal of the host animals. Also, computed parameters from the SEI model indicated that with the movement of dogs, there exist traveling waves in every subgroup of dogs. Thus, the dispersal of dogs induces the epidemic waves of rabies among the dog population. In this case, the researcher provided reasons for studying the dynamics of the introduced models. The important compon-

ents that the researcher mentioned are stability analysis, the existence of traveling solutions and threshold dynamics. One of the limitation to this study is that it is too general for our purpose. That is, it does not state the specific setting(s) to which the model fit for application. Also, the model miss one of the important classes. The vaccinated class.

In the N'Djamena, Chad, Laager *et al.* (2018) conducted a study to assess the impact of individual level heterogeneity on outbreak probability, effectiveness of vaccination campaigns and likely time to resurgence after a campaign. In this study, the researchers used empirical contact network data to develop a contact network model of dog rabies transmission incorporated into the deterministic model for rabies. At the end it showed that domestic dog mass vaccination (at least 70% of the population) would be sufficient to interrupt transmission for 6 years. Also, based on the analysis results, researchers recommended targeting dogs for vaccination based on the degree of centrality. Moreover, this study reveals that vaccination based on movement also reduces the outbreak probabilities and sizes. One of the shortcomings observed in this study is that, it does not specify which deterministic model applied. Adding to that, it fails to indicate the dynamics of the disease.

Chidumayo (2018) conducted a study on system dynamics modeling approach to explore the effect of dog demography on rabies vaccination coverage in Africa. In this study, a system dynamics approach was adopted to build a dog population model to simulate the effects of demographic processes on rabies vaccination coverage. The results of this study indicated that the vaccination coverage and adjusted vaccination coverage remained over 30% and 20% respectively at 12 months if annual mass vaccinations achieved at least 70% coverage. What inspires in this study is that, model validation was done using simulations techniques (though non mathematical) that involved studying the model behavior in relation to the data on owned dog population size, age specifying mortality rates, mean litter size, annual female reproduction probability, proportion of spayed females and proportion of: male, female, young (less than 12 months) and adult (more than 12 months) dogs from Machakos district in Kenya. From this study, one can see that there is no comparison between different strategies to combat rabies. The researchers did not show why they suggested mass vaccination as a strategy to combat rabies transmission apart from others. Also, the suggested strategy is not specific to a particular setting because methods vary with different factors one including setting. Further, Mathematical modeling approach which has always been supported by various scholars in understanding the disease dynamics and predicting is little bit missing in this study.

## CHAPTER THREE

### MATERIALS AND METHODS

#### 3.1 Model Formulation

In this study, a Mathematical model for dog rabies disease for areas near wildlife reservoirs was developed. The model has measured the effect of culling and vaccination. Statistical data analysis, specifically least square statistics, has been used to fit parameters.

The researcher developed a basic transmission risk model tailored to areas with similar settings as Arusha, which will measure the effect of culling and vaccination. The formulated model consists of three dog sub-populations, which are domestic dogs, stray dogs and Pastoralist dogs. Domestic dogs (*canis familiaris*) being defined as the dogs that live in a close relationship with human being (Dürr *et al.*, 2017), stray dogs being defined as the publicly roaming dogs (Totton *et al.*, 2010) and Pastoralist dogs being defined as Livestock Guardian Dogs (LGDs) for Pastoralist tribe in Arusha region (Cleaveland *et al.*, 2007). Each sub-population is categorized into four classes which are Susceptible, Exposed, Infectious and Vaccinated and hence a SEIV model for rabies transmission description has been formulated.

The susceptible class consists of individuals, who do not have rabies but they may get infected with rabies once they have contact with an infectious dog. The exposed class consists of individuals who have contracted the virus via bites or scratches by another rabid dog but they do not show signs and symptoms of being affected with the disease yet. The infectious class consists of individuals who were previously exposed to the disease and later they developed clinical symptoms of rabies. They can now infect other mammals and will die due to the nature of the disease. The vaccinated class of individuals are the ones who were formally susceptible or exposed to the disease but they got vaccinated. The formulated model is a system of differential equations, which has been derived from the compartmental diagram in Fig. 1.

Theoretical analysis of the model was done by using the MATHEMATICA program while numerical analysis of the model was done by using MATLAB. All model parameters are non negative. They're listed and described in Table 1.

**Table 1: Parameter Description**

<b>Parameter</b>	<b>Description</b>
$\alpha_d, \alpha_s, \alpha_m$	The annual births of domestic dog, stray dog and Pastoralist dog populations respectively
$\omega_d, \omega_s, \omega_m$	The vaccination immunity loss rate for domestic dog, stray dog and Pastoralist dog populations respectively.
$\mu_d, \mu_s, \mu_m$	Natural death rate of domestic dog, stray dog and Pastoralist dog populations respectively
$\beta_d, \beta_s, \beta_m$	Rate at which infectious stray dogs infect susceptible domestic dog, stray dog and Pastoralist dog populations respectively
$\rho_d, \rho_s, \rho_m$	The incubation period in domestic dog, stray dog and Pastoralist dog populations respectively
$\sigma_d, \sigma_s, \sigma_m$	Vaccination rate of susceptible domestic dog, stray dog and Pastoralist dog populations respectively
$\psi_{md}, \psi_{sd}, \psi_{ds}, \psi_{ms}$	Number of dogs migrated from Pastoralist to domestic, stray to domestic, domestic to stray and Pastoralist to stray dogs' populations respectively
$\mu_c$	Average culling rate of stray dogs

Data on bite injuries provide a useful and accessible source of epidemiological information that could be used effectively to improve rabies surveillance in human and animal populations, detect trends in disease incidence, improve the allocation of medical and veterinary resources and assess the impacts of rabies control measures (Cleaveland *et al.*, 2014).

Five years worth of survey data from Mbwa wa Africa on Arusha's dog population and vaccination coverage, data on dog bite and rabies deaths and the number of dogs killed per year from the Ministry of Livestock and Fisheries has been used for the model analysis and model validation.

Based on the results of the analysis, the researcher provides a recommendation for a model to describe the dynamics and transmission control of rabies disease in the region. This has helped to inform on the best method to control the transmission in urban areas near wildlife reservoirs.

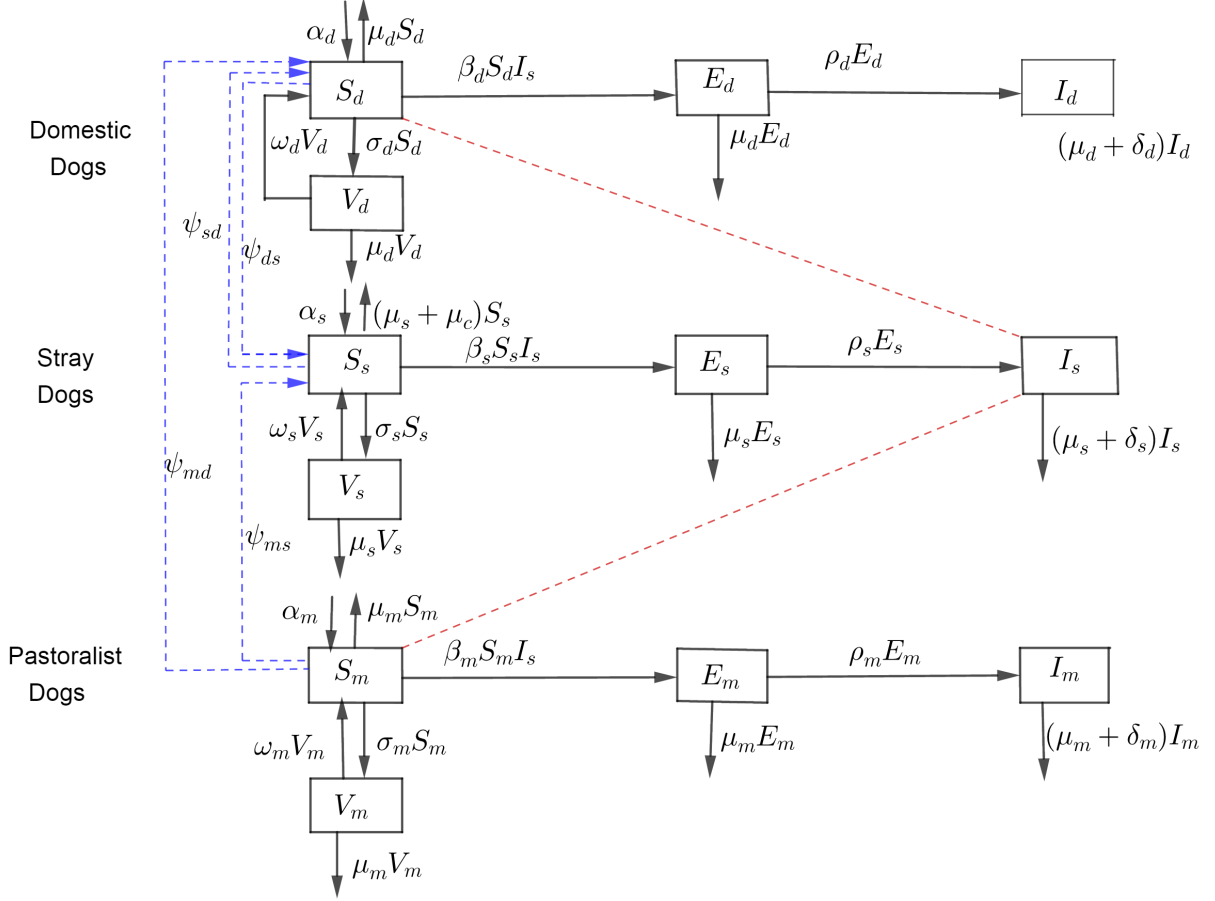
### **3.2 Model Assumptions**

The basic transmission risk model will be developed under the assumptions below:

- (i) The susceptible populations are recruited by birth rate  $\alpha$ ;
- (ii) Any kind of dog which is bitten or scratched or in contact with the saliva an infectious dog via any open part of its body, transforms to exposed;
- (iii) Dogs in every group are equal in natural death;
- (iv) Populations are homogeneous in a sense that every dog has a probability of being bitten or scratched by another dog and thereby contracting the disease;
- (v) Once a dog reaches the infectious stage there is no recovery and death is 100% certain;
- (vi) Pastoralist and domestic dog populations are controlled by humans, this means population growth is restricted; and
- (vii) We also assume a closed system where no new infected animals enter a dog population;

### **3.3 Model Compartment and Dynamics**

From the assumptions above, variables definitions and parameters descriptions, below is the model compartment diagram which illustrates the dynamics of rabies transmission among domestic dogs, stray dogs and Pastoralist dogs as shown in Fig. 1.



**Figure 1: Flow Diagram for Rabies Transmission Among Domestic Dogs, Stray Dogs and Pastoralist Dogs with Parameters as Described in Table 1**

The model parameters are positive.  $\alpha_i$  where,  $i = d, s, m$  represents the annual birth rates of domestic dogs, stray dogs and Pastoralist dogs populations respectively. The parameters  $\rho_i$  where,  $i = d, s, m$  represent the latency rates of domestic dogs, stray dogs and Pastoralist dogs so that  $1/\rho_i$  where,  $i = d, s, m$  are the respective incubation periods.

### 3.4 Model Equations

From the model compartment we formulate a set of twelve differential equations as shown in equation 3.1.

$$\begin{aligned}
\frac{dS_d}{dt} &= \alpha_d + \omega_d V_d + \psi_{sd} + \psi_{md} - \mu_d S_d - \sigma_d S_d - \psi_{ds} - \beta_d S_d I_s \\
\frac{dE_d}{dt} &= \beta_d S_d I_s - \mu_d E_d - \rho_d E_d \\
\frac{dI_d}{dt} &= \rho_d E_d - (\mu_d + \delta_d) I_d \\
\frac{dV_d}{dt} &= \sigma_d S_d - \omega_d V_d - \mu_d V_d \\
\\
\frac{dS_s}{dt} &= \alpha_s + \omega_s V_s + \psi_{ds} + \psi_{ms} - \sigma_s S_s - (\mu_s + \mu_c) S_s - \psi_{sd} - \beta_s S_s I_s \\
\frac{dE_s}{dt} &= \beta_s S_s I_s - \mu_s E_s - \rho_s E_s \\
\frac{dI_s}{dt} &= \rho_s E_s - (\mu_s + \delta_s) I_s \\
\frac{dV_s}{dt} &= \sigma_s S_s - \omega_s V_s - \mu_s V_s
\end{aligned} \tag{3.1}$$

$$\begin{aligned}
\frac{dS_m}{dt} &= \alpha_m + \omega_m V_m - \mu_m S_m - \psi_{ms} - \psi_{md} - \sigma_m S_m - \beta_m S_m I_s \\
\frac{dE_m}{dt} &= \beta_m S_m I_s - \mu_m E_m - \rho_m E_m \\
\frac{dI_m}{dt} &= \rho_m E_m - (\mu_m + \delta_m) I_m \\
\frac{dV_m}{dt} &= \sigma_m S_m - \omega_m V_m - \mu_m V_m
\end{aligned}$$

We add up the systems from each class to get the respective total populations derivatives as shown below; we know that:

$$\begin{aligned}
N_d(t) &= S_d(t) + E_d(t) + I_d(t) + V_d(t) \\
N_s(t) &= S_s(t) + E_s(t) + I_s(t) + V_s(t) \\
N_m(t) &= S_m(t) + E_m(t) + I_m(t) + V_m(t)
\end{aligned} \tag{3.2}$$

By applying  $\frac{d}{dt}$  to both sides we have:

$$\begin{aligned}
\frac{dN_d(t)}{dt} &= \frac{dS_d(t)}{dt} + \frac{dE_d(t)}{dt} + \frac{dI_d(t)}{dt} + \frac{dV_d(t)}{dt} \\
\frac{dN_s(t)}{dt} &= \frac{dS_s(t)}{dt} + \frac{dE_s(t)}{dt} + \frac{dI_s(t)}{dt} + \frac{dV_s(t)}{dt} \\
\frac{dN_m(t)}{dt} &= \frac{dS_m(t)}{dt} + \frac{dE_m(t)}{dt} + \frac{dI_m(t)}{dt} + \frac{dV_m(t)}{dt}
\end{aligned} \tag{3.3}$$

which implies:



$$\begin{aligned}
\frac{dN_d(t)}{dt} &= \alpha_d + \psi_{sd} + \psi_{md} - \mu_d S_d - \psi_{ds} - \mu_d E_d - (\mu_d + \delta_d) I_d - \mu_d V_d \\
\frac{dN_s(t)}{dt} &= \alpha_s + \psi_{ds} + \psi_{ms} - (\mu_s + \mu_c) S_s - \psi_{sd} - \mu_s E_s - (\mu_s + \delta_s) I_s - \mu_s V_s \\
\frac{dN_m(t)}{dt} &= \alpha_m - \mu_m S_m - \psi_{ms} - \psi_{md} - \mu_m E_m - (\mu_m + \delta_m) I_m - \mu_m V_m
\end{aligned} \tag{3.4}$$

Where  $N_i, i = d, s, m$  is the total of domestic dogs, stray dogs and Pastoralist dogs.

### 3.4.1 Invariant Region

The model represented by the system 3.1 of differential equations which deals with domestic dogs, Stray dogs and Pastoralist dogs, will be analysed in the feasible region  $\Phi$  and all state variables and parameters are assumed to be positive for all  $t \geq 0$ . The invariant region will be obtained through Theorem 3.1.

#### Theorem 3.1

All solutions of the system 3.1 are contained in the region  $\Phi \in \mathbb{R}^{12}$  and  $\Phi = \Phi_d \cup \Phi_s \cup \Phi_m$  where

$$\begin{aligned}
\Phi_d &= \{(S_d, E_d, I_d, V_d) \in \mathbb{R}_+^4 : 0 \leq N_d \leq \frac{\alpha_d}{\mu_d}\} \\
\Phi_s &= \{(S_s, E_s, I_s, V_s) \in \mathbb{R}_+^4 : 0 \leq N_s \leq \frac{\alpha_s}{\mu_s}\} \\
\Phi_m &= \{(S_m, E_m, I_m, V_m) \in \mathbb{R}_+^4 : 0 \leq N_m \leq \frac{\alpha_m}{\mu_m}\}
\end{aligned} \tag{3.5}$$

and  $\Phi$  is the positive invariant region.

#### Proof

Consider the first part of the system 3.1 of differential equations. The population for domestic dogs is:

$$\frac{dN_d(t)}{dt} = \frac{dS_d(t)}{dt} + \frac{dE_d(t)}{dt} + \frac{dI_d(t)}{dt} + \frac{dV_d(t)}{dt} \tag{3.6}$$

Therefore, the sum of total population of domestic dogs will satisfy:

$$\frac{dN_d(t)}{dt} = \alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds} - \mu_d N_d - \delta_d I_d \tag{3.7}$$

With an absence of rabies disease:

$$I_d = 0 \implies \delta_d I_d = 0 \quad (3.8)$$

Thus,

$$\begin{aligned} \frac{dN_d(t)}{dt} &\leq \alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds} - \mu_d N_d \\ \frac{dN_d(t)}{dt} + \mu_d N_d &\leq \alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds} \end{aligned} \quad (3.9)$$

This is a first order linear differential inequality with integrating factor  $e^{\mu_d t}$ .

$$\begin{aligned} e^{\mu_d t} \frac{dN_d(t)}{dt} + e^{\mu_d t} \mu_d N_d &\leq (\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}) e^{\mu_d t} \\ \frac{d}{dt} (e^{\mu_d t} N_d(t)) &\leq (\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}) e^{\mu_d t} \\ e^{\mu_d t} N_d(t) &\leq \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} e^{\mu_d t} + C \end{aligned} \quad (3.10)$$

Dividing by  $e^{\mu_d t}$  both sides of the inequality we have:

$$N_d(t) \leq \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} + C e^{-\mu_d t} \quad (3.11)$$

We now apply initial conditions when  $t = 0$ .

$$\begin{aligned} N_d(t=0) &= N_d(0) \\ N_d(0) &\leq \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} + C \\ N_d(0) - \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} &\leq C \end{aligned} \quad (3.12)$$

Substituting this expression into 3.11 we now have:

$$N_d(t) \leq \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} + (N_d(0) - \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d}) e^{-\mu_d t} \quad (3.13)$$

As  $t$  increases and become larger and larger the expression  $N_d(0) - \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} e^{-\mu_d t}$  goes to zero.

Thus we have:

$$N_d(t) \leq \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d} \quad (3.14)$$

Therefore:

$$0 \leq N_d \leq \frac{\alpha_d}{\mu_d} \quad (3.15)$$

This is the boundary for the domestic dog population. This implies that  $N_d(t) \geq 0 \forall t$ .

Similarly, if we consider the total of the stray dog and the Pastoralist dog populations of sub-systems of the system 3.1 we get the same results as in 3.15. That is  $N_s(t) \geq 0$  and  $N_m(t) \geq 0 \forall t$ .

Hence the set

$$\{(S_d, E_d, I_d, V_d \in \mathbb{R}_+^4), (S_s, E_s, I_s, V_s \in \mathbb{R}_+^4), (S_m, E_m, I_m, V_m \in \mathbb{R}_+^4)\}$$

is positively invariant set in  $\Phi$ .

### 3.4.2 Positivity of the Solution

For the model system 3.1 to be epidemiologically meaningful and well posed, we need to prove that all state variables are non-negative  $\forall t \geq 0$ .

#### Theorem 3.2

Let  $S_d(0), S_s(0), S_m(0) > 0, E_d(0), E_s(0), E_m(0) > 0, I_d(0), I_s(0), I_m(0) > 0, V_d(0), V_s(0), V_m(0) \in \Phi$ . Then the solution set  $S_d(t), E_d(t), I_d(t), V_d(t), S_s(t), E_s(t), I_s(t), V_s(t), S_m(t), E_m(t), I_m(t), V_m(t)$  of the model system 3.1 is positive  $\forall t \geq 0$ .

#### Proof

From the first equation of system 3.1 we have:

$$\frac{dS_d}{dt} = \alpha_d + \omega_d V_d + \psi_{sd} + \psi_{md} - \psi_{ds} - (\mu_d + \sigma_d + \beta_d I_s) S_d \quad (3.16)$$

This can be written as:

$$\frac{dS_d}{dt} \geq -(\mu_d + \sigma_d + \beta_d I_s) S_d \quad (3.17)$$

This is a first order linear differential inequality. By separation of variables we have:

$$\frac{dS_d}{S_d} \geq -(\mu_d + \sigma_d + \beta_d I_s) dt \quad (3.18)$$

With the absence of rabies disease:

$$\frac{dS_d}{S_d} \geq -(\mu_d + \sigma_d) dt \quad (3.19)$$

Through integrating both sides we get:

$$\int \frac{1}{S_d} dS_d \geq - \int (\mu_d + \sigma_d) dt \quad (3.20)$$

This gives:

$$\begin{aligned} \ln S_d &\geq - (\mu_d + \sigma_d)t \\ S_d &\geq S_d(0)e^{-(\mu_d + \sigma_d)t} > 0 \end{aligned} \quad (3.21)$$

We have shown that  $S_d$  is positive  $\forall t \geq 0$ .

Using similar process we have:

$$\begin{aligned} E_d &\geq E_d(0)e^{-(\mu_d + \rho_d)t} > 0, \forall t \geq 0 \\ I_d &\geq I_d(0)e^{-(\mu_d + \delta_d)t} > 0, \forall t \geq 0 \\ V_d &\geq V_d(0)e^{-(\omega_d + \mu_d)t} > 0, \forall t \geq 0 \\ S_s &\geq S_s(0)e^{-(\sigma_s + \mu_s + \mu_c)t} > 0, \forall t \geq 0 \\ E_s &\geq E_s(0)e^{-(\mu_s + \rho_s)t} > 0, \forall t \geq 0 \\ I_s &\geq I_s(0)e^{-(\mu_s + \delta_s)t} > 0, \forall t \geq 0 \\ V_s &\geq V_s(0)e^{-(\omega_s + \mu_s)t} > 0, \forall t \geq 0 \\ S_m &\geq S_m(0)e^{-(\mu_m + \sigma_m)t} > 0, \forall t \geq 0 \\ E_m &\geq E_m(0)e^{-(\mu_m + \rho_m)t} > 0, \forall t \geq 0 \\ I_m &\geq I_m(0)e^{-(\mu_m + \delta_m)t} > 0, \forall t \geq 0 \\ V_m &\geq V_m(0)e^{-(\omega_m + \mu_m)t} > 0, \forall t \geq 0 \end{aligned} \quad (3.22)$$

Therefore, the solution set  $\{S_d(t), E_d(t), I_d(t), V_d(t), S_s(t), E_s(t), I_s(t), V_s(t), S_m(t), E_m(t), I_m(t), V_m(t)\}$  of the model is positive  $\forall t > 0$ .

### 3.5 Model Analysis

#### 3.5.1 Disease Free Equilibrium (DFE) Points

The disease-free equilibrium point is defined as the point at which no disease is present in the population. In the absence of attack or in the absence of rabies,  $E_d = I_d = V_d = E_s = I_s = E_m = I_m = V_m = 0$ . Then, the DFE  $\varepsilon_0$  will be  $\varepsilon_0 = (s_d^0, 0, 0, 0, s_s^0, 0, 0, V_s^0, s_m^0, 0, 0, 0)$

where:

$$\begin{aligned}
S_d^0 &= \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d + \sigma_d} \\
S_s^0 &= \frac{(\mu_s + \omega_s)(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\
V_s^0 &= \frac{\alpha_s(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\
S_m^0 &= \frac{\alpha_m - \psi_{ms} - \psi_{md}}{\mu_m + \sigma_m}
\end{aligned} \tag{3.23}$$

The disease free equilibrium points for stray dogs populations that is  $V_s$  cannot be zero because once susceptible stray dog is vaccinated, it transfers to the vaccinated class. Hence the disease free equilibrium point of the system 3.1 exists and it is given by:

$$\begin{aligned}
\varepsilon_0 = & \left( \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d + \sigma_d}, 0, 0, 0, \frac{(\mu_s + \omega_s)(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)}, 0, 0, \right. \\
& \left. \frac{\alpha_s(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)}, \frac{\alpha_m - \psi_{ms} - \psi_{md}}{\mu_m + \sigma_m}, 0, 0, 0 \right)
\end{aligned} \tag{3.24}$$

### 3.5.2 The Basic Reproduction Number $R_0$

The basic reproduction number  $R_0$  can be defined as the expected number of secondary infections produced by an index case in a completely susceptible population (Van den Driessche & Watmough, 2008). The basic reproduction number can be used to assess whether a newly infectious disease can invade a population (Allen & Van den Driessche, 2008). If  $R_0 < 1$  it implies that, on average one infected individual brings less than one new infected individual into the population during its infectious period and hence, the infection cannot grow. Conversely, if  $R_0 > 1$  it indicates that, on average, each infected individual creates, more than one new infection and the disease can raid the population. It is also important when analysing important parameters which help to understand dynamics of the disease and stability analyses of DFE and endemic equilibrium points. To compute  $R_0$  it is crucial to pinpoint new infections from all other changes in the population. We used the next generation matrix method as proposed by Van den Driessche and Watmough (2008). We considered system 3.1 without vaccination i.e.  $\omega = \sigma = 0$ . In this case we also do not have culling, which means  $\mu_c = 0$ . Let  $f_i(x)$  be the rate of appearance of new infection in compartment  $i$ ,  $v_i^-(x)$  be the rate of transfer of individuals out of compartment  $i$  and  $v_i^+(x)$  be the rate of transfer of individuals into compartment  $i$  by all other means and it is assumed that each function is continuously differentiable at least twice in each variable. The disease transmission model of system 3.1 consists of non-negative initial

conditions together with the following system of equations:

$$\dot{x} = F_i(X) = f_i(x) - v_i(x), i = 1, \dots, 6$$

where  $v_i = v_i^- - v_i^+$

We now consider expressions in which the infection is in progress. These are:

$E_d, I_d, E_s, I_s, E_m, I_m$

$$\begin{aligned} \frac{dE_d}{dt} &= \beta_d S_d I_s - (\mu_d + \rho_d) E_d \\ \frac{dI_d}{dt} &= \rho_d E_d - (\mu_d + \delta_d) I_d \\ \frac{dE_s}{dt} &= \beta_s S_s I_s - (\mu_s + \rho_s) E_s \\ \frac{dI_s}{dt} &= \rho_s E_s - (\mu_s + \delta_s) I_s \\ \frac{dE_m}{dt} &= \beta_m S_m I_s - (\mu_m + \rho_m) E_m \\ \frac{dI_m}{dt} &= \rho_m E_m - (\mu_m + \delta_m) I_m \end{aligned} \tag{3.25}$$

By reorganizing equations of system 3.1 with the absence of vaccination from exposed to infectious class of domestic dog, stray dog and Pastoralist dog populations we have a system 3.25 of equations. Let  $F$  be a non-negative  $n \times n$  matrix and  $V$  be a non-singular N-matrix such that:

$$F = \left[ \frac{\partial f_i(\varepsilon_0)}{\partial x_j} \right]$$

and

$$V = \left[ \frac{\partial v_i(\varepsilon_0)}{\partial x_j} \right]$$

for  $1 \leq i, j \leq n$ . The point  $\varepsilon_0$  is the DFE point in 3.24 with no vaccination where:

$$f_i = \begin{bmatrix} \beta_d S_d I_s \\ 0 \\ \beta_s S_s I_s \\ 0 \\ \beta_m S_m I_s \\ 0 \end{bmatrix}$$

and

$$v_i = \begin{bmatrix} (\mu_d + \rho_d)E_d \\ (\mu_d + \delta_d)I_d - \rho_d E_d \\ (\mu_s + \rho_s)E_s \\ (\mu_s + \delta_s)I_s - \rho_s E_s \\ (\mu_m + \rho_m)E_m \\ (\mu_m + \delta_m)I_m - \rho_m E_m \end{bmatrix}$$

We consider classes in which the disease is in progress. Employing the Linearization approach, we get the Jacobian matrices of  $f$  and  $v$  at the disease free equilibrium point  $\varepsilon_0$  as shown below:

$$F = \begin{bmatrix} 0 & 0 & 0 & \frac{\beta_d(\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds})}{\mu_d} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_s(\alpha_s + \psi_{ds} + \psi_{ms} - \psi_{sd})}{\mu_s} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_m(\alpha_m - \psi_{ms} - \psi_{md})}{\mu_m} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \mu_d + \rho_d & 0 & 0 & 0 & 0 & 0 \\ -\rho_d & \mu_d + \delta_d & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_s + \rho_s & 0 & 0 & 0 \\ 0 & 0 & -\rho_s & \mu_s + \delta_s & 0 & 0 \\ 0 & 0 & 0 & 0 & \mu_m + \rho_m & 0 \\ 0 & 0 & 0 & 0 & -\rho_m & \mu_m + \delta_m \end{bmatrix}$$

Now solving for  $V^{-1}$  we get:

$$V^{-1} = \begin{bmatrix} \frac{1}{\mu_d + \rho_d} & 0 & 0 & 0 & 0 & 0 \\ -\frac{\rho_d}{(\delta_d + \mu_d)(\mu_d + \rho_d)(\mu_s + \rho_s)} & \frac{1}{\delta_d + \mu_d} & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{\mu_s + \rho_s} & 0 & 0 & 0 \\ 0 & 0 & \frac{\rho_s}{(\delta_s + \mu_s)(\mu_s + \rho_s)} & \frac{1}{\delta_s + \mu_s} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\mu_m + \rho_m} & 0 \\ 0 & 0 & 0 & 0 & \frac{\rho_m}{(\delta_m + \mu_m)(\mu_m + \rho_m)} & \frac{1}{\delta_m + \mu_m} \end{bmatrix}$$

We now multiply  $F$  and  $V^{-1}$  and then compute the eigen values of the resulting matrix  $FV^{-1}$  and hence we choose the maximum eigen values as the basic reproduction number.

$$FV^{-1} = \begin{bmatrix} 0 & 0 & \frac{\beta_d \rho_s (\alpha_d - \psi_{ds} + \psi_{md} + \psi_{sd})}{\mu_d (\delta_s + \mu_s) (\mu_s + \rho_s)} & \frac{\beta_d (\alpha_d - \psi_{ds} + \psi_{md} + \psi_{sd})}{\mu_d (\delta_s + \mu_s)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\beta_s \rho_s (\alpha_s + \psi_{ds} + \psi_{ms} - \psi_{sd})}{\mu_s (\delta_s + \mu_s) (\mu_s + \rho_s)} & \frac{\beta_s (\alpha_s + \psi_{ds} + \psi_{ms} - \psi_{sd})}{\mu_s (\delta_s + \mu_s)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{\beta_m \rho_s (\alpha_m - \psi_{md} - \psi_{ms})}{\mu_m (\delta_s + \mu_s) (\mu_s + \rho_s)} & \frac{\beta_m (\alpha_m - \psi_{md} - \psi_{ms})}{\mu_m (\delta_s + \mu_s)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Now the eigen values of matrix  $FV^{-1}$  are:

$$\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ \frac{\beta_s \rho_s (\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_s (\delta_s + \mu_s) (\mu_s + \rho_s)} \end{bmatrix}$$

Now from that we have the basic reproduction number  $R_0$  which is given by:

$$R_0 = \frac{\beta_s \rho_s (\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_s (\delta_s + \mu_s) (\mu_s + \rho_s)} \quad (3.26)$$

From the equation 3.26, we see that all parameters depend on stray dog population. This implies that, putting more effort into the stray dog population combating rabies transmission is very crucial.

### 3.5.3 The Effective Reproduction Number $R_e$

The effective reproduction number is defined as the average number of secondary cases that one index case generates over the course of its infectious period (Cowling *et al.*, 2010). The prevalence of infection increases or decreases according to whether  $R_e$  is greater than or less than one, respectively (Cintr3n-Arias *et al.*, 2009). Here we consider the presence of control methods in our case we have vaccination and culling. In this case  $\omega$ ,  $\mu_c$  and  $\sigma$  will not take on zero values, so we include them and follow the same procedures as we did in computing  $R_0$  and this will result to the following Eigen values of new matrix  $FV^{-1}$  which are:



$$\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ \frac{\beta_s \rho_s (\mu_s + \omega_s) (\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{(\delta_s + \mu_s) (\mu_s + \rho_s) (\mu_c \omega_s + \mu_c \mu_s + \mu_s \sigma_s + \mu_s \omega_s + \mu_s^2)} \end{bmatrix}$$

Therefore; The spectral radius (dominant eigenvalue) of  $FV^{-1}$  denoted by  $R_e = \rho(FV^{-1})$  will be obtained by:

$$R_e = \frac{\beta_s \rho_s (\mu_s + \omega_s) (\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{(\delta_s + \mu_s) (\mu_s + \rho_s) (\mu_c \omega_s + \mu_c \mu_s + \mu_s \sigma_s + \mu_s \omega_s + \mu_s^2)} \quad (3.27)$$

Numerical computations of  $R_0$  and  $R_e$  were done using the data collected from Mbwa wa Africa and the Ministry of Livestock and Fisheries of The United Republic of Tanzania (URT). We now substitute the values of the parameters to the expression found in 3.26 and 3.27.

$$R_0 = \frac{(1.7864 \times 10^{-4}) \times 0.83778234 \times (56 + 35 + 2.5 \times 10^3 - 17)}{0.32 \times (0.22 + 0.32) \times (0.32 + 0.83778234)} \approx 1.9 \quad (3.28)$$

With no any control strategy,  $R_0$  is greater than one which shows that the disease will still invade in the population.

$$R_e = \frac{(1.7864 \times 10^{-4}) \times 0.83778234 \times 0.42(56 + 35 + 2.5 \times 10^3 - 17)}{0.54 \times 1.15778234(0.001792 + 0.0057344 + 0.0805568 + 0.032 + 0.32^2)} \approx 1.2 \quad (3.29)$$

### 3.6 Stability Analysis

#### 3.6.1 Local Stability of the DFE Points

In this sub-section we are going to use the trace and determinant of the Jacobian matrix of system 3.1 at DFE to examine the local stability of the disease free equilibrium points.

#### Theorem 3.3

If  $R_e < 1$ , then:

- (i) The disease-free equilibrium  $\varepsilon_0$  of system 3.1 is locally asymptotically stable; and

(ii) The disease-free equilibrium  $\varepsilon_0$  of system 3.1 is globally asymptotically stable in the region  $\phi$ .

We have the disease free equilibrium point from 3.24 given by:

$$\varepsilon_0 = \left( \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d + \sigma_d}, 0, 0, 0, \frac{(\mu_s + \omega_s)(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)}, 0, 0, \right. \\ \left. \frac{\alpha_s(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)}, \frac{\alpha_m - \psi_{ms} - \psi_{md}}{\mu_m + \sigma_m}, 0, 0, 0 \right) \quad (3.30)$$

Next we derive the Jacobian matrix of the system 3.1 by differentiating every equation in the system 3.1 in terms of state variables  $S_d, E_d, I_d, V_d, S_s, E_s, I_s, V_s, S_m, E_m, I_m, V_m$  to have:

$$J_{\varepsilon_0} = \begin{pmatrix} -(\mu_d + \sigma_d) & 0 & 0 & \omega_d & 0 & 0 & A^* & 0 & 0 & 0 & 0 & 0 \\ 0 & -(\mu_d + \rho_d) & 0 & 0 & 0 & 0 & B^* & 0 & 0 & 0 & 0 & 0 \\ 0 & \rho_d & -(\delta_d + \mu_d) & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \sigma_d & 0 & 0 & -(\mu_d + \omega_d) & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & G & 0 & C^* & \omega_s & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -(\mu_s + \rho_s) & D^* & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \rho_s & -(\delta_s + \mu_s) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma_s & 0 & 0 & -(\mu_s + \omega_s) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & e & 0 & -(\mu_m + \sigma_m) & 0 & 0 & \omega_m \\ 0 & 0 & 0 & 0 & 0 & 0 & F & 0 & 0 & -(\mu_m + \rho_m) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \rho_m & -(\delta_m + \mu_m) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_m & 0 & 0 & -(\mu_m + \omega_m) \end{pmatrix}$$

where:

$$A^* = \frac{-\beta_d(\alpha_d - \psi_{ds} + \psi_{md} + \psi_{sd})}{\mu_d + \sigma_d} \\ B^* = \frac{\beta_d(\alpha_d - \psi_{ds} + \psi_{md} + \psi_{sd})}{\mu_d + \sigma_d} \\ C^* = \frac{-\beta_s(\mu_s + \omega_s)(\alpha_s + \psi_{ds} + \psi_{ms} - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ D^* = \frac{\beta_s(\mu_s + \omega_s)(\alpha_s + \psi_{ds} + \psi_{ms} - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ E = \frac{-\beta_m(\alpha_m - \psi_{ms} - \psi_{md})}{\mu_m + \sigma_m} \\ F = \frac{\beta_m(\alpha_m - \psi_{ms} - \psi_{md})}{\mu_m + \sigma_m} \\ G = -(\mu_c + \mu_s + \sigma_s) \quad (3.31)$$

The eigenvalues of the Jacobian Matrix are:

$$\begin{bmatrix} -\delta_d - \mu_d \\ -\mu_d \\ -\delta_m - \mu_m \\ -\mu_m \\ -\mu_d - \rho_d \\ -\mu_m - \rho_m \\ \frac{1}{2} \left( -\sqrt{4D^*\rho_s + (\delta_s - \rho_s)^2} - \delta_s - 2\mu_s - \rho_s \right) \\ \frac{1}{2} \left( \sqrt{4D^*\rho_s + (\delta_s - \rho_s)^2} - \delta_s - 2\mu_s - \rho_s \right) \\ -\mu_d - \sigma_d - \omega_d \\ -\mu_m - \sigma_m - \omega_m \\ \frac{1}{2} \left( -\mu_c - \sqrt{2\omega_s(\sigma_s - \mu_c) + (\mu_c + \sigma_s)^2 + \omega_s^2} - 2\mu_s - \sigma_s - \omega_s \right) \\ \frac{1}{2} \left( -\mu_c + \sqrt{2\omega_s(\sigma_s - \mu_c) + (\mu_c + \sigma_s)^2 + \omega_s^2} - 2\mu_s - \sigma_s - \omega_s \right) \end{bmatrix}$$

From the above eigenvalues we see that they are all negative but if

$$\sqrt{4D^*\rho_s + (\delta_s - \rho_s)^2} < \delta_s + 2\mu_s + \rho_s \quad (3.32)$$

and

$$\sqrt{2\omega_s(\sigma_s - \mu_c) + (\mu_c + \sigma_s)^2 + \omega_s^2} < \mu_c + 2\mu_s + \sigma_s + \omega_s \quad (3.33)$$

then the Disease Free Equilibrium points are locally asymptotically stable.

### 3.6.2 Global Stability of Disease Free Equilibrium Points

In this case we employ the method suggested by Iggidr *et al.* (2007) to scrutinize the global stability of the DFE points of the system 3.1.

Our model represented in system 3.1 has the following structure.

$$\begin{cases} \frac{dx}{dt} = A_0(x - x_{\varepsilon_0}) + A_3y \\ \frac{dy}{dt} = A_2y \end{cases} \quad (3.34)$$

whereby;  $x \in \mathbb{R}_+$  represents classes of susceptible and vaccinated individuals.  $y \in \mathbb{R}_+^n$  represents classes of exposed and infectious individuals.  $x_{\varepsilon_0}$  represents a vector at DFE point  $\varepsilon_0$  of

the vector length as  $x$ . With reference to the system 3.1 we define:

$$x = \begin{bmatrix} S_d \\ V_d \\ S_s \\ V_s \\ S_m \\ V_m \end{bmatrix}, y = \begin{bmatrix} E_d \\ I_d \\ E_s \\ I_s \\ E_m \\ I_m \end{bmatrix} \text{ and } x_{\varepsilon_0} = \begin{bmatrix} \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d + \sigma_d} \\ 0 \\ \frac{(\mu_s + \omega_s)(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ \frac{\alpha_s(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ \frac{\alpha_m - \psi_{ms} - \psi_{md}}{\mu_m + \sigma_m} \\ 0 \end{bmatrix}$$

$$x - x_{\varepsilon_0} = \begin{bmatrix} S_d - \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d + \sigma_d} \\ V_d \\ S_s - \frac{(\mu_s + \omega_s)(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ V_s - \frac{\alpha_s(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ S_m - \frac{\alpha_m - \psi_{ms} - \psi_{md}}{\mu_m + \sigma_m} \\ V_m \end{bmatrix}$$

To test for global stability of the disease free equilibrium we need to show that:

- (i)  $A_0$  should be a matrix whose eigenvalues are real and negative; and
- (ii)  $A_2$  should be a Metzler matrix.

Using system 3.1 and the representation in 3.34 the two equations can be rewritten as shown below:

$$\begin{aligned}
& \begin{bmatrix} \alpha_d + \omega_d V_d + \psi_{sd} + \psi_{md} - \psi_{ds} - (\mu_d + \sigma_d + \beta_d I_s S_d) \\ \sigma_d S_d - (\omega_d + \mu_d) V_d \\ \alpha_s + \omega_s V_s + \psi_{ds} + \psi_{ms} - \psi_{sd} - (\mu_s + \mu_c + \beta_s I_s) S_s \\ \sigma_s S_s - (\omega_s + \mu_s) V_s \\ \alpha_m + \omega_m V_m - \psi_{ms} - \psi_{md} - (\mu_m + \sigma_m + \beta_m I_s) S_m \\ \sigma_m S_m - (\omega_m + \mu_m) V_m \end{bmatrix} = A_0 \begin{bmatrix} S_d - \frac{\alpha_d + \psi_{sd} + \psi_{md} - \psi_{ds}}{\mu_d + \sigma_d} \\ V_d \\ S_s - \frac{(\mu_s + \omega_s)(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ V_s - \frac{\alpha_s(\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{\mu_c(\mu_s + \omega_s) + \mu_s(\mu_s + \sigma_s + \omega_s)} \\ S_m - \frac{\alpha_m - \psi_{ms} - \psi_{md}}{\mu_m + \sigma_m} \\ V_m \end{bmatrix} \\
& + A_3 \begin{bmatrix} E_d \\ I_d \\ E_s \\ I_s \\ E_m \\ I_m \end{bmatrix}
\end{aligned} \tag{3.35}$$

and

$$\begin{aligned}
& \begin{bmatrix} \beta_d S_d I_s - (\mu_d + \rho_d) E_d \\ \rho_d E_d - (\mu_d + \delta_d) I_d \\ \beta_s S_s I_s - (\mu_s + \rho_s) E_s \\ \rho_s E_s - (\mu_s + \delta_s) I_s \\ \beta_m S_m I_s - (\mu_m + \rho_m) E_m \\ \rho_m E_m - (\mu_m + \delta_m) I_m \end{bmatrix} = A_2 \begin{bmatrix} E_d \\ I_d \\ E_s \\ I_s \\ E_m \\ I_m \end{bmatrix}
\end{aligned} \tag{3.36}$$

Matrices  $A_0$ ,  $A_3$  and  $A_2$  are of order  $6 \times 6$ . Using elements of  $x$  of the Jacobian matrix of system 3.1 at  $\varepsilon_0$  and representation in 16 we get:

$$A_0 = \begin{bmatrix} -(\mu_d + \sigma_d) & \omega_d & 0 & 0 & 0 & 0 \\ \sigma_d & -(\omega_d + \mu_d) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu_s + \mu_c) & \omega_s & 0 & 0 \\ 0 & 0 & \sigma_s & -(\omega_s + \mu_s) & 0 & 0 \\ 0 & 0 & 0 & 0 & -(\mu_m + \sigma_m) & \omega_m \\ 0 & 0 & 0 & 0 & \sigma_m & -(\omega_m + \mu_m) \end{bmatrix}$$

$$A_3 = \begin{bmatrix} 0 & 0 & 0 & \beta_d S_d & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_s S_s & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_m S_m & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$A_2 = \begin{bmatrix} -(\mu_d + \rho_d) & 0 & 0 & \beta_d S_d & 0 & 0 \\ \rho_d & -(\mu_d + \sigma_d) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu_s + \rho_s) & \beta_s S_s & 0 & 0 \\ 0 & 0 & \rho_s & -(\mu_s + \delta_s) & 0 & 0 \\ 0 & 0 & 0 & \beta_m S_m & -(\mu_m + \rho_m) & 0 \\ 0 & 0 & 0 & 0 & 0 & -(\mu_m + \delta_m) \end{bmatrix}$$

Now we have deduced that, matrix  $A_0$  is an upper triangular matrix with eigenvalues being real and negative located in its main diagonal. The eigenvalues are  $-(\mu_d + \rho_d)$ ,  $-(\omega_d + \mu_d)$ ,  $-(\mu_s + \mu_c)$ ,  $-(\omega_s + \mu_s)$ ,  $-(\mu_m + \sigma_m)$  and  $-(\omega_m + \mu_m)$ . The off diagonal elements of matrix  $A_2$  are non-negative since all parameters are positive which proves that it is a Metzler matrix. This also shows that the disease free equilibrium points of system 3.1 is globally asymptotically stable in the region  $\Phi$ . This brings us to the following crucial theorem.

### Theorem 3.4

The disease free equilibrium point is globally asymptotically stable in the region  $\Phi$  if  $R_e < 1$  and unstable in the region  $\Phi$  if  $R_e > 1$ .

## 3.7 Endemic Equilibrium Points

### 3.7.1 Existence of Endemic Equilibrium Points

We equate the right hand side of system 3.1 to zero to be able to compute the equilibrium points of system 3.1. If the endemic equilibrium points of system 3.1 exist, they are given by:

$$\varepsilon_0^* = (S_d^*, E_d^*, I_d^*, V_d^*, S_s^*, E_s^*, I_s^*, V_s^*, S_m^*, E_m^*, I_m^*, V_m^*) \quad (3.37)$$

where:

$$\begin{aligned}
S_d^* &= \frac{\alpha_d + \omega_d V_d^* - \psi_{ds} + \psi_{md} + \psi_{sd}}{\mu_d + \beta_d I_s^* + \sigma_d} \\
E_d^* &= \frac{\beta_d I_s^* S_d^*}{\mu_d + \rho_d} \\
I_d^* &= \frac{\rho_d E_d^*}{\delta_d + \mu_d} \\
V_d^* &= \frac{\sigma_d S_d^*}{\mu_d + \omega_d}
\end{aligned} \tag{3.38}$$

$$\begin{aligned}
S_s^* &= \frac{\alpha_s + \omega_s V_s^* - \psi_{sd} + \psi_{ms} + \psi_{ds}}{\mu_s + \mu_c + \beta_s I_s^* + \sigma_s} \\
E_s^* &= \frac{\beta_s I_s^* S_s^*}{\mu_s + \rho_s} \\
I_s^* &= \frac{\rho_s E_s^*}{\delta_s + \mu_s} \\
V_s^* &= \frac{\sigma_s S_s^*}{\mu_s + \omega_s}
\end{aligned} \tag{3.39}$$

$$\begin{aligned}
S_m^* &= \frac{\alpha_m + \omega_m V_m^* - \psi_{ms} + \psi_{md}}{\mu_m + \beta_m I_s^* + \sigma_m} \\
E_m^* &= \frac{\beta_m I_s^* S_m^*}{\mu_m + \rho_m} \\
I_m^* &= \frac{\rho_m E_m^*}{\delta_m + \mu_m} \\
V_m^* &= \frac{\sigma_m S_m^*}{\mu_m + \omega_m}
\end{aligned} \tag{3.40}$$

### 3.7.2 Local Stability of the Endemic Equilibrium

We employed the following theorem as explained in El-Marhomy & Abdel-Sattar (2004) to explain and prove the local stability of the endemic equilibrium points of system 3.1.

#### Theorem 3.5

(Routh-Hurwitz Criterion)

Given a polynomial  $P(\lambda) = \lambda^n + a_1 \lambda^{n-1} + \dots + a_{n-1} \lambda + a_n$ .

Where the coefficients  $a_i$  are real constants,  $i = 1, \dots, n$  define the  $n$  Hurwitz matrices using the coefficients  $a_i$  of the characteristic polynomial:

$$H_1 = \begin{bmatrix} a_1 \\ a_1 \end{bmatrix}$$

$$H_2 = \begin{bmatrix} a_1 & 1 \\ a_3 & a_2 \end{bmatrix}$$

$$H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{bmatrix}$$

$$H_n = \begin{bmatrix} a_1 & 1 & 0 & 0 & \dots & 0 \\ a_3 & a_2 & a_1 & 1 & \dots & 0 \\ a_5 & a_4 & a_3 & a_2 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \dots & \vdots \\ 0 & 0 & 0 & 0 & \dots & a_n \end{bmatrix}$$

Note that,  $a_{i=0}$  iff  $j > 0$ . All of the roots of the polynomial  $P(\lambda)$  are negative or have negative real part iff the determinants of all Hurwitz matrices are positive:  $\det H_j > 0, j = 0, 1, 2, \dots, n$ . More details on Routh-Hurwitz criterion are given by (Aweya *et al.*, 2004; Gil *et al.*, 2004). Consider the first part of system 3.1. The Jacobian matrix of that part is given by:

$$J_{\lambda_{\varepsilon_0}} = \begin{bmatrix} -(\mu_d + \sigma_d + \beta_d I_s) & 0 & 0 & \omega_d \\ \beta_d I_s & -(\mu_d + \rho_d) & 0 & 0 \\ 0 & \rho_d & -(\mu_d + \delta_d) & 0 \\ 0 & 0 & 0 & -(\omega_d + \mu_d) \end{bmatrix}$$

Through computations, we derive the following characteristic polynomial.

$$P(\lambda) = \lambda^4 + A\lambda^3 + B\lambda^2 + C\lambda + D \quad (3.41)$$



where:

$$\begin{aligned}
A &= \delta_d + 4\mu_d + \rho_d + I_s\beta_d + \sigma_d + \omega_d \\
B &= 3\delta_d\mu_d + \delta_d\rho_d + \delta_d\sigma_d + \delta_d\omega_d + 3\mu_d\rho_d + 3\mu_d\sigma_d + 3\mu_d\omega_d + 6\mu_d^2 + \rho_d\sigma_d + \rho_d\omega_d + I_s\beta_d\delta_d \\
&\quad + 3I_s\beta_d\mu_d + I_s\beta_d\rho_d + I_s\beta_d\omega_d + \sigma_d\omega_d \\
C &= 2\delta_d\mu_d\rho_d + 2\delta_d\mu_d\sigma_d + 2\delta_d\mu_d\omega_d + 3\delta_d\mu_d^2 + \delta_d\rho_d\sigma_d + \delta_d\rho_d\omega_d + \delta_d\sigma_d\omega_d + 2\mu_d\rho_d\sigma_d + 4\mu_d^3 \\
&\quad + 3\mu_d^2\rho_d + 2\mu_d\sigma_d\omega_d + 3\mu_d^2\sigma_d + 3\mu_d^2\omega_d + \rho_d\sigma_d\omega_d + 2\mu_d\rho_d\omega_d + 2I_s\beta_d\delta_d\mu_d + I_s\beta_d\delta_d\rho_d \\
&\quad + I_s\beta_d\delta_d\omega_d + 2I_s\beta_d\mu_d\rho_d + 2I_s\beta_d\mu_d\omega_d + 3I_s\beta_d\mu_d^2 + I_s\beta_d\rho_d\omega_d \\
D &= \delta_d\mu_d\rho_d\sigma_d + \delta_d\mu_d\rho_d\omega_d + \delta_d\mu_d^2\rho_d + \delta_d\mu_d\sigma_d\omega_d + \delta_d\mu_d^2\sigma_d + \delta_d\mu_d^2\omega_d + \delta_d\mu_d^3 + \delta_d\rho_d\sigma_d\omega_d \\
&\quad + \mu_d\rho_d\sigma_d\omega_d + \mu_d^2\rho_d\sigma_d + \mu_d^2\rho_d\omega_d + \mu_d^3\rho_d + \mu_d^2\sigma_d\omega_d + \mu_d^3\sigma_d + \mu_d^3\omega_d + \mu_d^4 + I_s\beta_d\delta_d\mu_d\rho_d \\
&\quad + I_s\beta_d\delta_d\mu_d\omega_d + I_s\beta_d\delta_d\mu_d^2 + I_s\beta_d\delta_d\rho_d\omega_d + I_s\beta_d\mu_d\rho_d\omega_d + I_s\beta_d\mu_d^2\rho_d + I_s\beta_d\mu_d^2\omega_d + I_s\beta_d\mu_d^3
\end{aligned} \tag{3.42}$$

From the characteristic polynomial represented in 3.41 we have the following Hurwitz matrix

$$H_4 = \begin{bmatrix} A & 1 & 0 & 0 \\ C & B & A & 1 \\ 0 & D & C & B \\ 0 & 0 & 0 & D \end{bmatrix}$$

The determinant of the Hurwitz matrix is  $D(ABC - C^2 - A^2D)$ . From the Routh-Hurwitz criteria of Theorem 3.5, we see that the determinant of Hurwitz matrix will be positive if the following conditions hold true.  $A > 0, C > 0, D > 0$  and  $ABC > C^2 + A^2D$ . Recall that all parameters of our model are positive. Also recall that all coefficients of the characteristic polynomial are positive as shown in equation 3.24. Now combining all requirements, we deduce that all roots of the polynomial represented in 3.41 are negative and hence we prove that the first part of system 3.1 is locally asymptotically stable.

Moreover, we consider the second part of system 3.1. The Jacobian matrix is given by:

$$J_{\lambda_{\varepsilon_0}} = \begin{bmatrix} -(\sigma_s + \mu_s + \mu_c + \beta_s I_s) & 0 & -\beta_s S_s & \omega_s \\ \beta_s I_s & -(\mu_s + \rho_s) & \beta_s S_s & 0 \\ 0 & \rho_s & -(\mu_s + \delta_s) & 0 \\ \sigma_s & 0 & 0 & -(\omega_s + \mu_s) \end{bmatrix}$$

Consider the characteristic polynomial

$$P(\lambda) = \lambda^4 + A_1\lambda^3 + B_1\lambda^2 + C_1\lambda + D_1 \tag{3.43}$$

where:

$$\begin{aligned}
A_1 &= \mu_c + I_s \beta_s + \delta_s + 4\mu_s + \rho_s + \sigma_s + \omega_s \\
B_1 &= \mu_c \delta_s + \mu_c \rho_s + \mu_c \omega_s + 3\mu_c \mu_s + I_s \beta_s \delta_s + 3I_s \beta_s \mu_s + I_s \beta_s \rho_s + I_s \beta_s \omega_s + 3\delta_s \mu_s + \delta_s \rho_s \\
&\quad + \delta_s \sigma_s + \delta_s \omega_s + 3\mu_s \rho_s + 3\mu_s \sigma_s + 3\mu_s \omega_s + 6\mu_s^2 + \rho_s \sigma_s + \rho_s \omega_s - \beta_s \rho_s S_s \\
C_1 &= \mu_c \delta_s \rho_s + \mu_c \delta_s \omega_s + 2\mu_c \delta_s \mu_s + \mu_c \rho_s \omega_s + 2\mu_c \mu_s \rho_s + 2\mu_c \mu_s \omega_s + 3\mu_c \mu_s^2 - \mu_c \beta_s \rho_s S_s \\
&\quad + 2I_s \beta_s \delta_s \mu_s + I_s \beta_s \delta_s \rho_s + I_s \beta_s \delta_s \omega_s + 2I_s \beta_s \mu_s \rho_s + 2I_s \beta_s \mu_s \omega_s + 3I_s \beta_s \mu_s^2 + I_s \beta_s \rho_s \omega_s \\
&\quad + 2\delta_s \mu_s \rho_s + 2\delta_s \mu_s \sigma_s + 2\delta_s \mu_s \omega_s + 3\delta_s \mu_s^2 + \delta_s \rho_s \sigma_s + \delta_s \rho_s \omega_s + 2\mu_s \rho_s \sigma_s + 2\mu_s \rho_s \omega_s \\
&\quad + 3\mu_s^2 \rho_s + 3\mu_s^2 \sigma_s + 3\mu_s^2 \omega_s + 4\mu_s^3 - 2\beta_s \mu_s \rho_s S_s - \beta_s \rho_s \sigma_s S_s - \beta_s \rho_s S_s \omega_s \\
D_1 &= \mu_c \delta_s \rho_s \omega_s + \mu_c \delta_s \mu_s \rho_s + \mu_c \delta_s \mu_s \omega_s + \mu_c \delta_s \mu_s^2 + \mu_c \mu_s \rho_s \omega_s + \mu_c \mu_s^2 \rho_s + \mu_c \mu_s^2 \omega_s + \mu_c \mu_s^3 \\
&\quad - \mu_c \beta_s \rho_s S_s \omega_s - \mu_c \beta_s \mu_s \rho_s S_s + I_s \beta_s \delta_s \mu_s \rho_s + I_s \beta_s \delta_s \mu_s \omega_s + I_s \beta_s \delta_s \mu_s^2 + I_s \beta_s \delta_s \rho_s \omega_s + \\
&\quad I_s \beta_s \mu_s \rho_s \omega_s + I_s \beta_s \mu_s^2 \rho_s + I_s \beta_s \mu_s^2 \omega_s + I_s \beta_s \mu_s^3 + \delta_s \mu_s \rho_s \sigma_s + \delta_s \mu_s \rho_s \omega_s + \delta_s \mu_s^2 \rho_s + \delta_s \mu_s^2 \sigma_s \\
&\quad + \delta_s \mu_s^2 \omega_s + \delta_s \mu_s^3 + \mu_s^2 \rho_s \sigma_s + \mu_s^2 \rho_s \omega_s + \mu_s^3 \rho_s + \mu_s^3 \sigma_s + \mu_s^3 \omega_s + \mu_s^4 - \beta_s \mu_s \rho_s \sigma_s S_s - \beta_s \mu_s^2 \rho_s S_s \\
&\quad - \beta_s \mu_s \rho_s S_s \omega_s
\end{aligned} \tag{3.44}$$

From the characteristic polynomial represented by 3.25 we have the Hurwitz matrix being given by:

$$H_5 = \begin{bmatrix} A_1 & 1 & 0 & 0 \\ C_1 & B_1 & A_1 & 1 \\ 0 & D_1 & C_1 & B_1 \\ 0 & 0 & 0 & D_1 \end{bmatrix}$$

It comes behind that the determinant of the Hurwitz matrix given by  $D_1(A_1 B_1 C_1 - C_1^2 - A_1^2 D_1)$ . With reference to Theorem 3.5 the determinant of Hurwitz matrix become positive iff  $A_1 > 0, C_1 > 0, D_1 > 0$  and  $A_1 B_1 C_1 > C_1^2 + A_1^2 D_1$ . Again since  $A_1 > 0$ ,

$$B_1 > 0 \text{ iff } \mu_c \delta_s + \mu_c \rho_s + \mu_c \omega_s + 3\mu_c \mu_s + I_s \beta_s \delta_s + 3I_s \beta_s \mu_s + I_s \beta_s \rho_s + I_s \beta_s \omega_s + 3\delta_s \mu_s + \delta_s \rho_s + \delta_s \sigma_s + \delta_s \omega_s + 3\mu_s \rho_s + 3\mu_s \sigma_s + 3\mu_s \omega_s + 6\mu_s^2 + \rho_s \sigma_s + \rho_s \omega_s > \beta_s \rho_s S_s,$$

$$\begin{aligned}
C_1 > 0 \text{ iff } &\mu_c \delta_s \rho_s + \mu_c \delta_s \omega_s + 2\mu_c \delta_s \mu_s + \mu_c \rho_s \omega_s + 2\mu_c \mu_s \rho_s + 2\mu_c \mu_s \omega_s + 3\mu_c \mu_s^2 + 2I_s \beta_s \delta_s \mu_s + \\
&I_s \beta_s \delta_s \rho_s + I_s \beta_s \delta_s \omega_s + 2I_s \beta_s \mu_s \rho_s + 2I_s \beta_s \mu_s \omega_s + 3I_s \beta_s \mu_s^2 + I_s \beta_s \rho_s \omega_s + 2\delta_s \mu_s \rho_s + 2\delta_s \mu_s \sigma_s + \\
&2\delta_s \mu_s \omega_s + 3\delta_s \mu_s^2 + \delta_s \rho_s \sigma_s + \delta_s \rho_s \omega_s + 2\mu_s \rho_s \sigma_s + 2\mu_s \rho_s \omega_s + 3\mu_s^2 \rho_s + 3\mu_s^2 \sigma_s + 3\mu_s^2 \omega_s + 4\mu_s^3 > \\
&2\beta_s \mu_s \rho_s S_s + \beta_s \rho_s \sigma_s S_s + \beta_s \rho_s S_s \omega_s + \mu_c \beta_s \rho_s S_s,
\end{aligned}$$

$$\begin{aligned}
D_1 > 0 \text{ iff } & \mu_c \delta_s \rho_s \omega_s + \mu_c \delta_s \mu_s \rho_s + \mu_c \delta_s \mu_s \omega_s + \mu_c \delta_s \mu_s^2 + \mu_c \mu_s \rho_s \omega_s + \mu_c \mu_s^2 \rho_s + \mu_c \mu_s^2 \omega_s + \mu_c \mu_s^3 + \\
& I_s \beta_s \delta_s \mu_s \rho_s + I_s \beta_s \delta_s \mu_s \omega_s + I_s \beta_s \delta_s \mu_s^2 + I_s \beta_s \delta_s \rho_s \omega_s + I_s \beta_s \mu_s \rho_s \omega_s + I_s \beta_s \mu_s^2 \rho_s + I_s \beta_s \mu_s^2 \omega_s + \\
& I_s \beta_s \mu_s^3 + \delta_s \mu_s \rho_s \sigma_s + \delta_s \mu_s \rho_s \omega_s + \delta_s \mu_s^2 \rho_s + \delta_s \mu_s^2 \sigma_s + \delta_s \mu_s^2 \omega_s + \delta_s \mu_s^3 + \mu_s^2 \rho_s \sigma_s + \mu_s^2 \rho_s \omega_s + \mu_s^3 \rho_s + \\
& \mu_s^3 \sigma_s + \mu_s^3 \omega_s + \mu_s^4 > \beta_s \mu_s \rho_s \sigma_s S_s + \beta_s \mu_s \rho_s S_s \omega_s + \beta_s \mu_s^2 \rho_s S_s + \mu_c \beta_s \rho_s S_s \omega_s + \mu_c \beta_s \mu_s \rho_s S_s
\end{aligned}$$

When all conditions hold, similarly  $A_1 B_1 C_1 > C_1^2 + A_1^2 D_1$  holds. Hence we can conclude that all roots of polynomial 3.25 are negative. This verifies that the second part of system 3.1 is locally asymptotically stable.

Using the same procedure for the third part of system 3.1, will result in the same conclusion. Therefore, we can generally conclude that the endemic equilibrium point of system 3.1 is locally asymptotically stable.

### 3.8 Sensitivity Analysis

Sensitivity analysis helps to determine the most sensitive parameters to the model. It tells us how important each parameter is to disease transmission and is used to assess how sensitive a model is to variation in the value of the parameters of the model and to changes in the structure of the model (Peter *et al.*, 2018). This further helps to decide on which parameters to put more effort on combating disease transmission. Now, since we want to understand the dynamics of rabies in Arusha region and therefore control it by targeting the most sensitive parameters, sensitivity analysis will help us by playing a role to determine those parameters. Parameter values used in DFE are as in Table 2.

**Table 2: Values of Parameters Used at DFE**

Parameter	Description	Value ( $year^{-1}$ )	Source
$\alpha_s$	The annual births of stray dogs	$2.5 \times 10^3$	Totton <i>et al.</i> (2010)
$\delta_s$	Death rate due rabies for stray dogs	0.22	Amaku <i>et al.</i> (2010)
$\omega_s$	Loss rate of vaccination immunity for stray dogs	0.1	Assumption
$\mu_s$	Natural death rate of stray dogs	0.32	Paul <i>et al.</i> (2016)
$\beta_s$	Rate of infection of stray dogs	$1.7864 \times 10^{-4}$	Data
$\rho_s$	The incubation period of stray dogs	0.837 782 34	Leung & Davis (2017)
$\sigma_s$	Vaccination rate of the susceptible stray dogs	0.251 74	Data
$\psi_{ms}$	Average number of Pastoralist dogs that migrate to stray dog population	35	Fitting
$\psi_{sd}$	Average number of stray dogs that migrate to domestic dog population	17	Fitting
$\psi_{ds}$	Average number of domestic dogs that migrate to stray dog population	56	Fitting
$\mu_c$	Average culling rate of stray dogs	0.017 92	Data

### 3.8.1 Sensitivity Analysis of $R_e$

Sensitivity analysis tells us how important each parameter is to disease transmission and is used to assess how sensitive a model is to variation in the value of the parameters of the model and to changes in the structure of the model (Peter *et al.*, 2018). In this case, the normalised forward sensitivity index was employed by using the MATHEMATICA program.

The normalised forward sensitivity index is the ratio of relative change of a variable to the relative change in parameter. If the variable is a differentiable function of the parameter then the sensitivity index is defined as follows:

**Definition 3.1:** The normalised forward sensitivity index of variable  $V$  that depends on parameter  $\rho$  is defined as:

$$S_\rho^V = \frac{\partial V}{\partial \rho} \times \frac{\rho}{V} \quad (3.45)$$

For example in our case, we have the effective reproduction number  $R_e$  computed. The norm-

alised forward sensitivity with respect to the parameter  $\rho$  is given by:

$$S_{\rho}^{R_e} = \frac{\partial R_e}{\partial \rho} \times \frac{\rho}{R_e} \quad (3.46)$$

For instance, the sensitivity index of  $R_e$  with respect to parameter  $\beta_s$  is given by:

$$S_{\beta_s}^{R_e} = \frac{\partial R_e}{\partial \beta_s} \times \frac{\beta_s}{R_e} = +1 \quad (3.47)$$

By using the same idea, the sensitivity indices of  $R_e$  given by the expression below:

$$R_e = \frac{\beta_s \rho_s (\mu_s + \omega_s) (\psi_{ds} + \psi_{ms} + \alpha_s - \psi_{sd})}{(\delta_s + \mu_s) (\mu_s + \rho_s) (\mu_c \omega_s + \mu_c \mu_s + \mu_s \sigma_s + \mu_s \omega_s + \mu_s^2)} \quad (3.48)$$

Is calculated w.r.t all parameters fixed to  $R_e$  and are as shown in the Table 3.

**Table 3: Sensitivity Indices of  $R_e$**

Parameter	Value
$\alpha_s$	+0.9713
$\delta_s$	-0.4074
$\omega_s$	+0.0866
$\mu_s$	-1.5593
$\beta_s$	+1
$\rho_s$	+0.2764
$\sigma_s$	-0.3621
$\psi_{ms}$	+0.0136
$\psi_{sd}$	$-6.6045 \times 10^{-3}$
$\psi_{ds}$	+0.0218
$\mu_c$	-0.0338

According to the sensitivity indices, infection rate of stray dogs  $\beta_s$  is the most positive sensitive parameter followed by the annual births of stray dogs  $\alpha_s$  and the incubation period of stray dogs  $\rho_s$ . This means, increasing these parameters, will result to increase in the effective reproduction number  $R_e$ . For example, increasing  $\beta_s$  by 10% will result to increase in  $R_e$  by 10% also decreasing  $\beta_s$  by 10% will result to decrease in  $R_e$  by 10%. Average number of Pastoralist dogs that migrate to a stray dog population  $\psi_{ms}$ , loss rate of vaccination immunity of stray dogs  $\omega_s$  and average number of domestic dogs that migrate to a stray dog population  $\psi_{ds}$  are the less positively sensitive parameters.

Also, natural death rate of stray dogs  $\mu_s$  is the most negative sensitive parameter followed by death rate for stray dogs due to rabies  $\delta_s$  and vaccination rate of the susceptible stray dogs  $\sigma_s$ . This implies that increase in this parameter will result to decrease in the effective reproduction number  $R_e$ . For instance, increase in natural death rate  $\mu_s$  by 10% results to decrease in  $R_e$  by approximately 16%. Average number of stray dogs that migrate to domestic dog population  $\psi_{sd}$  and average culling rate of stray dogs  $\mu_c$  are the less negatively sensitive parameters.

We can deduce that, putting much emphasis on the most positive and most negative sensitive parameter will be the most effective way in combating dog-rabies transmission in the Arusha region.

## CHAPTER FOUR

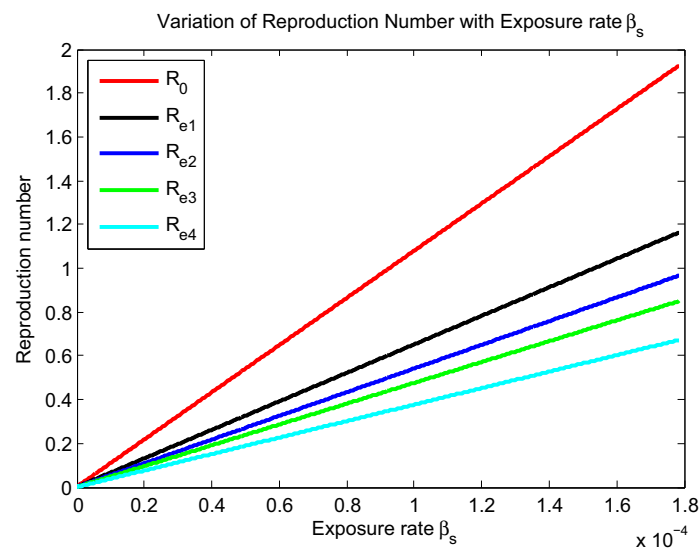
### RESULTS AND DISCUSSION

#### 4.1 Introduction

In this chapter, results of several numerical simulations and the interpretations of both our basic model and the modified model are presented. The ode45 MATLAB's ordinary differential equations (ODEs) standard solver was used. In this function a Runge-Kutta method with a variable time step for efficient computation is implemented. The 2013 to 2018 reported data from the Ministry of Livestock and Fisheries of the URT and also survey data from Mbwa wa Africa were used. Information on the number of dogs that migrate from one population to another was missing so the parameters were obtained through data fitting.

#### 4.2 Numerical Analysis of the Basic Model

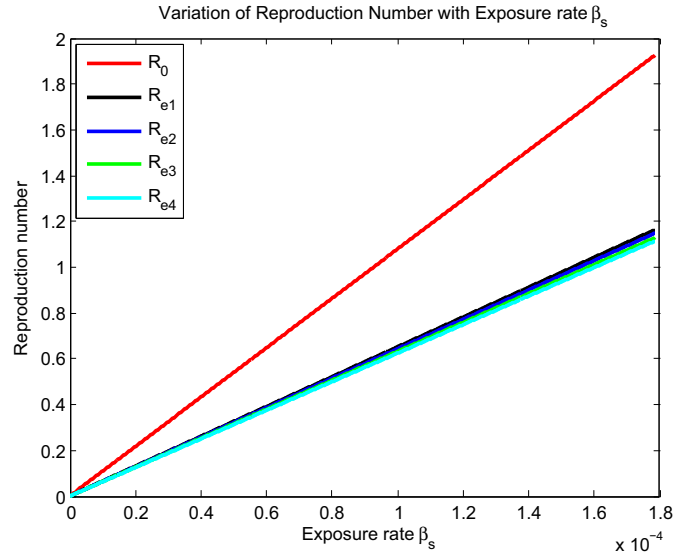
This sections presents and interpret the numerical results of the basic model. By starting we consider Fig. 2.



**Figure 2: Reproduction Numbers for Various Coverages in Vaccination and Combination of Vaccination and Culling**

From Fig. 2 we can see that,  $R_{e4} < R_{e3} < R_{e2} < R_{e1} < R_0$ . This indicates that if we increase vaccination of the stray dogs, the effective reproduction number will decrease to less

than one. Due to the high rabies transmission rate from stray dogs to domestic dogs and Pastor-  
alist dogs, increasing vaccination to stray dogs is highly recommended as it leads to a less than  
one effective reproduction number.



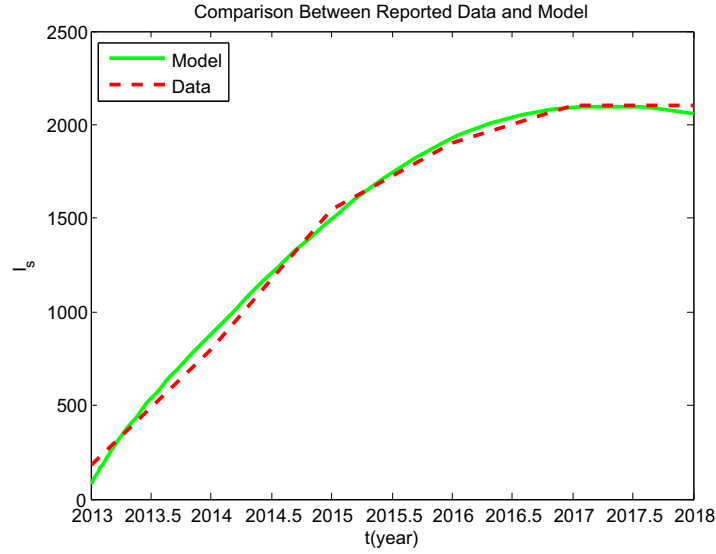
**Figure 3: Reproduction Numbers for Different Culling Coverages with the Current Vaccination Coverage Being Constant**

From Fig. 3 we see that culling alone has got a very minute impact in combating rabies transmission risk. The effect observed is for the current 25% vaccination coverage only. This study insists on using vaccination of stray dogs to control rabies transmission since culling is less advantageous due to the fact that it has a very small contribution in combating rabies transmission while it is very costly.

In the simulation results of Fig. 2,  $R_0$  is without any control,  $R_{e1}$  is the current 25% vaccination coverage,  $R_{e2}$  is the 40% vaccination coverage and  $R_{e3}$  is the 50% vaccination coverage and  $R_{e4}$  combination of 60% vaccination coverage and 40% culling.

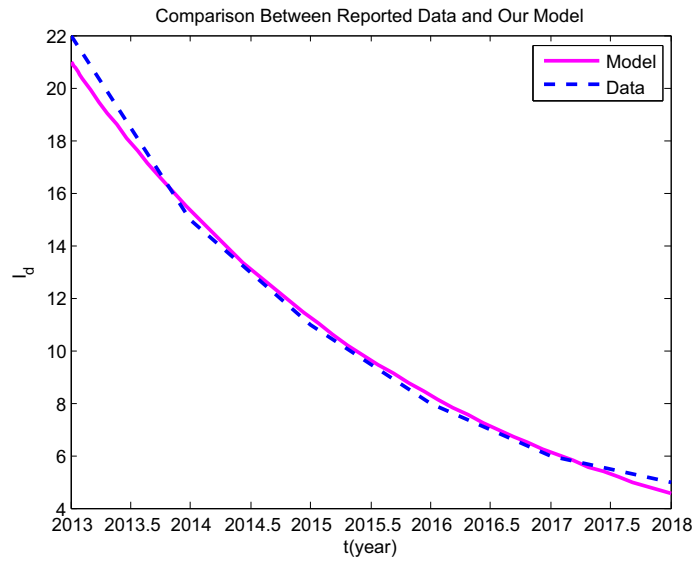
In Fig. 3,  $R_0$  is without control,  $R_{e1}$  is a combination of 25% vaccination coverage and 40% culling,  $R_{e2}$  is the 50% culling,  $R_{e3}$  is the 60% culling and  $R_{e4}$  is the 75% culling.





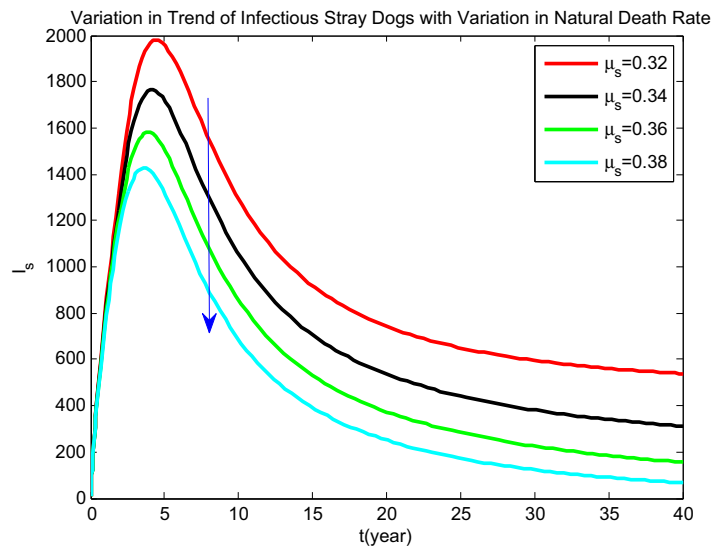
**Figure 4: Comparison Between the Reported Data and Simulation of System 3.1 for Rabies Infected Stray Dogs in the Arusha Region From 2013 to 2018**

In Fig. 4, we fit the data on infectious stray dogs to the model from the year 2013 to 2018. We compare the reported data and the simulation of our model system of differential equations. The dashed red line is for the data and the full green line is the simulation of our model system. We see that there is a good match between the reported data and our model. Also, our model predicts that, the number of infectious stray dogs will increase but later on the number will stabilize because the basic reproduction number of 1.9 for rabies will determine the maximum number of infectious stray dogs in the population. The initial conditions of the variables were obtained through the reported data from the Ministry of Livestock and Fisheries of the URT and Mbwa wa Africa, logical assumptions and data fitting. Thus,  $S_d(0) = 14063$ ,  $E_d(0) = 83$ ,  $I_d(0) = 21$ ,  $V_d(0) = 7276$ ,  $S_s(0) = 20000$ ,  $E_s(0) = 1500$ ,  $I_s(0) = 75$ ,  $V_s(0) = 0$ ,  $S_m(0) = 2500$ ,  $E_m(0) = 90$ ,  $I_m(0) = 15$ ,  $V_m(0) = 1500$ .



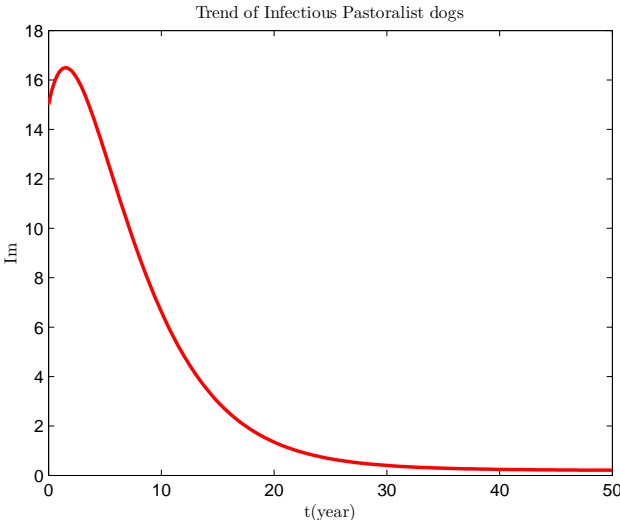
**Figure 5: Comparison Between Reported Data and Simulation of System 3.1 for Rabies Infected Domestic Dogs in Arusha Region From 2013 to 2018**

Using the same initial conditions, we fitted the data for rabies infected domestic dogs from the year 2013 to 2018 into the model. From Fig. 5 we see that the number of rabies infected domestic dogs is decreasing. This is because the infected dogs die and the increase in vaccination rate protects the remaining dogs. The full magenta line indicates our model and the dotted blue line stands for the data. We also observe that there is an outstanding resemblance between the reported data and our model.



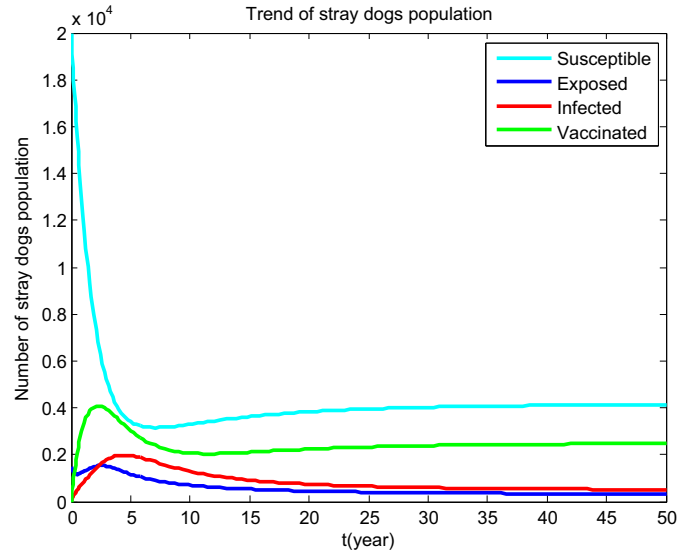
**Figure 6: The Effect of Natural Death Rate of Stray Dogs on Stray Dog Rabies Infection for the Next 40 Years**

From the sensitivity analysis we found that, natural death rate is the most sensitive parameter for controlling the dynamics of dog rabies transmission and dynamics. Figure 6 shows how a minor increase in the natural death rate of stray dogs results in a decrease in the number of infectious stray dogs. This means increasing the natural death rate by vaccinating more dogs than are born every year will reduce the number of infected dogs. However, this would be very costly.



**Figure 7: Trend of Infected Pastoralist Dogs for a Period of 50 Years**

From Fig. 7, we see that the population of infectious Pastoralist dogs will increase rapidly and it will reach the peak in 2020. The increase is because exposed Pastoralist dogs will move to the infectious group once they develop symptoms of rabies and hence it will result in an increase in the infectious group. Assuming that no new infections will enter the population from outside, the number of infected Pastoralist dogs will naturally decline since infection will die out when the population get vaccinated.



**Figure 8: Trend of Stray Dog Population for a Period of 50 Years**

From the Fig. 8 we see that the group of susceptible stray dogs will decline because once a susceptible dog is attacked and scratched or bitten, it become exposed. This results in an increase in the exposed stray dog class. The number of dogs in the susceptible group stabilizes because vaccination rate is assumed to stay constant. Before exposed stray dogs develop symptoms, if they are vaccinated, they also shift to the vaccinated group but if not, they become infectious and later on die. Therefore the number of infected dogs will now stabilize, due to  $R_0$ . In the first five years, the number of dogs in the vaccinated group increases as the vaccination rate increases. After that the vaccinated group will stabilize because of a now constant vaccination rate.

### 4.3 Analysing the Model with Impacts of Migration Being Treated as Functions

In the previous section we have seen the analysis results of the basic model with the impacts of migration being treated as scalar. In this section we have modified our model a little bit and analysed it with the impacts of migration being treated as function of some parameters. Below is the modification of the model and definition of some new parameters slotted into the model.

$$\begin{aligned}
\frac{dS_d}{dt} &= \alpha_d + \omega_d V_d + \theta_{sd} S_s + \theta_{md} S_m - \mu_d S_d - \sigma_d S_d - \theta_{ds} S_d - \beta_d S_d I_s \\
\frac{dE_d}{dt} &= \beta_d S_d I_s - \mu_d E_d - \rho_d E_d \\
\frac{dI_d}{dt} &= \rho_d E_d - (\mu_d + \delta_d) I_d \\
\frac{dV_d}{dt} &= \sigma_d S_d - \omega_d V_d - \mu_d V_d \\
\\
\frac{dS_s}{dt} &= \alpha_s + \omega_s V_s + \theta_{ds} S_d + \theta_{ms} S_m - \sigma_s S_s - (\mu_s + \mu_c) S_s - \theta_{sd} S_s - \beta_s S_s I_s \\
\frac{dE_s}{dt} &= \beta_s S_s I_s - \mu_s E_s - \rho_s E_s \\
\frac{dI_s}{dt} &= \rho_s E_s - (\mu_s + \delta_s) I_s \\
\frac{dV_s}{dt} &= \sigma_s S_s - \omega_s V_s - \mu_s V_s
\end{aligned} \tag{4.1}$$

$$\begin{aligned}
\frac{dS_m}{dt} &= \alpha_m + \omega_m V_m - \mu_m S_m - \theta_{ms} S_m - \theta_{md} S_m - \sigma_m S_m - \beta_m S_m I_s \\
\frac{dE_m}{dt} &= \beta_m S_m I_s - \mu_m E_m - \rho_m E_m \\
\frac{dI_m}{dt} &= \rho_m E_m - (\mu_m + \delta_m) I_m \\
\frac{dV_m}{dt} &= \sigma_m S_m - \omega_m V_m - \mu_m V_m
\end{aligned}$$

Whereby:

$\theta_{ds}$  →Rate of domestic dogs' migration to stray dog population.

$\theta_{sd}$  →Rate of stray dogs' migration to domestic dog population.

$\theta_{ms}$  →Rate of Pastoralist dogs' migration to stray dog population.

$\theta_{md}$  →Rate of Pastoralist dogs' migration to domestic dog population.

We define our  $\theta$ 's as shown in the Sub-section 4.3.1 below.

### 4.3.1 Analysing the Model After Inclusion of Mass Culling of Stray Dogs and Numerical Simulations Over a One Year Period

Based on the modified model, we want to analyse and get to know what happens if almost all stray dogs are culled. In this case we are going to consider the following logical conditions that;

$\theta_{md} S_m$  is constant  $\epsilon$  (it has nothing to do with stray dog population)

$\theta_{sd} \approx 0$  since we shall no longer have stray dogs so we do not expect any migrations from stray dogs population.

We define:

$$\theta_{ds} = \tau_d \left(1 - \frac{S_s + V_s}{M_s}\right)$$

$$\theta_{ms} = \tau_m \left(1 - \frac{S_s + V_s}{M_s}\right)$$

Where  $\tau_d$  is the percentage of domestic dogs that migrate to stray dog population.

$\tau_m$  is the percentage of Pastoralist dogs that migrate to stray dog population.

$M_s$  is the maximum possible number of stray dogs in the population.

From the definitions and the conditions above, we have our model as shown below.

$$\frac{dS_d}{dt} = \alpha_d + \omega_d V_d + \epsilon - \mu_d S_d - \sigma_d S_d - \tau_d \left(1 - \frac{S_s + V_s}{M_s}\right) S_d - \beta_d S_d I_s$$

$$\frac{dE_d}{dt} = \beta_d S_d I_s - \mu_d E_d - \rho_d E_d$$

$$\frac{dI_d}{dt} = \rho_d E_d - (\mu_d + \delta_d) I_d$$

$$\frac{dV_d}{dt} = \sigma_d S_d - \omega_d V_d - \mu_d V_d$$

$$\frac{dS_s}{dt} = \alpha_s + \omega_s V_s + \tau_d \left(1 - \frac{S_s + V_s}{M_s}\right) S_d + \tau_m \left(1 - \frac{S_s + V_s}{M_s}\right) S_m - \sigma_s S_s - (\mu_s + \mu_c) S_s - \beta_s S_s I_s$$

$$\frac{dE_s}{dt} = \beta_s S_s I_s - \mu_s E_s - \rho_s E_s$$

$$\frac{dI_s}{dt} = \rho_s E_s - (\mu_s + \delta_s) I_s$$

$$\frac{dV_s}{dt} = \sigma_s S_s - \omega_s V_s - \mu_s V_s$$

$$\frac{dS_m}{dt} = \alpha_m + \omega_m V_m - \mu_m S_m - \tau_m \left(1 - \frac{S_s + V_s}{M_s}\right) S_m - \epsilon - \sigma_m S_m - \beta_m S_m I_s$$

$$\frac{dE_m}{dt} = \beta_m S_m I_s - \mu_m E_m - \rho_m E_m$$

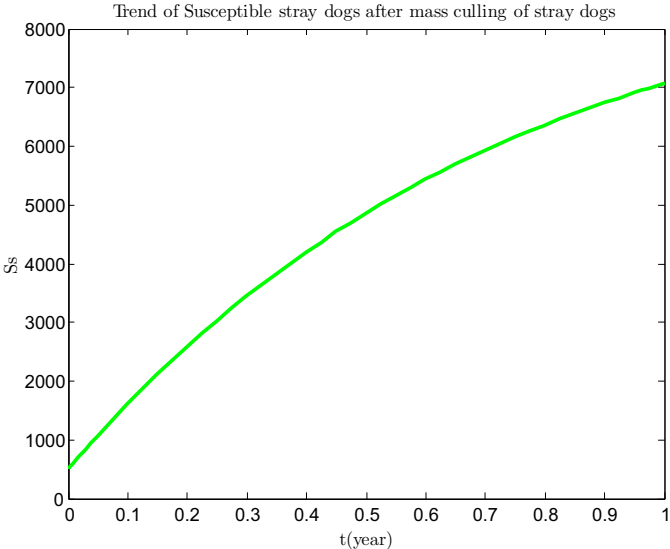
$$\frac{dI_m}{dt} = \rho_m E_m - (\mu_m + \delta_m) I_m$$

$$\frac{dV_m}{dt} = \sigma_m S_m - \omega_m V_m - \mu_m V_m$$

(4.2)

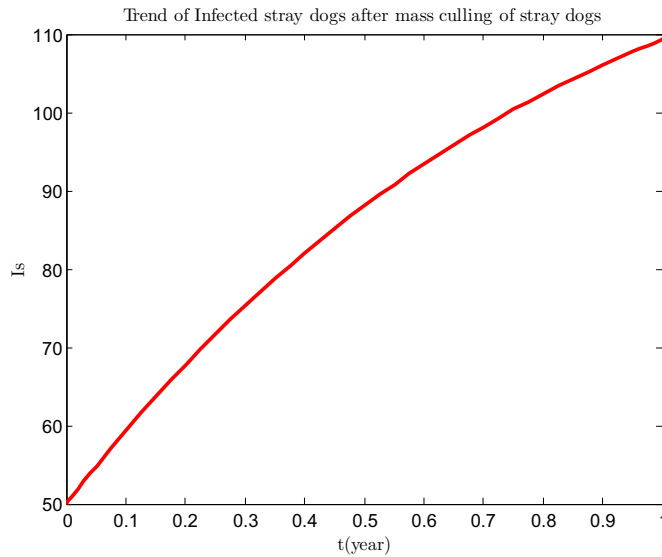
In the Fig. 9, one can notice that, the number of susceptible stray dogs will increase from the beginning of 2019 and reach its maximum at the end of the year. This is because after mass

culling there will be very few susceptible stray dogs left, something which will influence migration of dogs from domestic dog and Pastoralist dog sub-populations to the stray dog population and hence the number of susceptible stray dogs will grow.



**Figure 9: Trend of Susceptible Stray Dogs After Mass Culling of Stray Dogs**

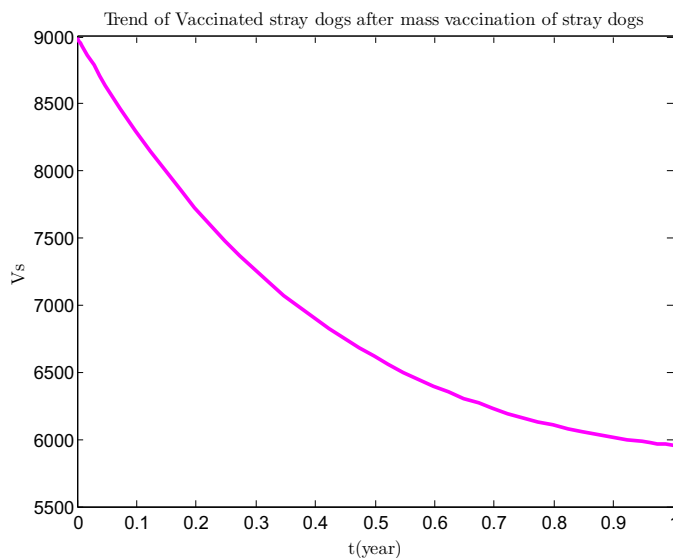
Based on the recorded data from laboratory brain tests of exposed stray dogs, up to the end of the year 2018, there were around 50 infectious stray dogs. Now, as per analysis, results show that if we cull almost all stray dogs the number of infectious stray dogs will actually increase. These results are also supported by literature, indicating that every culled stray dog will get replaced by an un-vaccinated newborn puppy after 6 to 8 months (Cleaveland, 1998). This is depicted in the Fig. 10.



**Figure 10: Trend of Infectious Stray Dogs After Mass Culling of Stray Dogs**

### 4.3.2 Analysing the Model After Mass Vaccination of Stray Dogs and Numerical Simulations Over a One Year Period

In this section, we have analyzed model system 4.1 by considering a case where mass vaccination of more than 75% of stray dogs is conducted. In addition to this case  $\theta_{sd} \approx 0$  since it is rare for people to adopt stray dogs hence we have taken the rate of migration from stray dogs to domestic dogs to be minimum close to zero.

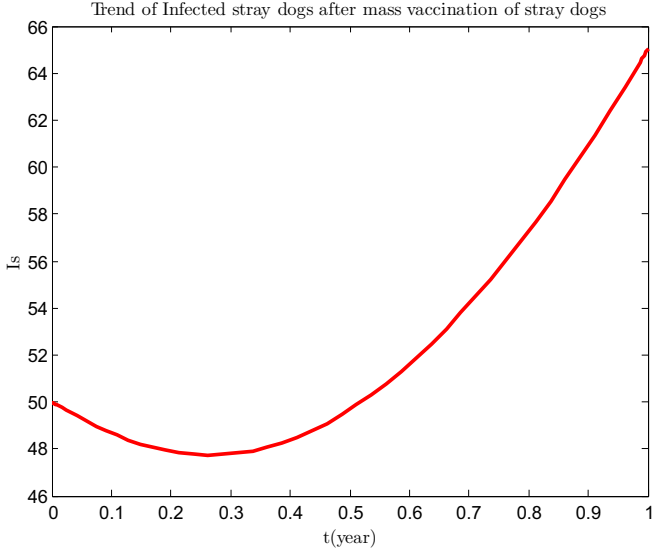


**Figure 11: Trend of Vaccinated Stray Dogs After Mass Vaccination of Stray Dogs**

Based on the reported data, up to the end of 2018, there were around 9000 vaccinated stray dogs.



From the Fig. 11 we can see that this number gradually decreases to around 6000 by 2020 as more un-vaccinated puppies are born and immunity of vaccinated dogs is lost. According to simulation results vaccinated stray dogs will shift to susceptible hence the number of stray dogs in the vaccinated class will decrease.



**Figure 12: Trend of Infectious Stray Dogs After Mass Vaccination of Stray Dogs**

Based on the results of model analysis, after mass vaccination of stray dogs, the number of infectious stray dogs will decrease in the first four months as shown in the Fig. 12. Yet, after the first four months of the year, the number will increase again, since some of exposed stray dogs will become infected and shift to the infectious class.

## CHAPTER FIVE

### CONCLUSIONS AND RECOMMENDATIONS

#### 5.1 Conclusions

After modeling, we conclude that the risk of transmission to humans is best controlled by mass vaccination of dogs in the long term, particularly by vaccinating the stray dog population. The results in this study are in line with existing literature reporting that immunity against rabies is present up to 3 years and longer after vaccination (Lakshmanan *et al.*, 2006). However, results also suggest that culling seems the best method to reduce transmission risk in the short term. While applying dog mass vaccination of stray dogs will help to control transmission over time, culling will help at the moment in time it is practiced, but after 6 to 8 months all culled dogs will get replaced by un-vaccinated new born puppies (Gsell *et al.*, 2012).

Due to meaningfulness, accuracy and reliability of the rabies data, three years predictions were done. The numerical simulations of the model formulated in this study predict that the number of infected stray dogs in Arusha will increase to nearly 1000 in 2020. The results further show that, rabies incidence for infected stray dogs will be the highest as compared to the 2 other dog sub populations. The number of rabies infected domestic dogs on the other hand is expected to decrease to approximately 4 and even less in 2020. This is the lowest rabies incidence among the dog sub groups. For the infected Pastoralist dogs, the numerical results predict that there will be around 17 infected Pastoralist dogs in 2020, a medium rabies incidence among dog sub population.

The analysis of the modified model also shows that, mass culling of stray dogs result in an exponential increase in the susceptible class, the infectious class and the vaccinated class of the model for a short period of one year. Also, the behaviour of the model after mass vaccination indicates that the number of infected stray dogs decreases but will increase after the first four months. Furthermore, mass vaccination of stray dogs results in an increase in the number of vaccinated stray dog sub-population.

The one year transient analysis of the model, has been done using the data for 2018 to 2019. At the same time, it is applicable for analysis of disease dynamics at any year if it will be started from initial conditions taken from the real data set of the analysed year. Therefore, we can

use the developed model as the predictive model describing the dynamics in dependence on the applied controls such as culling and vaccination.

The main problem of using the findings of this model to break rabies transmission in the Arusha setting remains that vaccinating stray dogs successfully has been reported to be hampered by the issue of safely catching and handling the animals so that they can be injected (Cliquet *et al.*, 2007). This is one of the reasons which make culling the preferred control method for untrained government workers. However, recent discoveries and developments make oral vaccination (distributing food bait containing causative oral vaccine in capsules) a viable alternative option for vaccinating stray dogs (Zhang *et al.*, 2011). Currently, other rabies hosts such as raccoons and foxes are frequently vaccinated using oral vaccination. These animals differ from dogs in their feeding habits, so this method still needs to be perfected to ensure a sufficient amount of vaccine is consumed by each dog.

The main limitation to this study is that vaccination data were not available for the year 2019 and vaccination numbers vary greatly among the years depending on available resources such as vaccines and trained volunteers.

## **5.2 Recommendations**

The following recommendations are the result of the information obtained by using actual data for a modeling approach to establish the best method for controlling rabies in the Arusha region:

- (i) Coordinated vaccination campaigns especially in areas where national parks are closest to urban areas.
- (ii) Proper surveillance system especially of mobile dog populations such as Pastoralist dogs and stray dogs.
- (iii) Law enforcement of obligatory dog vaccination of domestic dogs.
- (iv) Awareness campaigns to educate people on the importance of dog vaccination.
- (v) An economic cost-benefit analysis based on this model would give more information on the best control methods in resource limited settings.
- (vi) This study can be extended by applying optimal control theory for more detailed findings.
- (vii) Stochastic models can be applied to check random movements of dog sub-populations.

(viii) Future studies may take into account a consideration of distinct dog populations and other rabies hosts such as cats, wild dogs, lions etc.

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## APPENDICES

### Appendix 1: MATLAB Codes for Figure 2

Reproduction Number for Different Vaccination Coverages and Combination of Vaccination and Culling.

```
%R0andRe.m
%constant values of parameters of reproduction numbers
set(0,'defaulttextinterpreter','Latex');
rhos=0.83778234;
psids=56; psims=35; alphas=2500; psisd=17;
mus=0.32; deltas=0.22; omegas=0.1; muc=0.01792; sigmas1
    =0.25174; sigmas2=0.39351;
sigmas3=0.50825; sigmas4=0.75687; muc2=0.02503;
betas=0:0.00000001:1.7864*10^-4;
R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus)
    *(mus+rhos));
Re1=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas1
    )+(mus*omegas)+mus^2));
Re2=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas2
    )+(mus*omegas)+mus^2));
Re3=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas3
    )+(mus*omegas)+mus^2));
Re4=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc2*omegas)+(muc*mus)+(mus*
    sigmas4)+(mus*omegas)+mus^2));
Y=[R0' Re1' Re2' Re3' Re4']*4;
plot(betas,R0,'r-',betas,Re1,'k-',betas,Re2,'b-',betas,Re3,'g',
    betas,Re4,'c','LineWidth',2)
xlabel('Exposure rate \beta_s')
ylabel('Reproduction number')
```

```
legend('R_0', 'R_{e1}', 'R_{e2}', 'R_{e3}', 'R_{e4}')
title('Variation of Reproduction Number with Exposure rate \
      beta_s')
ylim([0 2])
```

## Appendix 2: MATLAB Codes for Figure 3

Reproduction Number for Different Culling Coverages with the Current Vaccination Coverage Being Constant.

```
%R0andRe.m
%constant values of parameters of reproduction numbers
set(0,'defaulttextinterpreter','Latex');
rhos=0.83778234;
psids=56; psims=35; alphas=2500; psisd=17;
mus=0.32; deltas=0.22; omegas=0.1; muc=0.01792; sigmas1
    =0.25174; sigmas2=0.39351;
sigmas3=0.50825; sigmas4=0.75687; muc2=0.02503;muc3=0.0343;
    muc4=0.0412;
betas=0:0.00000001:1.7864*10^-4;
R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus)
    *(mus+rhos));
Re1=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas1
    )+(mus*omegas)+mus^2));
Re2=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc2*omegas)+(muc2*mus)+(mus*
    sigmas1)+(mus*omegas)+mus^2));
Re3=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc3*omegas)+(muc3*mus)+(mus*
    sigmas1)+(mus*omegas)+mus^2));
Re4=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc4*omegas)+(muc4*mus)+(mus*
    sigmas1)+(mus*omegas)+mus^2));
Y=[R0' Re1' Re2' Re3' Re4']*4;
plot(betas,R0,'r-',betas,Re1,'k-',betas,Re2,'b-',betas,Re3,'g',
    betas,Re4,'c','LineWidth',2)
xlabel('Exposure rate \beta_s')
ylabel('Reproduction number')
```

```
legend('R_0', 'R_{e1}', 'R_{e2}', 'R_{e3}', 'R_{e4}')
title('Variation of Reproduction Number with Exposure rate \
      beta_s')
ylim([0 2])
```

### Appendix 3: MATLAB Codes for Figure 4

Comparison Between Reported Data and Simulation of System 3.1 for Rabies Infected Stray Dogs in Arusha Region From 2013 to 2018.

```
%stray_dogs_rabies_data_fitting.m
clc
clear all
set(0,'defaulttextinterpreter','Latex');
c=['b ','g ','c ','g- ','g ','b- ','r ','k- ','r--','m. ','b ','
    'y '];
%Parameter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589; sigmad=0.5751; psimd=13;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
    =1.7864*10^-4; rhos=0.83778234; sigmas=0.25174; psims=35;
    psids=17; psids=56; muc=0.01792;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124;

Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psid))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
R0=(betas*rhos*(psids+psims+alphas-psid))./(mus.*(deltas+mus)
    *(mus+rhos));
%y0=[Sd Ed Id Vd Ss Es Is Vs Sm Em Im Vm]. Compartment values
y0=[14063 83 21 7276 20000 1500 75 0 2500 90 15 1500];
tspan=[2013 2018];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psid
    ,psimd,mud,sigmad,psids,betad,rhod,deltad,alphas,omegas,
    psims,sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,
    sigmam,betam,rhom,deltam);
for i=7:7
plot(t,y(:,i),c(:,i),'LineWidth',2)
```

```
xlabel('t(year)');ylabel('I_{s}')
title('Comparison Between Reported Data and Model')
hold on
end
time = 2013:1:2018;
Is=[180 800 1550 1900 2100 2100];
plot(time,Is,'r--','LineWidth',2)
legend('Model','Data')
Ispan=[30 35 40 45 50 55];
hold on
```

## Appendix 4: MATLAB Codes for Figure 5

Comparison Between Reported Data and Simulation of System 3.1 for Rabies Infected Domestic Dogs in Arusha Region From 2013 to 2018

```
%Domestic_dogs_data_fitting.m
clc
clear all
set(0,'defaulttextinterpreter','Latex');
c=['b ','m ','c ','r- ','g ','b- ','r ','k- ','r--','m. ','b ','
    'y '];
%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589;sigmad=0.5751; psimd=13;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
    =1.7864*10^-4; rhos=0.83778234; sigmas=0.25174; psims=35;
    psisd=17; psids=56; muc=0.01792;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124;

%Effective and basic reproduction numbers
Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus)
    *(mus+rhos));
%y0=[Sd Ed Id Vd Ss Es Is Vs Sm Em Im Vm]. Compartment values
y0=[14063 83 21 7276 20000 1500 75 0 2500 90 150 1500];
tspan=[2013 2018];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psisd
    ,psimd,mud,sigmad,psids,betad,rhod,deltad,alphas,omegas,
    psims,sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,
    sigmam,betam,rhom,deltam);
for i=3:3
```



```
plot(t,y(:,i),c(:,i),'LineWidth',2)
xlabel('t(year)');ylabel('I_{d}')
hold on
end
time = 2013:1:2018;
Id=[22 15 11 8 6 5];
plot(time,Id,'b--','LineWidth',2)
legend('Model','Data')
Idspan=[0 5 10 15 20 25];
hold on
```

## Appendix 5: MATLAB Codes for Figure 6

### The Effect of Natural Death Rate of Stray Dogs to Stray dogs Rabies Infection

```
%naturaldeathofstraydogs
clc
clear all
set(0,'defaulttextinterpreter','Latex');
%changing the color of infected stray dogs for each mus
c=['b ','g ','r','c- ','g ','b- ','r ','k- ','r--','m. ','b ','y '];
% c=['b ','g ','r ','g ','b- ','g ','r ','k- ','r--','m. ','b ','y '];
%change the value of mus(naturaldeathofstraydogs) for each simulation of stray dogs infection
% mus=0.32;
% mus=0.34;
% mus=0.36;
mus=0.38;
%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
rhod=0.06109589;sigmad=0.5751; psimd=13;
alphas=2500; deltas=0.22; omegas=0.1; betas=1.7864*10^-4; rhos=0.83778234; sigmas=0.25174; psims=35; psisd=17; psids=56; muc=0.01792;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7; rhom=0.069863013; sigmam=0.3124;
Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)+(mus*omegas)+mus^2));
R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus)*(mus+rhos));
y0=[14063 83 21 7276 20000 1500 10 0 2500 90 15 1500];
tspan=[0 40];
```

```

[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psisd
,psimd,mud,sigmad,psids,betad,rhod,deltad,alphas,omegas,
psims,sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,
sigmam,betam,rhom,deltam);
for i=7:7
plot(t,y(:,i),c(:,i),'Linewidth',2)
legend('\mu_s=0.32','\mu_s=0.34','\mu_s=0.36','\mu_s=0.38')
xlabel('t(year)');ylabel('I_{s}')
hold on
end

```

## Appendix 6: MATLAB Codes for Figure 7

### Trend of Infected Pastoralist Dogs

```
%infectedmaasaidogs.m
clc
clear all
set(0,'defaulttextinterpreter','Latex');

%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589;sigmad=0.5751; psimd=13;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
    =1.7864*10^-4; rhos=0.83778234; sigmas=0.25174; psims=35;
    psisd=17; psids=56; muc=0.01792;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124;

Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus)
    *(mus+rhos));
y0=[14063 83 21 7276 20000 1500 10 0 2500 90 15 1500];
tspan=[0 50];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psisd
    ,psimd,mud,sigmad,psids,betad,rhod,deltad,alphas,omegas,
    psims,sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,
    sigmam,betam,rhom,deltam);
for i=11:11
plot(t,y(:,i),'r','Linewidth',2)
xlabel('t(year)');ylabel('I_{m}')
hold on
end
```

## Appendix 7: MATLAB Codes for Figure 8

### Trend of Stray Dog Population for a Period of 50 Years

```
%Transmission of rabies in stray dog population in 50 years
time
set(0,'defaulttextinterpreter','Latex');
clear all
clc
c=['b','g-','r','c-','r','g-','r','k-','r--','m.','b.','y'];

%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
rhod=0.06109589;sigmad=0.5751; psimd=13;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
=1.7864*10^-4; rhos=0.83778234; sigmas=0.25174; psims=35;
psisd=17; psids=56; muc=0.01792;
alphan=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
rhom=0.069863013; sigmam=0.3124;
Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
+(mus*omegas)+mus^2));
R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus)
*(mus+rhos));
y0=[14063 83 21 7276 20000 1500 10 0 2500 90 15 1500];
tspan=[0 50];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psisd
,psimd,mud,sigmad,psids,betad,rhod,deltad,alphas,omegas,
psims,sigmas,mus,muc,betas,rhos,deltas,alphan,omegam,mum,
sigmam,betam,rhom,deltam);
for i=5:8
plot(t,y(:,i),c(:,i),'Linewidth',2)
title('Trend of stray dogs population')
ylabel('Number of stray dogs population')
```

```
legend('Susceptible','Exposed','Infected','Vaccinated')
xlabel('t(year)');
hold on
end
```

## APPENDIX 8: MATLAB Codes for Figure 9

Trend of Susceptible Stray Dogs After Mass Culling of Stray Dogs.

```
clc
clear all
set(0,'defaulttextinterpreter','Latex');
c=['b ','b ','g ','r- ','b ','b- ','r ','k- ','r--','m. ','b ','
   'y '];
%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589;sigmad=0.5751; psimd=13;psisd=0;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
    =1.7864*10^-4; rhos=0.83778234; sigmas=0.15174; muc=0.7592;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124; taud=0.05;taum=0.03;Mus
    =10000;

% Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
% R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus
    )*(mus+rhos));
%y0=[Sd Ed Id Vd Ss Es Is Vs Sm Em Im Vm]. Compartment values
y0=[14063 83 21 7276 500 1500 50 5 2500 90 15 1500];
tspan=[0 1];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psimd
    ,mud,sigmad,taud,Mus,betad,rhod,deltad,alphas,omegas,taum,
    sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,sigmam,
    betam,rhom,deltam);
for i=5:5
plot(t,y(:,i),c(:,i),'LineWidth',2)
xlabel('t(year)');ylabel('Ss')
%legend('Susceptible','Exposed','Infectious')
```

```
title('Trend of Susceptible stray dogs after mass culling of  
      stray dogs')  
hold on  
end  
hold on  
% time = 2013:1:2018;  
% Is=[180 800 1550 1900 2100 2100];  
% plot(time,Is,'r--','LineWidth',2)  
% legend('Model','Data')  
% Ispan=[30 35 40 45 50 55];  
% hold on
```



## Appendix 9: MATLAB Codes for Figure 10

Trend of Infected Stray Dogs After Mass Culling of Stray Dogs.

```
clc
clear all
set(0,'defaulttextinterpreter','Latex');
c=['b ','b ','g ','r- ','b ','b- ','r ','k- ','r--','m. ','b ','
   'y '];
%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589;sigmad=0.5751; psimd=13;psisd=0;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
    =1.7864*10^-4; rhos=0.083778234; sigmas=0.15174; muc=0.7592;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124; taud=0.05;taum=0.03; Mus
    =10000;

% Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
% R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus
    )*(mus+rhos));
%y0=[Sd Ed Id Vd Ss Es Is Vs Sm Em Im Vm]. Compartment values
y0=[14063 83 21 7276 500 1500 50 5 2500 90 15 1500];
tspan=[0 1];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psimd
    ,mud,sigmad,taud,Mus,betad,rhod,deltad,alphas,omegas,taum,
    sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,sigmam,
    betam,rhom,deltam);
for i=7:7
plot(t,y(:,i),c(:,i),'LineWidth',2)
xlabel('t(year)');ylabel('Is')
%legend('Susceptible','Exposed','Infectious')
```

```
title('Trend of Infected stray dogs after mass culling of stray  
      dogs')  
hold on  
end  
hold on  
% time = 2013:1:2018;  
% Is=[180 800 1550 1900 2100 2100];  
% plot(time,Is,'r--','LineWidth',2)  
% legend('Model','Data')  
% Ispan=[30 35 40 45 50 55];  
% hold on
```

## Appendix 10: MATLAB Codes for Figure 11

Trend of Vaccinated Stray Dogs After Mass Vaccination of Stray Dogs.

```
clc
clear all
set(0,'defaulttextinterpreter','Latex');
c=['b- ','c ','g ','m- ','b- ','b- ','r ','k- ','r--','m. ','b
   ','y '];
%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589;sigmad=0.5751; psimd=13;psisd=0;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.82; betas
    =1.7864*10^-4; rhos=0.083778234; sigmas=0.75174; muc
    =0.01792;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124; taud=0.05;taum=0.03;Mus
    =10000;

% Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./(
    (deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
% R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus
    )*(mus+rhos));
%y0=[Sd Ed Id Vd Ss Es Is Vs Sm Em Im Vm]. Compartment values
y0=[14063 83 21 7276 500 1500 50 9000 2500 90 15 1500];
tspan=[0 1];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psimd
    ,mud,sigmad,taud,Mus,betad,rhod,deltad,alphas,omegas,taum,
    sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,sigmam,
    betam,rhom,deltam);
for i=8:8
plot(t,y(:,i),c(:,i),'LineWidth',2)
xlabel('t(year)');ylabel('Vs')
```

```
title('Trend of Vaccinated stray dogs after mass vaccination of  
      stray dogs')  
hold on  
end  
hold on  
% time = 2013:1:2018;  
% Is=[180 800 1550 1900 2100 2100];  
% plot(time,Is,'r--','LineWidth',2)  
% legend('Model','Data')  
% Ispan=[30 35 40 45 50 55];  
% hold on
```

## Appendix 11: MATLAB Codes for Figure 12

Trend of Infected Stray Dogs After Mass Vaccination of Stray Dogs.

```
clc
clear all
set(0,'defaulttextinterpreter','Latex');
c=['b ','c ','g ','r ','b ','b ','r ','k- ','r--','m. ','b ','y
   '];
%Paramter used for EEP
alphad=2450; deltad=0.33; omegad=0; mud=0.23; betad=1*10^-8;
    rhod=0.06109589;sigmad=0.5751; psimd=13;psisd=0;
alphas=2500; deltas=0.22; omegas=0.1; mus=0.32; betas
    =1.7864*10^-1; rhos=0.0083778234; sigmas=0.75174; muc
    =0.01792;
alpham=1674; deltam=0.11; omegam=0; mum=0.16; betam=1*10^-7;
    rhom=0.069863013; sigmam=0.3124; taud=0.05;taum=0.03;Mus
    =9000;

% Re=(betas.*rhos*(mus+omegas)*(psids+psims+alphas-psisd))./((
    deltas+mus).*(mus+rhos)*((muc*omegas)+(muc*mus)+(mus*sigmas)
    +(mus*omegas)+mus^2));
% R0=(betas*rhos*(psids+psims+alphas-psisd))./(mus.*(deltas+mus
    )*(mus+rhos));
%y0=[Sd Ed Id Vd Ss Es Is Vs Sm Em Im Vm]. Compartment values
y0=[14063 83 21 7276 0 1500 50 2000 2500 90 15 1500];
tspan=[0 1];
[t,y]=ode45(@rabiesmodelsystem1,tspan,y0,[],alphad,omegad,psimd
    ,mud,sigmad,taud,Mus,betad,rhod,deltad,alphas,omegas,taum,
    sigmas,mus,muc,betas,rhos,deltas,alpham,omegam,mum,sigmam,
    betam,rhom,deltam);
for i=7:7
plot(t,y(:,i),c(:,i),'LineWidth',2)
xlabel('t(year)');ylabel('Is')
```

```
title('Trend of Infected stray dogs after mass vaccination of  
    stray dogs')  
hold on  
end  
hold on  
% time = 2013:1:2018;  
% Is=[180 800 1550 1900 2100 2100];  
% plot(time,Is,'r--','LineWidth',2)  
% legend('Model','Data')  
% Ispan=[30 35 40 45 50 55];  
% hold on
```