Mathematical epidemiological models with finite time extinction: the case of African swine fever virus in wildlife areas

by:

Prashanthi Sivakumaran

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Summary

In Mathematical Epidemiology disease free states are commonly represented as equilibria of dynamical systems which model the respective epidemiological processes. However, in cases when the equilibrium is zero and is related to extinction (of the population), due to the uniqueness property of a complete dynamical system, solutions may converge to an equilibrium but never reach it. This may give rise to qualitatively unrealistic behaviour such as a population that is practically extinct but is able to grow. An example of a case when this problem may arise is when modelling the dynamics of African Swine Fever (ASF), a contagious disease affecting both domestic and wild pigs, in the Mkuze Game Reserve. In the paper by Arnot et. al.[3] it was established that although an increase in burrow infestation rates was observed, the disease was not detected within the game reserve. This situation cannot be captured using a model with exponential decay. In the following research project, we study various ODE and PDE models with the property that solutions approaching the disease free equilibrium 0, will reach it within finite time and remain at 0 thereafter. These include basic population models and epidemiological models with age and state structure. We then construct a model for ASF in order to accurately illustrate the phenomenon observed at the game reserve.

Declaration

I, the undersigned, declare that the dissertation, which I hereby submit for the degree Magister Scientiae at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at this or any other tertiary institution.

Signature:

Name: Prashanthi Sivakumaran

Date: July 14, 2016

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Chapter 1

Introduction

African Swine Fever (ASF) is a contagious viral disease that affects both domestic and wild pigs. The virus originally remained restricted within Africa amongst its natural hosts, namely the common warthog *Phacochoerus africanus*, bush pigs *Potamochoerus spp.* and soft ticks *Ornithodoros pornicus pornicus* [15]. As a result of the admittance of domestic pigs into Africa, ASF was transmitted into a population that is susceptible to the disease in which the virus manifests as an acute haemorrhagic disease [20] with mortality rates as high as 100% [14]. In particular, the disease is characterized by high fever, loss of appetite, vomiting, bleeding from the nose or rectum and death within 2-10 days.

ASF outbreaks in Portugal in 1957 and 1960 allowed the disease to become well established within the swine population of the Iberian Peninsula [20]. Successive outbreaks also took place in many European countries, Cuba, the Dominican Republic, Brazil and Haiti. As these outbreaks significantly affected the porcine production in countries with leading commercial pig industries and since disease extermination proved tedious and costly, ASF amassed international attention for the first time and triggered many research endeavours towards finding a vaccine. Unfortunately, these efforts have proven to be fruitless[20]. However, the studies conducted in Europe identified that argasid ticks from the genus *Ornithodoros* were able to maintain the virus for extended periods of time and were able to transmit ASFV (African Swine Fever Virus) to pigs. The following chapter provides an overview of the epidemiology of the disease and its significance within Africa as well as worldwide.

1.1 ASF in Africa

The FAO Yearbook for 1995 states that pig production in Africa accounts for less than 1% of the world's pork[20]. Although this industry has very little commercial value, it is of great importance locally in both urban and rural areas. Firstly, there

is a need to increase in pork production in order to meet the needs of a fast growing urban population within African countries. Furthermore, in rural areas where cattle production is not possible due to insufficient grazing area, pigs serve as the predominant source of animal protein. Pork is the cheapest source of high-quality protein and can be produced using nutritional sources of low value[20]. On a social level, pigs have become the traditional animal for numerous cultural practices and act as a mobile bank that can provide funds in order to meet basic needs for the poor. Hence, ASF is a crucial constraint for porcine production in sub-Saharan Africa and recent outbreaks of the disease have brought to light the need for new control measures that will be conducive to sustaining an inexpensive pig production in poverty-stricken countries.

In Africa, ASFV is maintained in at least three distinct cycles:

1. in the sylvatic cycle between wild pigs and soft ticks,

2. a cycle between domestic pigs and soft ticks that live in pig houses in Malawi; and

3. maintenance of ASFV independent of soft ticks and wild pigs, in domestic pig populations.

1.2 The sylvatic cycle between wild suids and argasid ticks

1.2.1 Warthogs

Warthogs play a vital role in the maintenance of ASFV in eastern and southern Africa since they inhabit burrows that are often infested with soft ticks[20]. Transmission of the virus occurs when ticks ingest a blood meal from an infected host (warthog) and then pass it on when feeding on susceptible animals. Infected warthogs are asymptomatic and virus levels in their blood are low. Neonatal warthogs, born in the burrows, develop high blood virus levels lasting upto two to three weeks [14] and hence are capable of infecting ticks when a blood meal is taken [19]. After this three week period, the blood virus levels drop abruptly and become too low for detection[20]. It has been established that vertical transmission of ASFV from a female warthog to her offspring in the womb is unlikely. Owing to the fact that warthog farrowing is seasonal (November to December)[3], the viral transmission between these two natural hosts also follows a cyclical pattern [14].

1.2.2 Bushpigs

Blood virus levels of six month old bushpigs were reportedly higher than those of experimentally infected warthogs within the same age range. However, since bushpigs exist in smaller numbers, do not inhabit burrows, and do not frequently come into contact with domestic pigs since they are nocturnal, there are very few circumstances under which they could encounter soft ticks[20]. Experimentally infected bushpigs are able to transmit ASFV to domestic pigs if there has been contact between them. Despite this, in areas where bush pigs are common, such as the Eastern Cape Province of South Africa, no outbreaks of the disease in domestic pigs has been reported [25] and they have low infection rates of ASF and hence their role in the spread of the ASF currently has not been established [14]. Therefore, in this research project, the warthog is considered to be the more significant of the free-living vertebrate hosts of the virus. Lastly, bushpigs are also asymptomatic to the disease.

1.2.3 Soft ticks

Ornithodoros porcinus porcinus are eyeless, soft-shelled ticks that occur in the savannah regions of eastern and southern Africa inhabited by warthogs[20]. Specifically, the species has been found predominantly within wildlife reserves in South Africa, Zimbabwe, Zambia, Tanzania, Kenya, Namibia and Uganda. It should be noted that the proportion of infested burrows as well as the number of ticks found per burrow tends to differ and may depend on the age of the burrow and how frequently the burrow was used. Due to their common habitat, *O.porcinus porcinus* are mostly dependant on warthogs for blood meals. However, they also feed on other vertebrate hosts that enter their burrows [6] such as porcupines, spotted hyaenas and aardvarks[20]. The availability of a food source affects the ageing process of the tick population since, with each blood meal the ticks engorge to their next life stage and hence when a blood meal is readily available more often, the time taken for the ticks to engorge to adulthood is shortened. If no animals enter the burrow for extended periods of time, then the ticks will remain at their current life stage indefinitely until their next blood meal and hence the ageing of the ticks becomes a discontinuous process. However, in this research project it was assumed that other sources of food were always available and hence, the ticks age continuously. Furthermore, this implies that when a warthog family inhabits a burrow, there ought to be an acceleration in the ageing of the tick population as well as higher infection rates of ASFV. This hypothesis was investigated with the aim of determining its effect on the spread of ASF.

The *Ornithodoros* tick population is able to maintain ASF and transmit the disease for many years[19]. In particular, transmission of the virus occurs in three ways [15]:

1. transtadially (from one life stage to another)
2. transovarially (parent to offspring)
3. sexually

In the paper by Plowright et al [21] it is established that sexual transmission of ASFV is unidirectional from infected males to females. Transmission from infected females to clean males was observed in only one of 35 observed mating instances and hence this is a rare occurrence that probably does not have any significant effect on the spread of ASF. This is possibly why the observed infection rates for female ticks is substantially higher than that of male ticks[20]. Additionally, the virus present in the seminal fluid of a tick may produce infected offspring following an extrinsic incubation period of 8-48 days.

Transovarial transmission occurs when the ovarian tissue of the female *Ornithodoros* tick is infected [23]. This provides a process by which the virus is maintained within the tick population when unfavourable conditions are experienced. For example during extended periods of time when the warthogs (or other vertebrate hosts) may be absent from the burrow [23]. The tick colony can maintain the disease for up to 15 months under these conditions [3]. Rates of transovrial transmission observed under experimental conditions are higher than those observed in nature [15] [23]. In the investigation conducted by Plowright et al in 1970 it was found that among naturally infected female ticks, infection rates from parent to offspring of up to 55-81% were reported [21]. However, studies conducted with higher numbers of infected females did not yield the same results.

Transtadial transmission ensures that the ticks remain infected with the virus from one life stage to the next. This is of particular significance with regards to maintenance of the disease within the tick population. Under experimental conditions, very high transtadial transmission rates (almost 100%) have been reported [15]. Therefore, regardless of the life stage at which initial infection takes place, most ticks will remain infected for the remainder of their lifetime. However, there is insufficient data in this regard for infected ticks in the field.

It has been observed that the rates of infection of ticks increases gradually with each life stage except between the last nymphal stage and adults, where a sudden six fold increase in infection rate occurs [20]. It should be noted that with each developmental stage the size of the blood meals increases considerably is possibly why the infection rates increase as the ticks age. In the paper by Rennie et al [22] , it is suggested that mortality rates of adult ticks that ingested a blood meal from an infected host were comparatively higher than the mortality rates observed for ticks that fed on an uninfected blood meal. This is an important result since it reduces

the probability of maintaining the disease within the tick population through biting alone and hence, places greater significance on transovaraial, transtadial and sexual transmission. It was also established that if the female ticks are able to ingest blood meals on a relatively regular basis, the number of female ticks that lay infected eggs increased. Therefore, it is possible that the warthogs play a role in the escalation and, to some extent, the maintenance of the disease within the tick population. It is important to note, however, that the joint presence of warthogs and soft ticks in a common locality does not always imply that ASF is prevalent in the region. Similarly, warthogs that inhabit areas that are tick-free are not necessarily free of ASF [14].

Transmission of ASFV between warthogs and domestic pigs or between warthogs as a result of direct contact is unlikely[15]. However, in a study Horak et. al. large numbers of soft ticks have been found on captured warthogs, as well as on warthog carcases located outside their burrows [11]. In particular it was found that a single individual carried 97 nymphal ticks and 107 others. It is suggested that the feeding of the ticks on the warthog was interrupted by the fact that the warthog left the burrows in the mornings and would remain attached to them until the warthog returned to its burrow in the evening. Therefore, despite the fact that soft ticks are burrow-dwelling, it is possible for them to be transported outside the burrow while attached to a host. This implies that indirect warthog to warthog transmission is possible (even outside the burrow). Infected ticks may come into contact with domestic pigs when attached to warthogs that graze in areas adjacent to land occupied by domestic pigs or while attached to infected warthogs that are transported back to pig farms for slaughter. Feeding ASFV contaminated garbage to domestic pigs is a possible but unlikely scenario leading to the infection of domestic pigs [14].

1.3 Control measures

As there is currently no vaccine for ASF, the disease is controlled by means of slaughter, separation of wild and domestic pigs using double fencing and strict quarantine procedures [15] [14]. However, the slaughter of large numbers of pigs is unethical and is difficult to implement successfully in countries where adequate funding and veterinary services are scarce [19]. Furthermore, since ASFV can be isolated in certain pork products,(e.g. Parma hams), for up to 300 days after processing [15], countries that are ASF free employ stringent import policies that ensure that no infected pigs or pork products are introduced into the region. These measures (particularly trade bans) directly result in major economic losses in the affected countries.

Owing to the fact that the virus is able to adapt and spread across borders easily, ASF poses a significant threat to porcine production worldwide. Furthermore, the

disease is endemic in sub-Saharan countries and since this region will remain a potential starting point of infection, it is important that an accurate understanding of the epidemiology of the disease in Africa is established, in order to further improve international control of ASF[25]. In the paper by Arnot et al.(2009) the prevalence of ASF in the Mkuze Game Reserve (MGR), which is an ASF controlled area in South Africa, is investigated. It was established that in comparison to a study conducted in 1978, a higher proportion of adult ticks was sampled and that the burrow infestation rate had increased by 27%. This would ideally suggest a high prevalence of ASF within the game reserve, however the disease was not detected within the 98 burrows that were sampled. Hence, the disease has either been eradicated from the game reserve or is only present in a few isolated areas of MGR.

In order to gain some insight into the situation at MGR, investigation of the behaviour of ASFV was done with the aim of finding conditions under which this situation may arose. One of the research questions that could possibly be answered through this project is if the conditions in the Mkuze Game Reserve can be replicated in other wildlife sites or areas in order to minimize or eliminate their effects on another swine population.

The organization of the thesis is as follows. Chapter 2 introduces mathematical concepts used to construct and analyse the model and includes a study of existing population models with significant features such as age structure and impulses. Chapter 3 investigates population models with extinction of the population in finite time. In Chapter 4, the ASFV model is formulated and analysed. Chapter 5 concludes and discusses some possible future work.

Chapter 2

Mathematical Introduction

In this chapter we provide mathematical preliminaries related to continuous dynamical systems defined via differential equations by following the book [24]. Additionally, we extend the standard theory by giving special consideration to forward (only) uniqueness, derived from the one-sided Lipschitz condition.

Consider the initial value problem

$$\frac{du}{dt} = f(u) \tag{2.1}$$

$$u(0) = u^0 \tag{2.2}$$

where $f \in C(W, \mathbb{R}^p)$, C is the continuous function space, $\mathbb{R}^p$ is the real coordinate space of dimension p, $W \subset \mathbb{R}^p$ and W is an open set.

A solution of the problem (2.1))-(2.2)) is a continuously differentiable function $u : I(u^0) \to W$ satisfying (2.1)) and (2.2)), where $I(u^0)$ is a real interval containing the origin.

2.1 Dynamical systems defined by ODE's

Definition 2.1.1. ***Dynamical system***

(i) Equation (2.1) *is said to define a* ***positive dynamical system*** *on* $W \subseteq \mathbb{R}^p$ *if for every* $u^0 \in W$ *there exists a unique solution* u *of* (2.1)-(2.2) *which is defined for all* $u(t) \in W,\ t \in [0, \infty)$.

(ii) Equation (2.1) *is said to define a* ***negative dynamical system*** *on* $W \subseteq \mathbb{R}^p$ *if for every* $u^0 \in W$ *there exists a unique solution* u *of* (2.1)- (2.2) *which is defined for all* $u(t) \in W,\ t \in (-\infty, 0]$.

(iii) Equation (2.1) *is said to define a* ***complete dynamical system*** *on* $W \subseteq \mathbb{R}^p$ *if it defines both a positive and negative dynamical system on* W.

We recall here several theorems, from the book by Stuart and Humphries [24], that are relevant to the existence and uniqueness of the solutions of (2.1)-(2.2).

Theorem 2.1.2. ***Existence***
Let $W \subseteq \mathbb{R}^p$ *be open and let* $f \in C(W, \mathbb{R}^p)$. *Then for any* $u^0 \in W$ *there exists a real interval* $I(u^0)$ *containing the origin and a continuously differentiable function* $u : I(u) \to W$ *which satisfies* (2.1)-(2.2).

Theorem 2.1.3. ***Global Existence***
Let K *be a compact subset of* $W \subseteq \mathbb{R}^{\prime}$ *and* $u^0 \in K$. *If every solution of* (2.1)-(2.2) *that is of the form* $u : [0, \beta] \to W$ *satisfies* $u(t) \in K, t \in [0, \beta]$ *then there exists a solution* $u : [0, \infty) \to W$. *Similarly, if every solution of* (2.1)-(2.2) *in the form* $u : [-\beta, \beta] \to W$ *satisfies* $u(t) \in K, t \in [-\beta, \beta]$ *then there exists a solution* $u : (-\infty, \infty) \to W$.

Theorem 2.1.4. ***Uniqueness***
If f *is locally Lipschitz on* W, *then any solution of* (2.1)-(2.2) *is unique on its domain.*

Definition 2.1.5. ***One-sided Lipschitz condition***
A function $f : \mathbb{R}^p \to \mathbb{R}^p$ *is called* ***one-sided Lipschitz on*** $\mathbf{R^p}$ *if*

$$< f(y_1) - f(y_2), y_1 - y_2 > \ \leq \ L\|y_1 - y_2\|^2 \tag{2.3}$$

for some real positive constant L *and all* $y_1, y_2 \in \mathbb{R}^p$.

In the special case where $p = 1$, condition (2.3) can be written as follows:

$$\frac{f(y_1) - f(y_2)}{|y_1 - y_2|} \leq L \tag{2.4}$$

for some real positive constant L and all $y_1, y_2 \in \mathbb{R}$ such that $y_1 \neq y_2$.

The application of the Lipschitz condition in proving the uniqueness of solutions often utilizes the following result [24].

Theorem 2.1.6. ***Gronwall's Inequality***
If $y(t)$ *satisfies*

$$y_t \leq ay + b, \ y(0) = y_0,$$

where a *and* b *are constant, then for* $t \geq 0$

$$y(t) \leq e^{at} y_0 + \frac{b}{a}(e^{at} - 1), \quad a \neq 0$$

and

$$y(t) \leq e^{at} + y_0, \quad a = 0$$

Theorem 2.1.7. ***Forward Uniqueness***
If f is one-sided Lipschitz on $W \subset \mathbb{R}^p$, then any solution $u : [0, \beta) \to W$ of (2.1)-(2.2) is unique on its domain.

Proof. Let $v_1, v_2 : [0, \beta) \to W$ be two distinct solutions of (2.1)-(2.2).

If $Q(t) = \|v_1(t) - v_2(t)\|^2$ then using (2.4) we obtain

$$\begin{aligned} Q'(t) &=< v_1'(t) - v_2'(t), v_1(t) - v_2(t) > \\ &=< f(v_1(t)) - f(v_2(t)), v_1(t) - v_2(t) > \\ &\leq L\|v_1(t) - v_2(t)\|^2 \\ &= LQ(t) \quad \forall t \in [0, \hat{t}] \end{aligned}$$

From Theorem 2.1.6 and using the fact that $Q(0) = \|v_1(0) - v_2(0)\|^2$ we have,

$$Q(t) \leq Q(0)e^{Lt} = 0 \quad \forall t \in [0, \hat{t}]$$

Hence, $v_1(t) = v_2(t), \quad \forall t \in [0, \beta)$. □

Let (2.1) define a dynamical system on W. Below we define a few concepts related to this dynamical system.

For every $t \geq 0$ we define the operator $S(t) : W \to W$ as follows:

$$S(t)u^0 = u(t)$$

where $u(t)$ is the solution of (2.1)-(2.2). It is clear that S satisfies the following properties:

$$S(t) \circ S(r) = S(t + r) \tag{2.5}$$
$$S(0) = I \tag{2.6}$$

Due to properties (2.5)-(2.6) S is called an **evolution semigroup**[24].

Definition 2.1.8. ***Action of evolution semigroups***
Consider the evolution semigroup S associated with dynamical system (2.1). Given $B \subset \mathbb{R}^p$, the set

$$S(t)B = \cup_{u^0 \in B} S(t)u^0 \tag{2.7}$$

is called action of S on B.

Definition 2.1.9. ***Orbits***

*(i) A **positive orbit**, of the point $u^0 \in W$, is the set $\Gamma^+(u^0) = \{S(t)u^0 : t \geq 0\}$.*

*(i) A **negative orbit**, of the point u^0, is the set $\Gamma^-(u^0) = \{u(t) : t \leq 0\}$.*

*(iii) $\Gamma(u^0) = \Gamma^-(u^0) \cup \Gamma^+(u^0)$ is called a **complete orbit** of u^0.*

2.2 Existence and uniqueness under one-sided local Lipschitz condition

In existing literature, the Lipschitz condition has been widely used in order to establish uniqueness of a solution. In the following section, we intend to show that existence and uniqueness can be attained using the 1-sided local Lipschitz condition. This will allow a less stringent condition to be imposed on the function f.

Definition 2.2.1. ***Convex Set***
A set $W \subset \mathbb{R}^p$ is said to be ***convex*** *if for every $x,\ y \in W$, W contains all closed segments joining x and y. That is,*

$$M = \{z \in X : z = \alpha x + (1-\alpha)y,\ 0 \leq \alpha \leq 1\} \subset W \tag{2.8}$$

where M is a closed segment with boundary points x and y and $z \in M$ is an interior point of M [24].

Definition 2.2.2. ***Convex Hull*** *Let Q be a subset of a linear space. Then the convex hull $co(Q)$ of Q is the smallest convex set containing Q [24]. One can also write*

$$co(Q) = \bigcap_{P-convex\ \ Q\subset P} P. \tag{2.9}$$

Theorem 2.2.3. ***Carathéodory***
Every element of the convex hull of a set $Q \subset \mathbb{R}^p$ is a convex linear combination of at most p elements of Q. That is, for every $y \in co(Q)$ there exist $x_1, x_2, \ldots, x_m$ for $m \leq p+1$ and $\mu_1, \mu_2 \ldots \mu_m$ with $\sum_{j=1}^m \mu_j = 1,\ \mu_j \geq 0$ such that $y = \sum_{j=1}^m \mu_j x_j$ [24].

Definition 2.2.4. ***Locally Lipschitz***
f is said to be locally Lipschitz on $W \subset \mathbb{R}^p$ if for every $x \in W$ there exists δ such that f is Lipschitz on $\{y \in W : \|x-y\| < \delta\}$ [24].

Similarly, in the case when f is said to be **locally one-sided Lipschitz** on $W \subset \mathbb{R}^p$ if f is one-sided Lipschitz on every neighbourhood of W.

Lemma 2.2.5. *Let Q be a compact subset of $\mathbb{R}^p$. Then $co(Q)$ is also compact.*

Proof. Let $\mathcal{M} = \left\{\mu_1, \mu_2, \ldots \mu_p : \mu_j \geq 0,\ \sum_{j=1}^p \mu_j = 1\right\}$. It is clear that $\mathcal{M}$ is a compact subset of $\mathbb{R}^{p+1}$. Consider the mapping Φ defined by $\Phi(x_1, x_2, \ldots, x_p, \mu) = \sum_{j=1}^{p+1} \mu_j x_j$. Using the result of Theorem 2.2.3, it is clear that $co(Q) = \Phi(Q \times \cdots \times \mu)$. Further we infer that Φ is continuous. Then it maps a compact set onto a compact set. The set $\{Q \times Q \times \cdots \times Q \times \mathcal{M}\}$ is a compact subset of the domain of Q. Therefore, $co(Q) = \Phi(Q \times Q \times \cdots \times Q \times \mathcal{M})$. □

Theorem 2.2.6. *If W is convex and f is locally Lipschitz on W, then f is Lipschitz on every compact subset of W.*

Proof. Let K be a compact, proper subset of W. It then follows from Lemma 2.2.5 that $co(K) \subset W$ is compact. For every $x \in co(K)$ there exists δ_x such that f is Lipschitz on

$$V_x = \{y \in W : \|x - y\| < \delta_x\}. \tag{2.10}$$

Then $\{V_x : x \in co(K)\}$ is an open cover of $co(K)$. Since $co(K)$ is compact, it can be deduced that there exists a sequence $x_1,\ x_2 \dots x_m\ \in co(K)$ such that $co(K) \leq \bigcup_{i=1}^{m} V_{x_i}$.

Denote by $L_1, L_2 \dots L_m$ the Lipschitz constant of f on each of the sets $V_{x_1}, V_{x_2} \dots V_{x_m}$ respectively and let $L = \max\{L_1, L_2 \dots L_m\}$. Suppose $y, z \in K$. It then follows that the line segment connecting y and z, denoted by $\bar{yz}$, lies entirely in $co(K)$. Now, using geometrical arguments, $\overline{yz}$ can be partitioned into individual line segments, such that each segment lies entirely in one of the sets $V_{x_i},\ i = 1, 2, \dots, m$. Denote each line segment by $\overline{\xi_j \xi_{j+1}},\ j = 0, \dots, q-1$, where $\xi_0 = y$ and $\xi_q = z$.

Then

$$\begin{aligned}
\|f(z) - f(y)\| &= \|\sum_{j=1}^{q-1} (f(y_{j+1}) - f(y_j))\| \\
&\leq \sum_{j=1}^{q-1} \|f(y_{j+1}) - f(y_j)\| \\
&\leq \sum_{j=1}^{q-1} L\|y_{j+1} - y_j\|.
\end{aligned}$$

Due to the fact that all points $y_j,\ j = 0, , 1 \dots, q$ lie on the line segment $\bar{yz}$ and since y_j is between y_{j-1} and y_{j+1} (i.e. the points y_j are consecutive) we can conclude that

$$\sum_{j=1}^{q-1} \|y_{j+1} - y_j\| = \|z - y\|.$$

The result follows. □

In the case where f is locally one-sided Lipschitz the following result holds true.

Theorem 2.2.7. *If W is convex and f is locally one-sided Lipschitz on W, then f is one-sided Lipschitz on every compact subset of W.*

Proof. Let K be a compact, proper subset of W. It then follows from Lemma 2.2.5 that $co(K) \subset W$ is compact. For every $x \in co(K)$ there exists δ_x such that f is Lipschitz on

$$V_x = \{y \in W : \|x - y\| < \delta_x\}. \tag{2.11}$$

Then $\{V_x : x \in co(K)\}$ is an open cover of $co(K)$. Since $co(K)$ is compact, it can be deduced that there exists a sequence $x_1,\ x_2 \dots x_m\ \in co(K)$ such that $co(K) \leq \bigcup_{i=1}^{m} V_{x_i}$.

Denote by $L_1, L_2 \dots L_m$ the Lipschitz constant of f on each of the sets $V_{x_1}, V_{x_2} \dots V_{x_m}$ respectively and let $L = \max L_1, L_2 \dots L_m$. Suppose $y, z \in K$. It then follows that the line segment connecting y and z, denoted by $\bar{yz}$, lies entirely in $co(K)$. Now, using geometrical arguments, $\bar{yz}$ can be partitioned into individual line segments, such that each segment lies entirely in one of the sets $V_{x_i},\ i = 1, 2, \dots, m$. Denote each line segment by $y_j\bar{y}_{j+1},\ j = 0, \dots, q-1$, where $y_0 = y$ and $y_q = z$.

Using the fact that $z - y = \frac{\|z-y\|}{\|y_{j+1}-y_j\|}.(y_{j+1} - y_j)$, since the vectors $z - y$ and $y_{j+1} - y_j$ have the same direction, the following can be obtained:

$$\begin{aligned}
< f(z) - f(y), z - y > &= < \sum_{j=0}^{q-1} \left(f(y_{j+1}) - f(y_j)\right), z - y > \\
&= \sum_{j=0}^{q-1} < f(y_{j+1} - f(y_j), z - y > \\
&= \sum_{j=0}^{q-1} < f(y_{j+1} - f(y_j), \frac{\|z-y\|}{\|y_{j+1}-y_j\|}.(y_{j+1} - y_j) > \\
&= \sum_{j=0}^{q-1} \frac{\|z-y\|}{\|y_{j+1}-y_j\|} < f(y_{j+1} - f(y_j), (y_{j+1} - y_j) > \\
&\leq \sum_{j=0}^{q-1} \frac{\|z-y\|}{\|y_{j+1}-y_j\|} L\|y_{j+1} - y_j\|^2 \\
&= L\|z - y\|
\end{aligned}$$

Once again, equality was achieved in the final step since the points $y_j,\ j = 0, , 1 \dots, q$ lie consecutively on the line segment $\bar{yz}$.

□

Theorem 2.2.8. ***Lipschitz continuity with respect to the initial condition***

Suppose that W is a convex open set, $f : W \to \mathbb{R}^p$ is locally one-sided Lipschitz on W and $u = u(t),\ v = v(t)$ are two solutions of (2.1) which exist on $[0, T],\ T > 0$. It then follows that there exists $L > 0$ such that

$$\|u(t) - v(t)\| \leq e^{Lt}\|u(0) - v(0)\|. \tag{2.12}$$

Proof. Let $K = \{u(t) : t \in [0, T]\} \bigcup \{v(t) : t \in [0, T]\}$. Since both u and v are continuous the set K is compact. From Theorem 2.2.7 it follows that f is one-sided

Lipschitz on K. Let L be the Lipschitz constant of f on K. Then we obtain the following:

$$\begin{aligned}\frac{d}{dt}\|u(t)-v(t)\|^2 &= 2 < u_t - v_t, u(t)-v(t) > \\ &= 2 < f(u(t)) - f(v(t)), u(t)-v(t) > \\ &\leq 2L\|u(t)-v(t)\|^2\end{aligned}$$

From (2.1.6),

$$\|u(t)-v(t)\|^2 \leq e^{2Lt}\|u(0)-v(0)\|^2 \tag{2.13}$$

Taking the square root on both sides of the equation yields the desired result. □

Corollary 2.2.9. *Let* (2.1) *define a dynamical system on* $\Omega \subset W$. *Then for every* T *there exists* L *such that*

$$\|S(t)u^0 - S(t)v^0\| \leq e^{Lt}\|u^0 - v^0\| \tag{2.14}$$

Corollary 2.2.10. *If* f *is locally one-sided Lipschitz on* $W \in \mathbb{R}^p$, *then any solution* $u : [0, \beta) \to W$ *of* (2.1)-(2.2) *is unique on its domain.*

2.3 Limit sets

Definition 2.3.1. ***Invariant Sets***
Consider an arbitrary set B.

(i) B *is* ***positively invariant*** *under* $S()$ *if* $S(t)B \subseteq B$ *for all* $t \geq 0$.

(ii) B *is* ***negatively invariant*** *under* $S()$ *if* $B \subseteq S(t)B$ *for all* $t \geq 0$

(iii) If B *satisfies both (i) and (ii) (i.e.* $S(t)B \equiv B$ *for all* $t \geq 0$*), then* B *is* ***invariant*** *under* S.

Theorem 2.3.2. ***Conditions for set Invariance***

(i) A set B *is positively invariant if and only if there exists a positive orbit* $\Gamma^+(u^0)$ *such that* $\Gamma^+(u^0) \subseteq B$ *for all* $u^0 \in B$.

(ii) B *is negatively invariant if and only if for every* $u^0 \in B$ *there exists a negative orbit* $\Gamma^-(u^0)$ *such that* $\Gamma^-(u^0) \subseteq B$.

(iii) B *is invariant if and only if for every* $u^0 \in B$ *there exists a complete orbit* $\Gamma(u^0)$ *such that* $\Gamma(u^0) \subseteq B$.

Definition 2.3.3. *Let $x \in \mathbb{R}^p$ and suppose that there exists a sequence $\{t_i\}_{i=1}^{\infty}$, $t_i \to \infty$, such that $S(t_i)u^0 \to x$ as $i \to \infty$. Then x is an* ***ω-limit point*** *of u^0. For a given u^0, the set, $\omega(u^0)$, containing all such points is called the* ***ω-limit set*** *of u^0 and*

$$\omega(u^0) = \left\{x \in \mathbb{R}^p : \exists_k \to \infty,\ S(t_k)u^0 \to x\right\}. \tag{2.15}$$

In the same manner, the ω-limit set of a bounded set B is defined as follows:

$$\omega(B) = \{x \in \mathbb{R}^p : \exists t_k \to \infty, yk \in B, S(t_k)y_k \to x_k\} \tag{2.16}$$

Theorem 2.3.4. ***Properties of Limit Sets***
Suppose that $S(t)$ is continuous. The ω-limit set of any bounded set $B \subset \mathbb{R}^p$, $\omega(B)$, is a closed positively invariant set. Furthermore, if $\cup_{t\geq 0} S(t)B$ is bounded then $\omega(B)$ is invariant. Lastly, if $\omega(B)$ is bounded for some $u^0 \in \mathbb{R}^p$ then it is connected.

2.4 Structured population models

Population models for biological species have been traditionally constructed with the assumption that the populations are homogeneous with respect to physical characteristics such as age, size, maturity etc. However, this assumption is not valid in the case of organisms where natural processes influencing the chance of an individuals survival are directly affected by these characteristics [1]. In this section we undertake a brief historical recollection of how continuous time structured population models were formulated and rose to prominence in population biology.

2.4.1 Early population models

In 1992 the simplest model to capture population dynamics was developed by Malthus, who speculated that the human population would grow exponentially with time [1]. This model was formulated under the following assumptions:

1. individuals in the population are physiologically indistinguishable,
2. the population inhabits a fixed and secluded location,
3. individuals have access to limitless resources.

Hence, the model only takes into account the size of the population at time t, denoted by $P(t)$. The following linear ordinary differential equation is known as *Malthus' Law*:

$$\frac{d}{dt}P(t) = \delta P(t) \tag{2.17}$$

for $\delta = \alpha - \mu$, where α and μ are constant birth and death rates respectively. However, this law does not apply in instances when the population competes for resources, since in these cases δ would depend on the size of the population, which would give rise to a non-linear model.

Verhulst endeavoured to amend this shortcoming by enforcing a maximum population size K, also known as the *carrying capacity*.

$$\frac{d}{dt}P(t) = r\left(1 - \frac{P(t)}{K}\right)P(t) \tag{2.18}$$

This model is analogous to the Malthusian model with fixed birth rate and death rate proportional to the ratio of the total population size to the carrying capacity. That is, $\alpha = r$ and $\mu = r\frac{P(t)}{K}$ in (2.17). The validity of the logistic model was verified by using laboratory experiments on simple organisms, such as bacteria and yeast, where the populations are subject to invariable environmental conditions, no predators and have an adequate supply of food [1]. Growth curves that were obtained from conducting these experiments were found to be consistent with the predictive results of the logistic equation. However, these results could not be replicated in the case of organisms with intricate life cycles(e.g. flies, ticks, beetles), with multiple life stages where the dynamics of the population greatly changes subject to an individuals physiological characteristics. It was found that proceeding a length of time where the population grows logistically, these populations display fluctuations.

The inability of these models to replicate biological actuality lead to the development of more mathematically complex models where individuals are differentiated with respect to characteristics such as age, size, epidemiological state etc [1]. These models are formulated under the fundamental assumption that the dynamical behaviour of the population is solely determined by the structure of a population with respect to these individual characteristics at a specified time, together with time dependant environmental factors.

The Sharpe-Lotka-McKendrick model

Structured population models in continuous time were first pioneered by Sharpe and Lotka (1911), where age was considered to be the sole structuring variable for the population [27]. Furthermore, an integral formulation where the birth and death rates for the population are age-dependant was also developed. In 1926 McKendrick devised an age-structured population model using the following first-order, linear partial differential equation , where $u(t, a)$ represents the density of the distribution of individuals in the population at time $t > 0$ and age $a > 0$.

$$u_t(a, t) + u_a(a, t) = -\mu(a)u(a, t) \tag{2.19}$$

Hence, the total number of individuals in the population between the ages of a_1 and a_2, at time t is given by:

$$\int_{a_1}^{a_2} u(a,t)da \tag{2.20}$$

and

$$P(t) = \int_0^{\infty} u(a,t)da \quad , t > 0 \tag{2.21}$$

is the total population at a specific point in time. Furthermore, $\mu(a)$ is a non-negative age-dependant function referred to as the *'age-specific mortality modulus'* [27] and hence the number of individuals leaving the population due to death is given by $\mu(a)u(a,t)$. Moreover, the number of individuals entering the population at age 0 (i.e. birth process) satisfies the integral equation

$$u(0,t) = \int_0^{\infty} \beta(a)u(a,t)da \ , \quad t > 0 \tag{2.22}$$

where $\beta(a)$ is a non-negative, age-dependant function referred to as the *'age specific fertility modulus'* [27]. Equation (2.22) is the non-local boundary condition for the model [1]. Lastly,

$$u(a,0) = u_0(a), \quad a \geq 0 \tag{2.23}$$

is the initial age distribution of the population, where $u_0(a)$ is a non-negative function of age. Observe that it is not necessary for the boundary condition (2.22) to be satisfied at $t = 0$. However, if (2.22) holds at $t = 0$ then, it is required that the compatibility condition

$$\int_0^{\infty} \beta(a)u_0(a)da = u_0(0) \tag{2.24}$$

is met. Equation (2.19) was used by Von Förster in 1959 to model the dynamics of cell populations. It is realistic to assume that there exist situations where conditions within a population are not conducive to survival (i.e. high death rate and low fertility rate) which are attained when the population size reaches a certain threshold value[1]. However, since the functions governing vital dynamics in the McKendrick-von Förster model do not depend on the total population, such situations cannot be reproduced mathematically by this model. In order to counter this problem, in 1974 Gurtin and MacCamy [10] and Hoppensteadt [12] formulated the first non-linear continuous age-structured models.

2.4.2 Non-linear structured models

Gurtin-MacCamy Model

In 1974 Gurtin and MacCamy [10] proposed the first continuous time non-linear age-structured models where the vital processes were non-linear functions of the total

population $P(t)$. The model consists of the following non-linear partial differerential equation where the age-specific mortality modulus $\mu(a, P(t))$ is non-negative.

$$u_t(a,t) + u_a(a,t) = -\mu(a, P(t))u(a,t), \quad a > 0, \ t > 0 \tag{2.25}$$

The renewal equation plays the role of a non-local boundary condition with non-negative age-specific fertility modulus $\alpha(a, P(t))$.

$$u(t,0) = \int_0^\infty \alpha(a, P(t))u(a,t)da \quad t > 0 \tag{2.26}$$

Lastly, after taking the initial state of the population (given by (2.23)) into account, the age-density function is determined. Gurtin and MacCamy also carried out a theoretical study of this model and provide existence, uniqueness and stability results which further emphasize the abundance in dynamics of non-linear models in comparison to their linear counterparts.

We will now briefly outline the approach used in [10] to show existence of a unique solution. Consider,

$$\frac{\partial u}{\partial t} + \frac{\partial u}{\partial x} + \mu(a,P)u = 0, \quad a > 0, 0 < t < T \tag{2.27}$$

$$u(0,t) = \int_0^\infty \alpha(a,P)u(a,t)da, \quad 0 < t \leq T \tag{2.28}$$

$$u(a,0) = \phi(a), \quad a \geq 0 \tag{2.29}$$

where,

$$P(t) = \int_0^\infty u(a,t)da. \tag{2.30}$$

As in [10], we will commence by reducing problem (2.27)-(2.29) into non-linear functional equations for $P(t)$ (total population) and $B(t) = u(0,t)$ (birth rate).

Observe that equations (2.27)-(2.29) will only be physically meaningful in the context of modelling a population if $\alpha(a,P)$, $\mu(a,P)$ as well as the initial condition $\phi(a)$ are non-negative. in order to ensure that the initial total population is finite, it is assumed that $\phi \in L_1(\mathbb{R}^+)$, where L_1 is as defined below.

Definition 2.4.1. *L_1 Space: The L_1 space is a functional space where each element is Lebesque integrable [15].*

$$\|f\|_1 = \int_{\mathbb{R}^+} |f(t)|. \tag{2.31}$$

A solution for (2.27)-(2.29) is defined up to some arbitrary time $T > 0$ as a non-negative function u on $\mathbb{R}^+ \times [0,T]$ such that:

(*i*) the terms $\frac{\partial u}{\partial t}$ and $\frac{\partial u}{\partial x}$ exist on $\mathbb{R}^+ \times [0,T]$,

(*ii*) $u(.,t) \in L_1(\mathbb{R}^+)$,

(*iii*) (2.30) is continuous for all $0 \leq t \leq T$,

(*iv*) (2.27)-(2.29) are satisfied.

Now, let $(a_0, t_0) \in \mathbb{R}^+ \times [0,T]$ and suppose that

$$\bar{u}(h) = u(a_0 + h, t_0 + h), \quad \bar{\mu}(h) = \mu(a_0 + h, t_0 + h).$$

This allows us to rewrite (2.27) as

$$\frac{d\bar{u}}{dh} + \bar{\mu}(h)\bar{u} = 0. \tag{2.32}$$

Through separation of variables, (2.32) has a unique solution in the form,

$$\bar{u}(h) = \bar{u}(0)e^{-\int_0^h \bar{\mu}(\xi)d\xi}.$$

That is,

$$u(a_0 + h, t_0 + h) = u(a_0, t_0)e^{-\int_0^h \bar{\mu}(\xi)d\xi}. \tag{2.33}$$

This allows us to determine the values of the solution u at all points along the characteristic starting at (a_0, t_0), in terms of the value of u at (a_0, t_0). Without loss of generality, setting $(a_0, t_0) = (a - t, 0)$, $h = t$ and substituting into (2.29) yields,

$$u(a,t) = \phi(a-t)e^{-\int_0^t \mu(a-t+\tau, P(\tau))d\tau} \quad for \quad a \geq t. \tag{2.34}$$

Similarly, setting $(a_0, t_0) = (0, t - a)$, $h = a$ and substituting into (2.33) yields,

$$u(a,t) = B(t-a)e^{-\int_0^a \mu(k, P(t-a+k))dk} \quad for \quad t < a. \tag{2.35}$$

Therefore, substituting (2.34) and (2.35) into (2.29) and (2.28), respectively, we obtain

$$P(t) = \int_0^\infty u(a,t)da = \begin{cases} \int_0^\infty B(t-a)e^{-\int_0^a \mu(k,P(t-a+k))dk}da & for \quad a < t, \\ \int_0^\infty \phi(a-t)e^{-\int_0^t \mu(a-t+\tau,P(\tau))d\tau}da & for \quad a \geq t, \end{cases}$$

and

$$B(t) = \int_0^\infty u(a,t)da = \begin{cases} \int_0^\infty \alpha(a,P(t))B(t-a)e^{-\int_0^a \mu(k,P(t-a+k))dk}da & for \quad a < t, \\ \int_0^\infty \alpha(a,P(t))\phi(a-t)e^{-\int_0^t \mu(a-t+\tau,P(\tau))d\tau}da & for \quad a \geq t. \end{cases}$$

Now,

$$\begin{aligned} P(t) &= \int_0^t B(a)F(t-a,t;P)da + \int_0^\infty \phi(a)G(a,t;P)da \\ B(t) &= \int_0^t \alpha(t-a,P(t))B(a)F(t-a,t;P)da \\ &\quad + \int_0^\infty \alpha(t+a,P(t))\phi(a)G(a,t;P)da \end{aligned}$$

where

$$F(k,t;P) = e^{-\int_{t-k}^{t}\mu(k+\tau-t,P(\tau))d\tau}$$
$$G(k,t;P) = e^{-\int_{0}^{t}\mu(k+\tau,P(\tau))d\tau} \; for \; 0 \leq k \leq t.$$

Existence is then established in [10] within the time interval $[0,T]$ resulting in the following theorem.

Theorem 2.4.2. *There exists a $T > 0$ such that the population problem has a unique solution up to time T.*

It is also proven that if the fertility modulus α is uniformly bounded, then the existence and uniqueness result can be extended to include all possible values of t.

Theorem 2.4.3. *Assume that*

$$\alpha = \sup_{a\geq 0, P\geq 0} \alpha(a,P) < \infty \tag{2.36}$$

holds. Then the population problem has a unique solution for all time.

Lastly global existence is established in the following theorem.

Theorem 2.4.4. *Assume that $\phi \in C^1(\mathbb{R}^+)$ with $\dot{\phi} \in L_1(\mathbb{R}^+)$. Additionally, assume that $\mu, \alpha \in C^1(\mathbb{R}^+ \times \mathbb{R}^+)$ and that the mappings carrying (t,P) into the functions $a \to \alpha_a(a+t,P)$ and $a \to \alpha_p(a+t,P)$ belong to $C^1(\mathbb{R}^+ \times \mathbb{R}^+ : L_\infty(\mathbb{R}^+))$. Let ρ be a solution of the population problem upto time T. Then $\rho \in C^1(\mathbb{R}^+ \times [0,T])$ if and only if ϕ satisfies the compatibility conditions*

$$\phi(0) = \int_0^\infty \alpha(a,\psi)\phi(a)da$$

and

$$\dot{\phi(0)} = [\mu(0,\psi) - \alpha(0,\psi)]\phi(0) \quad - \int_0^\infty [\alpha_a(a,\psi) + \alpha_p(a,\psi)\dot{\psi} - \alpha(a,\psi)\mu(a,\psi)]\phi(a)da$$

where

$$\dot{\psi} = \phi(0) - \int_0^\infty \mu(a,\psi)\phi(a)da, \quad \psi = \int_0^\infty \phi(a)da.$$

In our case the compatibility condition above is not enforced, hence an alternative theorem is proposed for existence.

Hoppenstead Model

Frank Hoppenstead developed an age-structured population model where the population on which the infectious disease is acting is partitioned into four non-overlapping compartments [12], namely: (S) susceptibles, (Q) quarentined infectives, (I) infectives, (R) recovered. The distinguishing feature of this model is that together with an individuals chronological age a, the amount of time an individual has spent in a specific compartment is tracked for each of the four compartments is tracked. Hoppensteadt refers to this variable as the 'class age' c of the compartment. Essentially this variable describes an individuals current epidemiological state. The resulting model is given by the following set of non-linear structured partial differential equations,

$$\begin{cases} \frac{\partial S}{\partial t} + \frac{\partial S}{\partial a} + \frac{\partial S}{\partial c} = m(a,c,t) - S(a,c,t)\int_0^\infty \int_0^\sigma r(a,c,t,a',c')I(a',c',t)dc'da' \\ \frac{\partial I}{\partial t} + \frac{\partial I}{\partial a} + \frac{\partial I}{\partial c} = -[q(a,c,t) + \Delta(a,c,t)]I \\ \frac{\partial Q}{\partial t} + \frac{\partial Q}{\partial a} + \frac{\partial Q}{\partial c} = q(a,c,t)I \\ \frac{\partial R}{\partial t} + \frac{\partial R}{\partial a} + \frac{\partial R}{\partial c} = 0 \end{cases} \tag{2.37}$$

with initial age distribution,

$$\begin{cases} S(a,c,0) = S_0(a,c), \quad I(a,c,0) = I_0(a,c), \\ Q(a,c,0) = Q_0(a,c), \quad R(a,c,0) = R_0(a,c), t > 0. \end{cases} \tag{2.38}$$

and boundary conditions,

$$\begin{cases} S(0,0,t) = \int_0^\infty \int_0^\infty [\beta_1(a,c,t)S(a,c,t) + \beta_2(a,c,t)I(a,c,t) \\ \qquad + \beta_3(a,c,t)Q(a,c,t) + \beta_4(a,c,t)R(a,c,t)]dadc \\ I(0,0,t) = Q(0,0,t) = R(0,0,t) = 0, \ t > 0. \end{cases} \tag{2.39}$$

This model assumes that all newly born individuals are susceptible to the disease and hence enter into S. Each group S, I, Q, R has known reproductive measures denoted by β_i, $i = 1,2,3,4$, which then contribute to the birth rate in the susceptible compartment. Furthermore, migration into S occurs at a rate of m. Q is a subclass of the group of infectives and the rate at which individuals are quarantined is given by q. Moreover, individuals who are infective may die at rate Δ. Individuals may remain infective for a fixed period of time σ, after which they are immune to the disease permanently. The rate at which individuals become immune (transition from I to R) is given by $I(a,\sigma,t) + Q(a,\sigma,t)$.

The term

$$S(a,c,t)\int_0^\infty \int_0^\sigma r(a,c,t,a',c')I(a',c',t)dc'da' \tag{2.40}$$

in (2.37) describes the rate at which susceptible individuals exit the compartment S and become infective (enter I) due to mixing with other infective individuals in

the population. This is akin to the law of mass action, where r is the sufficient rate of contact between susceptible organisms of age (a, c) and the infective organisms of age (a', c'), required to cause the transition from S to I. Observe that in this instance 'age' is interpreted as the pair of variables for class age and chronological age.

In order to ensure that individuals do not reach age older than their chronological age, an additional condition is introduced.

$$S(0, c, t) = I(0, c, t) = Q(0, c, t) = R(0, c, t) = 0 \tag{2.41}$$

Hoppensteadt concludes that despite being a very general model it is also difficult and impractical since the tracking of class ages of susceptibles and recovereds may not be necessary. Furthermore, in practice it observing the dependence of the population on class age might not be possible and hence reducing the dependence of variables r, Δ, q and β_i (for $i = 1, 2, 3, 4$) to time and chronological age.

Other significant structured models

It should be noted that the models considered thus far have provided a foundation for problems in various areas of study. For example, in 1975 Hoppensteadt[13] proposed a population model with gender differentiation, Busenberg et al [7] modelled situations in epidemiology, Venturino [26] formulated models that capture interactions between many species such as predators and prey and parasitism and Langlais [18] studied models with space diffusion.

In this research project, we consider non-linear continuous time models with age and epidemiological state structure, that were formulated using approaches similar to that of Gurtin and MacCamy and Hoppensteadt. This is done with the objective of developing structured models for vector-borne diseases such as ASFV. Instead of tracking class ages of susceptibles and recovereds as in [12], we will construct models where only the class age of infectives is tracked. In other words,the infectives will be structured with respect to their current epidemiological state.

2.5 Impulsive Differential Equations

There exist evolutionary processes with dynamics characterized by the occurrence of sudden and short-lived perturbations at specific moments in time. These perturbations are brief in duration in comparison to the duration of the process itself. Therefore it may be assumed that they occur instantaneously and hence are referred to as 'impulses'. Mathematically this causes certain model parameters to remain

smooth in variation for prolonged periods of time, followed by rapid short-term changes in values. These abrupt changes can take on the form of harvesting, natural disasters, shocks etc.

Consider an arbitrary evolution process described by the following:

(i) a system of differential equations

$$\frac{d}{dt} = f(x,t) \tag{2.42}$$

where $f : \mathbb{R}_+ \times \Omega \to \mathbb{R}^p$, and $\Omega \subset \mathbb{R}^p$ is an open set.

(ii) operator $A(t) : M(t) \to N(t)$ where $M(t),\ N(t) \subset \Omega$, for all $t \in \mathbb{R}_+$.

Suppose that $x(t) = x(t, t_0, x_0)$ is a solution for (2.42) with starting point (t_0, x_0). Moments of impulsive effect are denoted by τ_k and can be chosen in numerous ways to suit practical purposes.

The process defined by the system of impulsive differential equations $(i) - (ii)$ behaves as follows: the point denoted by $P_t = (t, x(t))$ commences its motion at point (t_0, x_0) and travels along the curve $\{(t, x) : t \geq t_0,\ x = x(t)\}$ until time $\tau_1 > t_0$ when P_t encounters set $M(t)$. At time $t = \tau_1$ operator $A(t)$ maps $P_{\tau_1} = (\tau_1, x(\tau_1))$ to the point $P_{\tau_1^+} = (\tau_1, x_1^+)$ on set $N(\tau_1)$, where $x_1^+ = A(\tau_1)x(\tau_1)$. $P(t)$ continues travelling along the curve with $x(t) = (t, \tau_1, x_1^+)$ as the solution to (2.42) with starting point P_{τ_1}, until the set $M(t)$ is met at the next instant $\tau_2 > \tau_1$. Once again, $P_{\tau_2} = (\tau_2, x(\tau_2))$ is shifted to the point $P_{\tau_2^+} = (\tau_2, x_2^+) \in N(\tau_2)$, where $x_2^+ = A(\tau_2)x(\tau_2)$ and P_t continues its trajectory along the curve with $x(t) = (t, \tau_2, x_2^+)$ as the solution to (2.42) with starting point P_{τ_2}. The evolution process continues thus for as long as the solution of (2.42) exists.

The curve described by the point P_t is referred to as the integral curve. The solutions $x(t)$ of the impulsive differential system are assumed to be **left continuous** at the moments of impulsive effect $\tau_k,\ k = 1, 2, \ldots$. That is,

$$x(\tau_k^-) = \lim_{h \to 0^+} x(\tau_k - h) = x(\tau_k). \tag{2.43}$$

The theory of impulsive differential equations has been explored extensively in many literature sources (see[4] and [17]) and hence the existence and uniqueness of these equations will not be discussed in this dissertation. τ_k can be chosen in various ways, some of which are discussed here.

1. *Fixed moments of impulsive effect*
These equations are of the following form:

$$\begin{cases} \frac{dx}{dt} &= f(x,t),\ t \neq \tau_k \\ \Delta x &= I_k,\ t = \tau_k. \end{cases} \tag{2.44}$$

Define a sequence $\tau_k : \tau_k < \tau_{k+1},\ k \in B \subset \mathbb{Z}$. Clearly, when $t \in (\tau_k, \tau_{k+1}]$, the solution $x(t)$ of (2.44) satisfies $\frac{dx}{dt} = f(x,t)$, while at the moment of impulsive effect $t = \tau_k$, $x(t)$ satisfies $x(\tau_k^+) = \psi_k(x(\tau_k)) = x(\tau_k) + I_k(x(\tau_k))$.

2. *Unfixed moments of impulsive effect*
Equations belonging to this class are written as follows:

$$\begin{cases} \frac{dx}{dt} &= f(x,t),\ t \neq \tau_k \\ \Delta x &= I_k(x),\ t = \tau_k. \end{cases} \tag{2.45}$$

where $\tau_k : \Omega \to \mathbb{R},\ \tau_k(x) < \tau_{k+1}(x),\ k \in B \subset \mathbb{Z},\ x \in \Omega$. In this case moments of impulsive effect occur when (x,t) touches an arbitrary set of hypersurfaces denoted by σ_k, when $t = \tau_k(x(t))$ for some $k \in B$.

3. *Autonomous impulsive equations*
Let $\sigma \in \Omega \subset \mathbb{R}^n$ be an $(n-1)$ dimensional manifold. Autonomous impulsive equations are written as follows.

$$\begin{cases} \frac{dx}{dt} &= f(x),\ x \neq \sigma \\ \Delta x &= I(x),\ x \in \sigma \end{cases} \tag{2.46}$$

The instances of impulsive effect can be characterised by the moments when the point $x(t) \in \Omega$ meets σ.

4. *Random moments of impulsive effect*
Instantaneous changes at moments that cannot be predetermined occur in many real world processes [2]. In order to model these random changes, probability laws are utilised to determine moments of impulsive effect. In such cases, random variables must be incorporated into jump conditions and impulsive differential equations occurring at random moments.

Consider the probability space $(\Omega, \mathcal{F}, P)$ and define a sequence of random variables, $\{\eta_k\}_{k=1}^{\infty}$. Let $\{\xi_k(\omega)\}_{k=0}^{\infty}$ be an increasing sequence of random variables where $\xi_k = T_0 + \Sigma_{i=1}^{k}\eta_i,\ k = 1,2,3,\ldots,\ \xi_0 = T_0$ and T_0 is a positive fixed point. η_k denotes the time between the occurrence of two consecutive impulses and it is assumed that $\sum_{k=1}^{\infty}\eta_k = \infty$ with probability 1. Suppose that $t \geq T_0$ is a fixed point and the events $S_k(t)$ for $k = 1,2\ldots$ are defined as follows [2],

$$S_k(t) = \{\omega \in \Omega : \xi_k(\omega) < t < \xi_{k+1}(\omega)\}.$$

For each fixed $k = 1, 2, \ldots$ the points t_k denote random values of η_k. In the same manner, the points $T_k = \sum_{i=0}^{k} \eta_i, k = 1, 2, \ldots$ denote the values of ξ_k . This then yields the following initial value problem for the scalar impulsive differential equation with fixed points of impulses,

$$\begin{cases} \frac{dx}{dt} & = & f(t, x(t)) \quad for\ t \geq T_0,\ T_k < t < T_{k+1}, \\ x(T_k + 0) & = & I_k(\eta_k, x(T_k - 0)) \quad for\ k = 1, 2, \ldots, \\ x(T_0) = x_0 & & \end{cases} \tag{2.47}$$

where $x \in \mathbb{R}^p,\ f : [0, \infty) \times \mathbb{R}^p \to \mathbb{R}^p$ and $x_0 \in \mathbb{R}^p$.

The solution of (2.47), denoted by $x(t; T_0, x_0, \{t_k\})$, is dependant on the initially chosen random values t_k for $\eta_k,\ k = 1, 2, \ldots$. It is assumed that $x(T_k; T_0, x_0, \{t_k\}) = \lim_{t \to T_k{}^{-0}} x(t; T_0, x_0, \{t_k\})$. Now, $x(t; T_0, x_0, \{t_k\})$ generates a stochastic process in $\mathbb{R}^p$ for any arbitrary values t_k for $\eta_k, k = 1, 2, \ldots$ and is a solution to the following impulsive differential equation with impulses at random moments.

$$\begin{cases} \frac{dx}{dt} & = & f(t, x(t)) \quad for\ t \geq \eta_0,\ \eta_k < t < \eta_{k+1}, \\ x(\eta_k + 0) & = & I_k(\eta_k, x(\eta_k - 0)) \quad for\ k = 1, 2, \ldots, \\ x(\eta_0) = x_0 & & \end{cases} \tag{2.48}$$

Solutions of impulsive differential equations are piecewise continuous functions where instances of impulsive effect create points of discontinuity. All solutions of (2.44) will share the same points of discontinuity since all impulses will occur at the same instance. However, solutions of (2.45) and (2.46) have varying points of discontinuity. This makes the analysis of such equations complex [4].

It is hypothesized in this research project that warthogs act as an amplifying factor of ASF in the tick population. That is, the event of a warthog family inhabiting a burrow is assumed to cause a spike in the number of infected ticks within the burrow due to the abrupt availability of blood meals. Furthermore, since it is known that the time spent by the warthogs in the burrow during farrowing season makes up a very short portion of a ticks lifespan, we can interpret this event as an impulse.

In order to simulate reality, ideally random moments of impulsive effect should be used. However, since the introduction of stochastic variables would complicate the model and would be more difficult to implement, this possibility was excluded. Instead, fixed instances of impulsive effect were imposed on the ASFV model.

Chapter 3

Population and epidemiological models with extinction in finite time

It is common in differential equation models that solutions approach a stable equilibrium without actually reaching it. In many situations this is not a problem since the solutions are treated as approximations. However, in instances when the equilibrium is zero, qualitatively unrealistic behaviour may be obtained. In Mathematical Epidemiology disease free states are typically represented as equilibria of dynamical systems which model the respective epidemiological process. In other words, asymptotic stability of disease free equilibria is interpreted as disease extinction. In the case of a complete dynamical system, the uniqueness property ensures that no two solutions of the initial value problem may meet. Hence a solution that tends towards the disease free equilibria and the steady state solution at 0 cannot meet which implies that disease extinction can never occur. Despite the fact that in constant conditions this may not be problematic, when epidemiological factors are varied this will lead to significant modelling errors. The time taken to eradicate a disease from a population is a significant factor that will assist in determining appropriate conservation strategies.

As an illustrative example, we consider the generalised logistic model given by,

$$\frac{dP}{dt} = rP^{1-\alpha}(P^{\alpha} - \lambda)(M - P) \qquad r > 0,\ M > 0,\ \alpha \in [0, 1],\ \lambda \in \mathbb{R} \tag{3.1}$$

The following observations can be made:

(*i*) If $\alpha = 0$ or $\lambda = 0$ equation (3.1) is a logistic model.

(*ii*) For large P equation (3.1) is an approximately logistic model

(*iii*) If $\lambda < 0$ equation (3.1) is an approximately logistic model

(*iv*) If $\alpha > 0$ and $\lambda > 0$, equation (3.1) has a second positive equilibrium representing Alee effect ($\hat{P} = \lambda^{\frac{1}{\alpha}}$). If $P(0) < \hat{P} \leq M$ extinction occurs in finite time.

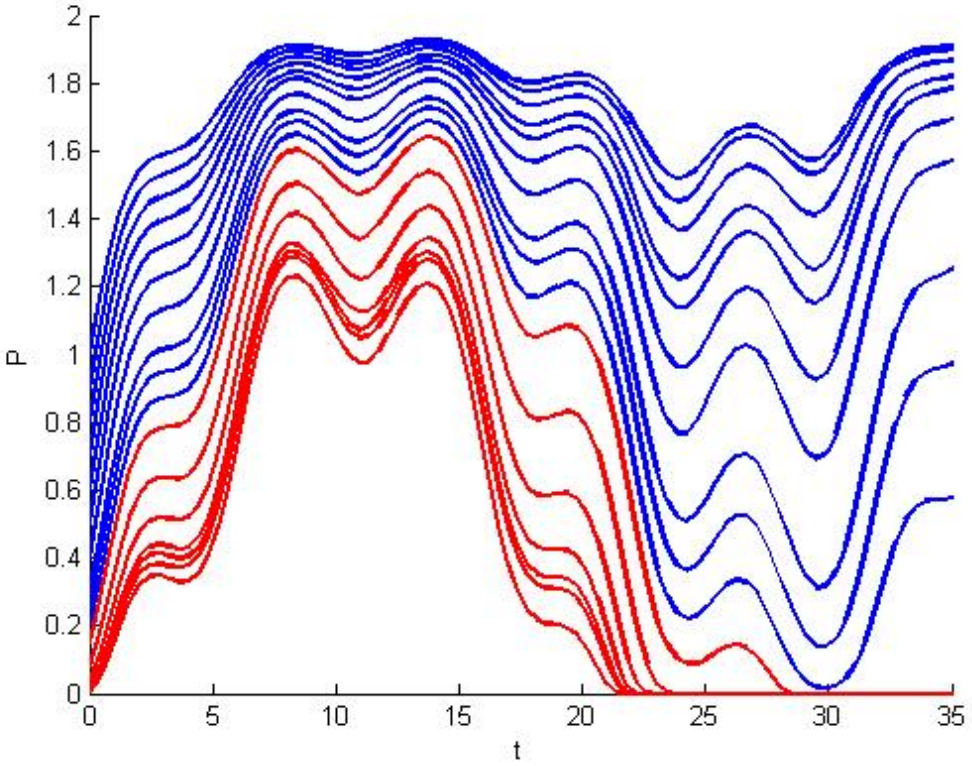


Figure 3.1: General logistic model

Zero is an attractive equilibrium when $\lambda > 0$ or a repelling equilibrium when $\lambda < 0$. We will consider (3.1) when λ is a function of t given by

$$\lambda(t) = 0.6 - 2\cos(t) - 2\cos(t/6).$$

Due to properties (*iii*) and (*iv*), given that λ remains positive long enough, the population becomes extinct and will remain extinct irrespective of any future changes of λ. This phenomenon is clearly illustrated in Figure 3.1 for the parameters $M = 2,\ r = 0.1,\ \alpha = 0.5$. Observe the solution trajectories indicated in red where extinction occurs in finite time. The trajectories indicated in blue tend towards the non-zero equilibrium $M = 2$ due to property (*ii*) above.

Remark
It is clear that $P \equiv 0$ is a solution of (3.1). Then, it follows from (*iv*) that in general

the solution of (3.1) is not unique. However, we can prove forward uniqueness thus showing that (3.1) defines a positive dynamical system on $\mathbb{R}^+$. We apply Theorem 2.1.7 with f being the right hand aside of (3.1). It is easy to see that $f'(P)$ is bounded above on $(0, +\infty)$. Hence, f is one-sided Lipschitz. Then the forward uniqueness follows from Theorem 2.1.7.

Our objective is to find favourable conditions that will persist for a sufficiently long period of time, so that extinction of a disease or host population can occur and the disease/host population will remain extinct even if the conditions change. In the following chapter ODE and PDE models with suitable conditions under which extinction can occur will be investigated. These include basic population models, state and age structured epidemiological models and models of vector borne diseases and these tools will be used to model the dynamics of ASFV and capture the situation in Mkuze Game Reserve where unexplained cases of extinction have been observed.

3.1 Basic population models

Consider models of the form

$$\frac{dN}{dt} = g(N).N \tag{3.2}$$

where N is the size of the population and g is a demographic function such that

$$g(N) \leq -cN^{-\alpha} \tag{3.3}$$

for $c > 0,\ \alpha > 0,\ \epsilon > 0$ and $0 < N < \epsilon$.

Theorem 3.1.1. *If a solution of* (3.2) *satisfying* (3.3) *is such that* $\lim_{t\to\infty} N(t) = 0$ *then there exist* t^* *such that* $N(t) = 0$ *for* $t \geq t^*$.

Proof. Let N be a non-repetitive solution of (3.2) such that $\lim_{t\to\infty} N(t) = 0$. Hence, there exists $t = t_1$ such that $N(t_1) < \epsilon$. Since $g(N) < 0$ for $N < \epsilon$ we have $N(t) < \epsilon$ for $t > t_1$. Hence, N satisfies

$$\frac{dN}{dt} = g(N) \leq -cN^{-\alpha} \quad for \quad t > t_1$$

Consider

$$\frac{dy}{dt} = -cy^{-\alpha}$$

Solving for y using separation of variables, we obtain

$$y(t) = [(K - ct)(1 - \alpha)]^{\frac{-1}{1-\alpha}} \quad , K \in R$$

Now $y(t) \leq 0 \iff K \leq ct$, i.e. $\frac{K}{c} \leq t$. Hence, $y(t) = 0 \iff t \geq t^* \quad for \quad t^* = \frac{K}{c}$. Since $0 \leq N(t) \leq y(t)$, it then follows that $N(t) = 0$ for $t \geq t^*$. □

This result implies that under assumption (3.3), if the population decreases to 0 eventually, then it reaches 0 in some finite time. The following example illustrates this result for a specific choice of function g.

Example

For $0 < \theta < 1$, $0 < \beta < 1$ and $0 < m < M$ consider

$$g(N) = \left(1 - \left(\frac{N}{M}\right)^{\beta}\right)\left(1 - \left(\frac{N}{m}\right)^{-\theta}\right) \tag{3.4}$$

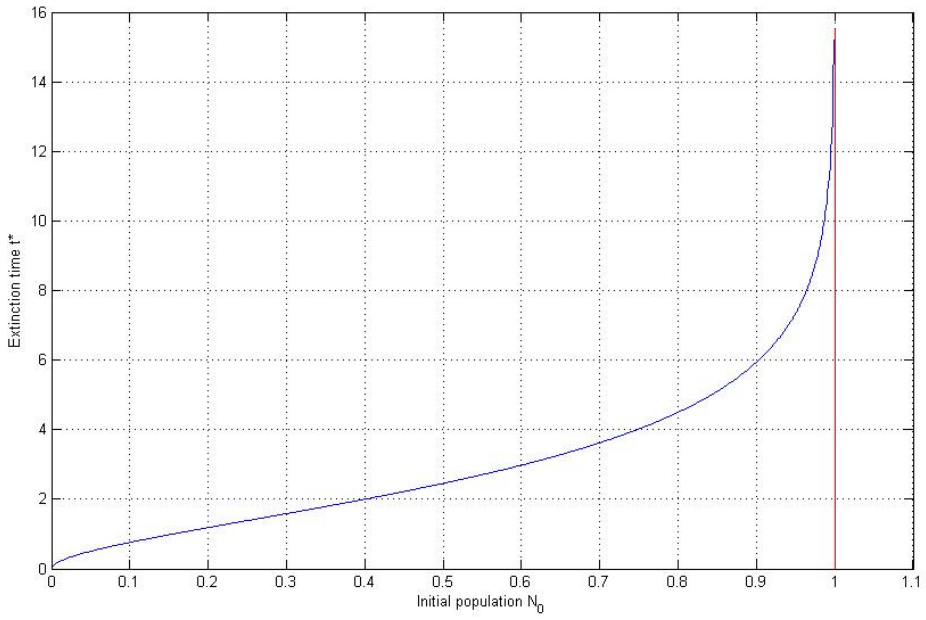


Figure 3.2: The relationship between extinction times t^* and N_0

The first factor models overcrowding with M being the carrying capacity. The second factor represents a strong Allee effect with minimum survival level m. Clearly, g satisfies the assumption (3.3). Therefore, all solutions with $N(0) < M$ equal zero in finite time.

Observe that $f(N) = g(N).N$ (where g is (3.4))and

$$\begin{aligned} f'(N) &= \left(1-\left(\frac{N}{M}\right)^{\beta}\right)\left(1-\left(\frac{N}{m}\right)^{-\theta}\right) + N\left(-\beta\left(\frac{N}{M}\right)^{\beta-1}\frac{1}{M}\right)\left(1-\left(\frac{N}{m}\right)^{-\theta}\right) \\ &\quad + \frac{N\theta}{m}\left(1-\left(\frac{N}{M}\right)^{\beta}\right)\left(\frac{N}{m}\right)^{-\theta-1} \\ &= \left(1-\left(\frac{N}{M}\right)^{\beta}\right)\left(1-\left(\frac{N}{m}\right)^{-\theta}\right) - \beta\left(\frac{N}{M}\right)^{\beta}\left(1-\left(\frac{N}{m}\right)^{-\theta}\right) \\ &\quad + \theta\left(\frac{N}{m}\right)^{-\theta}\left(1-\left(\frac{N}{M}\right)^{\beta}\right). \end{aligned}$$

Now,

$$\lim_{N\to 0} f'(N) = \lim_{N\to 0}\left(\frac{N}{m}\right)^{-\theta}\left[-1+\left(\frac{N}{M}\right)^{\beta}+\beta\frac{N}{M}^{\beta}+\theta-\theta\left(\frac{N}{M}\right)^{\beta}\right] = \infty.$$

Therefore, f' is locally bounded above on $[0,\infty)$ and hence the solution is forward unique by Corollary 2.2.10.

Figure 3.2 represents the relationship between extinction times t^* and N_0 for parameters $\theta = \beta = 0.5,\ m = 1,\ M = 2$. Additionally, observe that

$$\begin{aligned} g(N) &= \left(1-\left(\frac{N}{M}\right)^{\beta}\right)\left(1-\left(\frac{N}{m}\right)^{-\theta}\right) \\ &= -\left(\frac{N}{m}\right)^{-\theta}\left(1-\left(\frac{N}{M}\right)^{\beta}\right) + \left(1-\left(\frac{N}{M}\right)^{\beta}\right). \end{aligned}$$

Now,

$$g(N) \leq 1-\left(\frac{N}{m}\right)^{-\theta} = 1-\frac{1}{2}\left(\frac{N}{m}\right)^{-\theta}-\frac{1}{2}\left(\frac{N}{m}\right)^{-\theta}.$$

Let $N \leq m$. Then $\lim_{N\to 0} -\frac{1}{2}\left(\frac{N}{m}\right)^{-\theta} \to -\infty$. Therefore, there exists ϵ such that $-\frac{1}{2}\left(\frac{N}{m}\right)^{-\theta} < -1$. Hence, for $N < \epsilon$ we have, $1-\frac{1}{2}\left(\frac{N}{m}\right)^{-\theta} < 0$. Then for $0 < N < \epsilon$ we have

$$g(n) \leq -\frac{1}{2}\left(\frac{N}{m}\right)^{-\theta}.$$

Hence condition (3.3) holds and we have extinction in finite time. We will now extend this concept to epidemiological models that consist of systems of equations. In the next section, we will study the importance of utilising a nonstandard interaction term in order to construct a model where disease extinction occurs within finite time.

3.2 Significance of nonlinear force of infection

In epidemiological models the force of infection takes into account two factors that determine how a disease is transmitted: unique population behavioural patterns and the disease itself [9]. Standard force of infection which linearly depends on the number of individuals who have been infected is unrealistic when modelling certain diseases. In the paper by Capasso and Serio [8] it is suggested that a nonlinear, saturating force of infection is more appropriate, as it will accurately reflect the saturation phenomena for large numbers of infective individuals. To illustrate the relevance of using a nonlinear force of infection in order to ensure disease eradication, we begin by considering the classical SIR model.

The disease spreads with respect to the following system of differential equations:

$$\begin{cases} \frac{dS}{dt} = -\beta IS \\ \frac{dI}{dt} = \beta IS - \gamma I \\ \frac{dR}{dt} = \gamma I \end{cases} \tag{3.5}$$

with initial conditions

$$S(0) = S_0 > 0, \quad I(0) = I_0 > 0, \quad R(0) = 0 \tag{3.6}$$

such that $S_0 + I_0 = N$. That is, the sum of the initial number of individuals who are infected and the individuals who can contract the disease is equal to the total size of the population N. Furthermore, $\beta > 0$ denotes the rate at which the infection is transmitted, while $\gamma > 0$ denotes the rate of recovery. Kermack and McKendrick [8] derived a threshold theorem for (3.5), which states that all points along the S-axis (refer to Figure 3.3)are equilibrium points, where all points $S > \frac{\gamma}{\beta}$ are unstable and $S < \frac{\gamma}{\beta}$ are stable.

The theorem also states that if $S_0 < \frac{\gamma}{\beta}$, then $I(t)$ decreases to zero as t tends to positive infinity. Additionally number of susceptible individuals $S(t)$ is always a decreasing function of t and attains a limit $\lim_{t\to\infty} S(t) = S_\infty > 0$. This is clearly illustrated in Figure 3.3 where $\frac{\gamma}{\beta} = 0.3$. It is clear that this implies that the although the solution tends to 0 asymptotically, it does not actually reach $S = 0$ within finite time and so the disease is never fully eradicated from the population.

In order to counter this problem, following the approach in [8], model (3.5) can be extended as follows:

$$\begin{cases} \frac{dS}{dt} = -\beta g(I)S \\ \frac{dI}{dt} = \beta g(I)S - \gamma I, \quad t > 0 \\ \frac{dR}{dt} = \gamma I \end{cases} \tag{3.7}$$

where $g : \mathbb{R}^+ \to \mathbb{R}^+$ is a continuous, bounded function such that

(i) $g(x) \geq 0, \quad \forall x \in \mathbb{R}^+,$

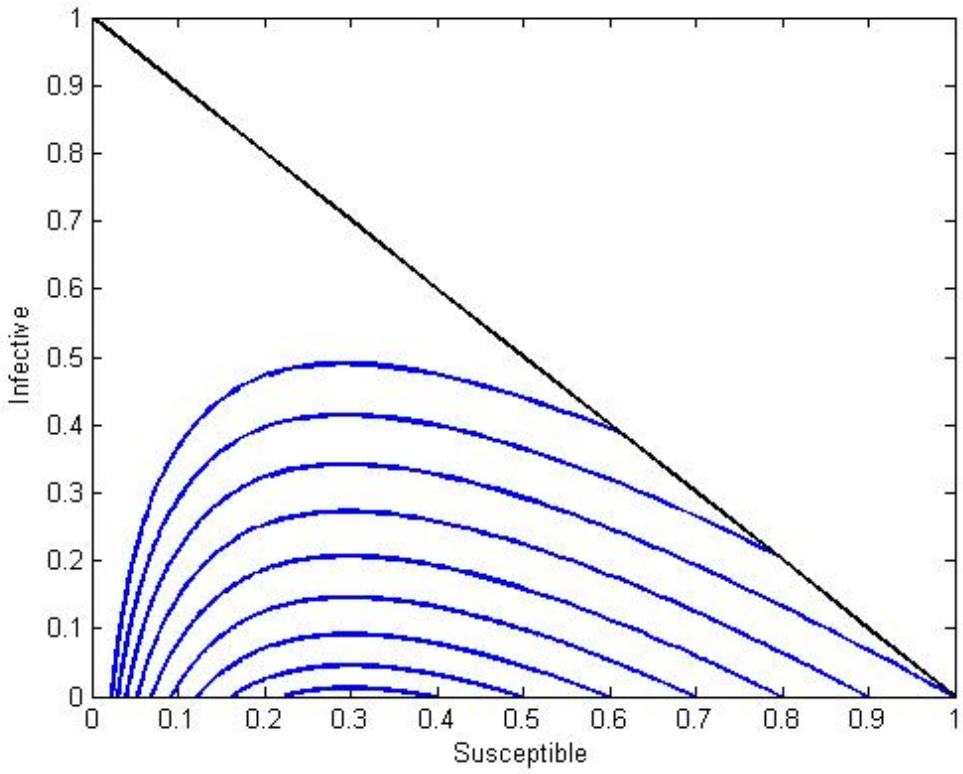


Figure 3.3: SIR epidemic model with nonlinear force of infection

(*ii*) $g(0) = 0$,

(*iii*) $g(x) \leq c, \quad \forall x \in \mathbb{R}^+$ where $c \in \mathbb{R}^+$,

(*iv*) the derivative of g exists and is bounded on any compact interval of $\mathbb{R}^+$ and $g'(0) > 0$,

(*v*) $g(x) \leq g'(0)x, \quad \forall x \in \mathbb{R}^+$.

Observe that the introduction of a nonlinear bounded function g alters the interaction term so that there is nonlinear dependence on the number of infective individuals. Additionally, for very large numbers of infectives, function g will tend to a "saturation level" C (refer to Figure 3.4). This ensures that the disease will not spread without a bound. In [9] the authors further expand this idea and propose a transmission rate of the form

$$g(I;t)S^r(t), \ r > 0. \tag{3.8}$$

Clearly, only when $r = 1$ can we refer to g as a force of infection.

In the following sections we will use similar nonstandard forces of infection in order to construct structured epidemiological models with finite time disease extinction.

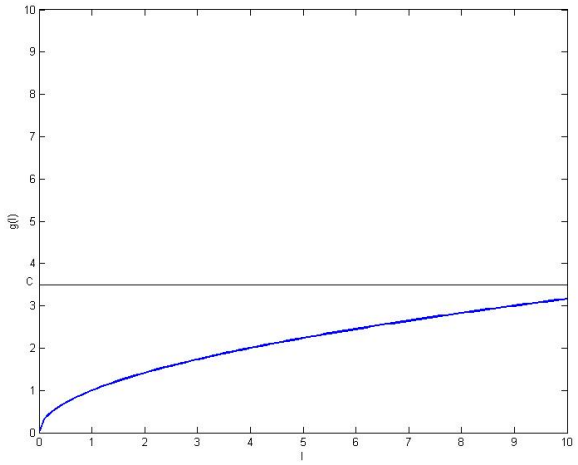


Figure 3.4: Example of an asymptotically saturating g

3.3 Structured population models with finite time extinction

3.3.1 State structured epidemiological models

Here we consider a classical epidemic SIR model with no vital dynamics, where the force of infection is βI^α and $\beta > 0,\ 0 < \alpha < 1$. The infectives are structured with respect to epidemiological state x (e.g. time since infection took place), where $x \in (0, \bar{x})$ and $\bar{x} < \infty$ is the state of transition to recovery.

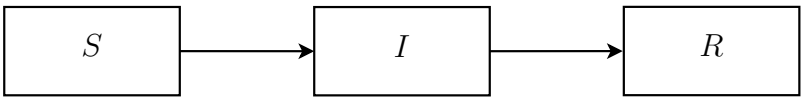
As in [8], the equation for recovered can be decoupled so that the model is as follows:

$$\begin{cases} \frac{dS(t)}{dt} = -\beta I^\alpha S(t) \\ \frac{\partial J(t,x)}{\partial t} + \frac{\partial J(t,x)}{\partial x} = 0 \\ J(t,0) = \beta I^\alpha(t) S(t) \\ \frac{dR(t)}{dt} = J(t,\bar{x}) \end{cases} \tag{3.9}$$

where,

$$I(t) = \int_0^{\bar{x}} J(t,x)dx$$

- S: Susceptibles at time t.
- J: Density of the distribution of infectives at time t over the epidemiological state x .
- I: Number of infectives at time t.



Theorem 3.3.1. *If a solution of the model* (3.9) *is such that*

$$I'(t) \leq -cI(t), \quad t \geq \hat{t} \tag{3.10}$$

for some $c > 0$ *and* $\hat{t} > 0$*, then there exists* t^* *such that* $I(t) = 0$ *for* $t > t^*$.

Proof. We have

$$\begin{aligned}
\frac{dI(t)}{dt} &= \int_0^{\bar{x}} J_t(t,x)dx \\
&= \int_0^{\bar{x}} -J_x(t,x)dx \\
&= J(t,0) - J(t,\bar{x}) \\
&= \beta I(t)^\alpha S(t) - J(t-\bar{x},0) \\
&= I(t)^\alpha \phi(t),
\end{aligned}$$

where

$$\phi(t) = \beta \left\{ S(t) - \frac{I(t-\bar{x})^\alpha S(t-\bar{x})}{I(t)^\alpha} \right\}.$$

We must show that there exists $k > 0$ such that

$$\phi(t) \leq -k$$

for all sufficiently large t. For $t > \hat{t} + \bar{x}$ we have

$$\frac{I(t-\bar{x})^\alpha}{I(t)^\alpha} \geq \frac{I(t-\bar{x})^\alpha}{I(t-\bar{x})^\alpha \exp^{-\alpha c\bar{x}}} = e^{\alpha c\bar{x}}$$

Therefore,

$$\phi(t) \leq \beta \left\{ S(t) - e^{\alpha c\bar{x}} S(t-\bar{x}) \right\}$$

Hence,

$$\limsup_{t\to\infty} \phi(t) \leq \beta \left\{ S_\infty - S_\infty e^{\alpha r\bar{x}} \right\} = -(e^{\alpha r\bar{x}} - 1)S_\infty \beta$$

Let $k = \frac{\beta}{2}(\exp^{\alpha r\bar{x}} - 1)S_\infty > 0$, so that $\limsup_{t\to\infty} \phi(t) \leq -2k < -k$. Then there exists $t_1 > \hat{t} + \hat{x}$ such that $\phi(t) < -k$ for $t > t_1$. Now $I(t)$ satisfies

$$\frac{dI(t)}{dt} \leq -kI(t)^\alpha, \ t > t_1.$$

Therefore $I(t) \leq y(t)$ for $t \geq t_1$, where $y(t)$ satisfies the following

$$\frac{dy(t)}{dt} = -ky(t)^\alpha \quad \textit{and} \quad y(t_2) = I(t_2)$$

By separation of variables,

$$y(t) = \begin{cases} \{(C-kt)(1-\alpha)\}^{\frac{1}{1-\alpha}} & for\ t \leq \frac{C}{k}, \\ 0 \quad for\ t \geq \frac{C}{k} \end{cases}$$

where

$$C = \frac{I(t_2)^{1-\alpha}}{1-\alpha} + kt_2.$$

Therefore, since $0 \leq I(t) \leq y(t)$, we have $I(t) = 0$ when $t \geq t^* = \frac{C}{k}$. □

Remark
Condition (3.10) stipulates that the number of infectives must tend to 0 atleast exponentially in order to ensure finite time extinction.

3.3.2 Age structured epidemiological models

Here we consider an SI endemic model, with vital dynamics, where the force of infection is βI^α and $\beta > 0,\ 0 < \alpha < 1$. Individuals are distinguished by age a, where $a \in (0, \bar{a})$ and $\bar{a} < \infty$ is the maximum age. In this model individuals cannot attain an age higher than $\bar{a}$.

$$\begin{cases} \frac{\partial S(t,a)}{\partial t} + \frac{\partial S(t,a)}{\partial a} = -\beta I(t) S(t,a) - \mu S(t,a), \\ \frac{\partial J(t,a)}{\partial t} + \frac{\partial J(t,a)}{\partial a} = \beta I(t) S(t,a) - \mu J(t,a) - \delta(I) J(t,a), \\ J(t,0) = 0, \\ S(t,0) = \Lambda, \end{cases} \tag{3.11}$$

where

$$I(t) = \int_0^{\bar{a}} J(t,a)da$$

and

$$\delta(I) = \delta_1 + \delta_2 I(t)^{-\alpha}, \quad \alpha \in (0,1).$$

- $\underline{a}$: Age of reproductive maturity.
- S: Density of the distribution of susceptible vectors at time t over age a.
- J: Density of the distribution of infective vectors at time t over age a.
- I: Number of infectives at time t.
- δ_1, δ_2: Disease induced death rates.
- β: Birth rate.

- μ: Natural death rate.
- Λ: Recruitment function.

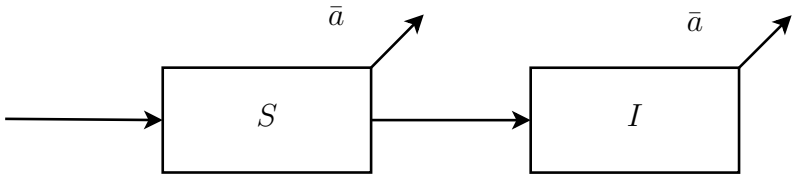


Figure 3.5: Diagram of dynamics for an age structured epidemiological model

Theorem 3.3.2. *If a solution of the model* (3.11) *is such that* $\lim_{t\to\infty} I(t) = 0$ *then there exists* t^* *such that* $I(t) = 0$ *for* $t > t^*$.

Proof. Consider

$$\begin{aligned}
\frac{dI(t)}{dt} &= \int_0^{\bar{a}} J_t(t,a)dt \\
&= \int_0^{\bar{a}} -J_a(t,a) + \beta I(t)S(t,a) - \mu J(t,a) - \delta(I)J(t,a)da \\
&= J(t,0) - J(t,\bar{a}) + \beta I(t)\int_0^{\bar{a}} S(t,a)da - \int_0^{\bar{a}} J(t,a)da\left(\mu + \delta_1 + \delta_2 I^{-\alpha}(t)\right) \\
&\leq \beta I(t)\int_0^{\bar{a}} S(t,a)da - I(t)\left(\mu + \delta_1 + \delta_2 I^{-\alpha}(t)\right)
\end{aligned}$$

Observe that,

$$\frac{\partial S(t,a)}{\partial t} + \frac{\partial S(t,a)}{\partial a} \leq -\mu S(t,a)$$

Hence,

$$\frac{d}{dt}\left\{\int_0^{\bar{a}} S(t,a)da\right\} \leq \Lambda - \mu\int_0^{\bar{a}} S(t,a)da \tag{3.12}$$

Letting $y(t) = \int_0^{\bar{a}} S(t,a)da$ and assuming equality in (3.12), we need only solve the initial value problem given by

$$\begin{aligned}
\frac{dy(t)}{dt} &= \Lambda - \mu y(t) \\
y(0) &= y_0
\end{aligned}$$

using the integrating factor method:

$$\begin{aligned} e^{\mu t}\frac{dy(t)}{dt} + \mu e^{\mu t}y(t) &= \Lambda e^{\mu t} \\ \frac{d}{dt}\left(e^{\mu t}y(t)\right) &= \Lambda e^{\mu t} \\ e^{\mu t}y(t) - y_0 &= \frac{\Lambda}{\mu}\left(e^{\mu t}y(t) - 1\right) \\ y(t) = y_0 e^{-\mu t}y(t) + \frac{\Lambda}{\mu}\left(1 - e^{-\mu t}y(t)\right) & \end{aligned}$$

Hence ,

$$y(t) \leq \max\left\{\frac{\Lambda}{\mu}, y_0\right\}.$$

That is,

$$\int_0^{\bar{a}} S(t,a)da \leq \max\left\{\frac{\Lambda}{\mu}, \int_0^{\bar{a}} S(0,a)da\right\} = \kappa.$$

and

$$\begin{aligned} \frac{dI(t)}{dt} &\leq \beta I(t)\kappa - I(t)\left(\mu + \delta_1 + \delta_2 I^{-\alpha}(t)\right) \\ &= I^{1-\alpha}(t)\left(AI^{\alpha}(t) - \delta_2\right) \end{aligned}$$

where $A = \beta\kappa - \mu - \delta_1$ is a constant. We now observe that the ODE

$$\frac{dI(t)}{dt} = I^{1-\alpha}(t)\left(AI^{\alpha}(t) - \delta_2\right)$$

has 2 constant solutions, namely 0 and $\left(\frac{\delta_2}{A}\right)^{\frac{1}{\alpha}}$. Furthermore, since we know that $\lim_{t\to\infty} I(t) = 0$, 0 is an attractive equilibrium, and so there exists a point $t > t_1$ such that

$$AI(t) - \delta_2 < -\frac{\delta_2}{2}.$$

That is,

$$\frac{dI(t)}{dt} \leq -\frac{\delta_2}{2}I(t)^{1-\alpha} \quad for \quad t > t_1.$$

Therefore, by separation of variables,

$$I(t) \leq \begin{cases} (\alpha C - \alpha\frac{\delta_2}{2}t)^{\frac{1}{\alpha}} & t_1 < t \leq \frac{2C}{\delta_2} \\ 0 & t > \frac{2C}{\delta_2} \end{cases}$$

where $C = \frac{I^{\alpha}(0)}{\alpha} - \frac{\delta_2 t_0}{2}$, $t_0 > t_1$. It is clear that for $t^* \geq \frac{2C}{\delta_2} > t_1$, $I(t) = 0$. □

3.3.3 A generic model of a vector borne disease

Vector-borne diseases are infections transmitted by the bite of infected arthropod species (e.g. mosquitoes, ticks).The following two sets of equations model the dynamics of an infectious disease between a vector and a host. Both the vector and the host are divided into compartments on the basis of whether they are susceptible or infectious. Age structure is taken into account in the case of the vectors, due to their short lifespan, as in model (3.11). State structure is used to model the infectives in the host population as in (3.9).

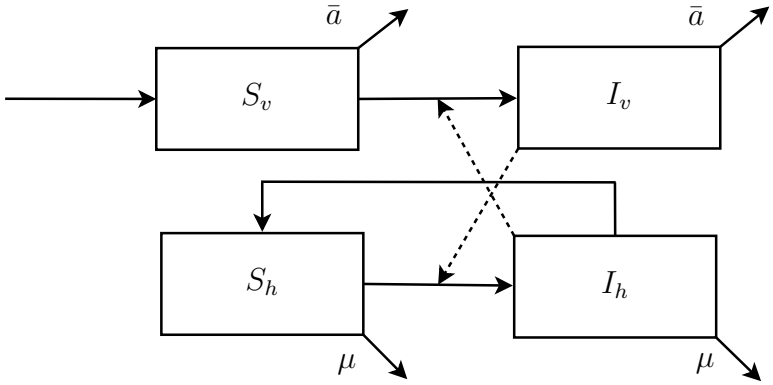


Figure 3.6: Diagram of dynamics for vector borne disease model

Vector

$$\begin{cases} \frac{\partial S_v}{\partial t} + \frac{\partial S_v}{\partial a} = -\beta_{hv} I_h^\alpha S_v \\ \frac{\partial J_v}{\partial t} + \frac{\partial J_v}{\partial a} = \beta_{hv} I_h^\alpha S_v \\ J_v(t,0) = 0 \\ S_v(t,0) = \int_{\underline{a}}^{\bar{a}} f(a)\left(S_v(t,a) + J_v(t,a)\right) da \\ I_v(t) = \int_0^{\bar{a}} J_v(t,a) da \end{cases} \tag{3.13}$$

- S_v: Density of the distribution of susceptible vectors at time t over age $a \in (0, \bar{a})$.
- J_v: Density of the distribution of infective vectors at time t over age $a \in (0, \bar{a})$.
- I_v: Infective vectors at time t.
- $\beta_{hv} I_h^\alpha$: Force of infection from host to vector where $0 < \alpha < 1$.
- f: Fertility function.

Host

$$\begin{cases} \frac{dS_h}{dt} = -\beta_{vh} I_v^{\gamma} S_h + \psi(S_h, J_h, t) \\ \frac{\partial J_h}{\partial t} + \frac{\partial J_h}{\partial x} = 0 \\ J_h(t,0) = \beta_{vh} I_v^{\gamma} S_h \\ I_h(t) = \int_0^{\bar{x}} J_h(t,x)dx \end{cases} \tag{3.14}$$

- S_h: Susceptible hosts at time t.
- J_h: Density of the distribution of infective hosts at time t over epidemiological state $x \in (0, \bar{x})$.
- I_h: Infective hosts at time t.
- $\beta_{vh} I_v^{\gamma}$: Force of infection from vector to host where $0 < \gamma < 1$.
- ψ: Auxiliary function of S_h, J_h and t that may be used to incorporate vital dynamics into this model.

Theorem 3.3.3. *If a solution of the model given by* (3.14) *and* (3.13) *is such that*

1. $\lim_{t\to\infty} S_h(t) = S_h^{\infty} > 0$,
   $\lim_{t\to\infty} S_v(t,a) = S_v^{\infty}(a) > 0$ *uniformly on* a,
2. $I_h'(t) \leq -cI_h(t)$,
   $I_v'(t) \leq -cI_v(t)$

for $c > 0$ *and* $t \geq \hat{t}$, *then there exists* t^* *such that* $I_h(t) = 0$ *and* $I_v(t) = 0$ *for* $t > t^*$.

Proof. Consider

$$\begin{aligned} \frac{dI_h(t)}{dt} &= \int_0^{\bar{x}} \frac{\partial J_h(t,x)}{\partial t} dx \\ &= \int_0^{\bar{x}} -\frac{\partial J_h(t,x)}{\partial x} dx \\ &= J_h(t,0) - J_h(t,\bar{x}) \\ &= \beta I_v(t)^{\gamma} S_h(t) - J_h(t-\bar{x},0) \\ &= \beta I_v(t)^{\gamma} \left\{ S_h(t) - \frac{I_v(t-\bar{x}) S_h(t-\bar{x})}{I_v(t)^{\gamma}} \right\} \end{aligned}$$

Using a similar approach to that of the proof for Theorem 3.3.1 it can be show that $\exists\ k > 0$ such that

$$S_h(t) - \frac{I_v(t-\bar{x})^{\gamma} S_h(t-\bar{x})}{I_v(t)^{\gamma}} \leq -k \tag{3.15}$$

Therefore

$$\frac{dI_h(t)}{dt} \leq -kI_v(t)^\gamma \quad , t > t_2.$$

$$\begin{aligned}
\frac{dI_v(t)}{dt} &= \int_0^{\bar{a}} \frac{\partial J_v(t,a)}{\partial t} da \\
&= -\int_0^{\bar{a}} \frac{\partial J_v(t,a)}{\partial a} da + \beta_{hv} I_h(t)^\alpha \int_0^{\bar{a}} S_v(t,a) da \\
&= -\left[J_v(t,\bar{a}) - J_v(t,0)\right] + \beta_{hv} I_h(t)^\alpha \int_0^{\bar{a}} S_v(t,a) da \\
&= -\left[J_v(t-\bar{a},0) + \beta_{hv} \int_0^{\bar{a}} I_h(t-\bar{a}+\theta)^\alpha S_v(t-\bar{a}+\theta,\theta) d\theta\right] + \beta_{hv} I_h(t)^\alpha \int_0^{\bar{a}} S_v(t,a) da \\
&\leq \beta_{hv} \int_0^{\bar{a}} I_h(t)^\alpha S_v(t,a) - I_h(t-\bar{a}+\theta)^\alpha S_v(t-\bar{a}+\theta,\theta) da \\
&\leq \beta_{hv} I_h(t)^\alpha \int_0^{\bar{a}} S_v(t,a) - e^{-c\alpha(\bar{a}-\theta)} S_v(t-\bar{a}+\theta,\theta) da
\end{aligned}$$

since $I_h(t)^\alpha \leq I_h(t-\bar{a}+\theta)^\alpha e^{-c\alpha(\bar{a}-\theta)}$.
Denote

$$\omega(t,\theta) = S_v(t,\theta) - e^{\alpha c(\bar{a}-\theta)} S_v(t-\bar{a}+\theta,\theta).$$

Then

$$\lim_{t\to\infty} \omega(t,\theta) = S_\infty(\theta)(1 - e^{\alpha c(\bar{a}-\theta)})$$

uniformly on θ. Let

$$k(\theta) = -\frac{S_\infty(\theta)}{2}(1 - e^{c(\bar{a}-\theta)}) > 0$$

Hence

$$\lim_{t\to\infty} \omega(t,\theta) = -2k(\theta) < -k(\theta)$$

Hence there exists $t = t_3$ such that $\omega(t,\theta) < -k(\theta)$ for $t > t_3$, which implies that

$$\frac{dI_v(t)}{dt} \leq -rI_h(t)^\alpha \quad for\ t > t_3\ and\ r = \beta \int_0^{\bar{a}} k(\theta) d\theta.$$

Now, for $t > \bar{t} = \max(t_2, t_3)$, let us consider

$$\begin{aligned}
\frac{dI_h(t)}{dt} &\leq -kI_v(t)^\gamma \\
\frac{dI_v(t)}{dt} &\leq -rI_h(t)^\alpha.
\end{aligned}$$

Suppose $s = \min(k, r)$ and $\lambda = \max(\gamma, \alpha)$, then

$$\begin{aligned}\frac{d(I_v + I_h)}{dt} &\leq -s(I_v^\gamma + I_h^\alpha) \\ &\leq -s(I_v^\lambda + I_h^\lambda) \\ &\leq -s(I_v + I_h)^\lambda.\end{aligned}$$

That is,

$$\frac{d(I_v(t) + I_h(t))}{dt} \leq -s(I_v + I_h)^\lambda, \;\; t > t_3.$$

Therefore $I_v(t) + I_h(t) \leq y(t)$ for $t \geq t_3$, where $y(t)$ satisfies the following

$$\frac{dy(t)}{dt} = -sy(t)^\lambda \;\; and \;\; y(t_3) = I_v(t_3) + I_h(t_3).$$

By seperation of variables,

$$y(t) = \begin{cases} \{(C - st)(1 - \lambda)\}^{\frac{1}{1-\lambda}} & for\ t \leq \frac{C}{s}, \\ 0 \;\; for\ t \geq \frac{C}{s} \end{cases}$$

where

$$C = \frac{(I_v(t_3) + I_h(t_3))^{1-\lambda}}{1 - \lambda} + st_3.$$

Therefore since $0 \leq I_h + I_v \leq y(t)$, we have $I_h(t) + I_v = 0$ (i.e.$I_h = I_v = 0$) when $t \geq t^* = \frac{C}{s}$. □

Clearly this result is valid regardless of the choice of function ψ, as long as the conditions of Theorem 3.3.3 are met.

Furthermore, it should be noted that the condition in all three theorems, that the solutions tend to 0 with time at least exponentially, is central to ensuring this result. Further mathematical analysis can possibly lead to relaxing the condition for convergence of infectives to 0 at least exponentially. This work provides useful mathematical tools for modelling extinction and characterizing possible pathways to extinction.

Chapter 4

African swine fever virus model

In this chapter we formulate and analyse a proposed model for African Swine Fever. It is our primary objective to accurately simulate and study the situation in the Mkuze Game Reserve, where ASF could only be traced in remote areas of the game reserve despite the following two observations [3]:

1. a higher proportion of adult ticks were sampled in each burrow and,
2. a significant increase in the number of burrows that were infested with soft ticks.

Firstly, since soft ticks engorge to their next state with each bloodmeal, and also since they prefer to feed on warthogs, it can be inferred that a larger number of adult ticks are present due to the fact that bloodmeals were more readily available. That is, warthog families had frequently visited the burrows that were sampled. Secondly, we have established that warthogs play a role in the maintenance of ASF within the tick population (see section 1.2.1) and the increased access to their preferred host should cause an increase in the infection rate. Hence, these observations indicate that conditions are ideal for the virus to spread throughout the tick population; but despite this the disease has been practically eradicated from the game reserve within the space of approximately 3 decades.

4.1 Model formulation

We will utilise two sets of equations to model the dynamics of ASFV between the tick and warthog population.

Owing to the fact that ticks age based on each engorgement and since the age of the tick or 'current stage of engorgement' dictate the way in which the disease is spread,

it is clear that age structure must be utilised. Let $\rho_v(t,a)$ denote the distribution of the tick population at time t over the age interval $[0,\bar{a}]$ where $\bar{a} < \infty$ is the maximum age. Observe that although we established that ticks can effectively "stop ageing" when bloodmeals are not readily available (see section 1.2.3) and survive for many years, we make the assumption that the ticks die of natural causes and are removed from the population once they reach age $\bar{a}$ and at death rate μ.

The following model is used to model the dynamics of the tick population, under the assumption that the tick population is at equilibrium:

$$\frac{\partial \rho_v(t,a)}{\partial t} + \frac{\partial \rho_v(t,a)}{\partial a} = -\mu P_v(t), \;\; \rho_v(t,0) = \psi(\rho_v(t,.)). \tag{4.1}$$

Note that,

$$P_v(t) = \int_0^{\bar{a}} \rho_v(t,a)da$$

is the total tick population at time t. Then,

$$\begin{aligned}\frac{dP_v(t)}{dt} &= \int_0^{\bar{a}} \frac{\partial \rho_v(t,a)}{\partial t} da \\ &= -\int_0^{\bar{a}} \frac{\partial \rho_v(t,a)}{\partial a} da - \mu P_v(t) \\ &= \rho_v(t,0) - \rho_v(t,\bar{a}) - \mu P_v(t).\end{aligned}$$

Clearly, if the tick population is at equilibrium, then

$$\rho_v(t,0) = \rho_v(t,\bar{a}) + \mu P_v(t).$$

Hence,

$$\psi(\rho_v(t,.)) = \rho_v(t,\bar{a}) + \mu P_v(t). \tag{4.2}$$

We partition the tick population into two compartments, namely susceptible S and infectious J. Note that soft ticks do not develop immunity to ASF and transtadial transmission from one life stage to the next ensures that once they are infected they cannot recover.

Tick population

$$\begin{cases} \frac{\partial S_v}{\partial t} + \frac{\partial S_v}{\partial a} = -\beta_{hv} I_h S_v - \mu S_v \\ \frac{\partial J_v}{\partial t} + \frac{\partial J_v}{\partial a} = \beta_{hv} I_h S_v - (\mu + \delta_1 + \delta_2 I_v^{-\gamma}) J_v \end{cases} \tag{4.3}$$

where

$$I_v(t) = \int_0^{\bar{a}} J_v(t,a)da. \tag{4.4}$$

- S_v: Density of the distribution of susceptible ticks at time t over age $a \in (0,\bar{a})$.

- J_v: Density of the distribution of infective ticks at time t over age $a \in (0, \bar{a})$.
- I_v: Infective ticks at time t.
- δ_1: Disease induced death rate.
- δ_2: Disease induced death rate.
- μ: Natural death rate.
- γ: Constant between $0 < \gamma < 1$.
- $\beta_{hv} I_h$: Force of infection from warthog to tick.

The recruitment rate into the population (i.e. eggs hatched per unit in time) is $\psi(\rho_v(t,.))$. We assume that the proportion of new recruits entering due to the infective part of the population is the same as the proportion of the infectives in the current population of the infectives in the current population. Then using (4.2) the boundary conditions are

$$\begin{cases} J_v(t,0) = c(J_v(t,\bar{a}) + \mu I_v(t)) \\ S_v(t,0) = \psi(\rho_v(t,.)) - c(J_v(t,\bar{a}) + \mu I_v(t)), \end{cases} \tag{4.5}$$

where $c \in (0,1)$ is the probability of vertical transmission. Due to the fact that low transovarial transmission rates have been observed in the field and in laboratory situations (see section 1.2.3), we will take this into account when accounting for the recruitment of new born ticks into the infective class by introducing a probability of transovarial transmission c. Additionally, if it is chosen that $c = 0$ (i.e. no new born ticks are born with ASF or $J_v(t,0) = 0$), then vertical transmission of the disease from female ticks to their offspring (transovarial transmission) is eliminated from the model. Lastly, note that due to the fact that this model does not take into account the gender of soft ticks, one directional sexual transmission is not explicitly taken into account.

The following model describes the dynamics of the warthog population.

Warthog population

$$\begin{cases} \frac{dS_h}{dt} = -\beta_{vh} I_v S_h^{\alpha} \\ \frac{\partial J_h}{\partial t} + \frac{\partial J_h}{\partial x} = 0 \\ J_h(t,0) = \beta_{vh} I_v S_h^{\alpha} \\ I_h(t) = \int_0^{\bar{x}} J_h(t,x)dx \end{cases} \tag{4.6}$$

- S_h: Susceptible warthogs at time t.
- J_h: Density of the distribution of infective warthogs at time t over epidemiological state $x \in (0, \bar{x})$.

- I_h: Infective warthogs at time t.
- α: Constant between $0 < \alpha < 1$.
- β_{vh}: Rate of infection from ticks to warthogs.

Warthogs are partitioned into three compartments on the basis of whether they are susceptible S, infectious J or recovered R. This is due to the fact that, unlike ticks warthogs gain immunity to ASFV as soon as they enter the burrow. Since only neonatal warthogs have blood virus levels that are high enough to spread the disease into the tick population, we need only to take into account the dynamics of these individuals and we are only interested in the short interval of time between the initial infection and recovery. Hence, using the approach suggested by Hoppensteadt [13](see section 2.4.2) only the infective compartment will be state structured with respect to epidemiological state x, which is the time since infection took place (i.e. time since the infective bloodmeal), where $x \in (0, \bar{x})$ and $\bar{x} < \infty$ is the final infective state. Therefore, the warthogs transition to the recovered compartment after $\bar{x}$.

Impulses are inserted into the model in order to signify that a warthog family has entered the burrow. For $k = 1, 2, 3, \ldots$,at time T_k a warthog family enters the burrow to rear its young. Hence the number of warthogs in the burrow increases sharply from 0 to Γ at time T_k. After δ units in time(impulse termination), the number of susceptible hosts is once again 0 and same goes for number of infected hosts, since warthogs develop immunity. Also, after time $T_k + \Delta$, the warthogs family exits the burrow and the number of susceptible hosts is 0.

$$\begin{cases} S_h(T_k) = \Gamma \\ S_h(T_k + \Delta) = 0 \\ J_h(T_k + \Delta, a) = 0, \quad a \in [0, \bar{a}] \end{cases} \tag{4.7}$$

In order for a mathematical model to accurately portray the MGR situation, it is required that extinction of the infective compartment I_v occurs within finite time. Therefore, we have incorporated similar techniques to those studied in Chapter 3 such as using a saturating force of infection $-\beta_{hv} I_h$ and $-\beta_{vh} I_v$ (refer to Figure 4.1) and using disease dependant death rates δ_1 and δ_2 to ensure that the infective vectors will reach 0. Figure 4.1 illustrates the dynamics of the model for ASF.

Remark
Observe that when $\alpha = 1$, this is a classic SIR model with mass action. In our numerical simulations we found that if $\alpha < 1$ and δ is sufficiently large, then the warthog population is disease free by the time it leaves the burrow. However, taking into account the impulsive conditions this fact does not play a role in this model. Indeed at time $T_k + \Delta$ there are no susceptible or infective hosts.

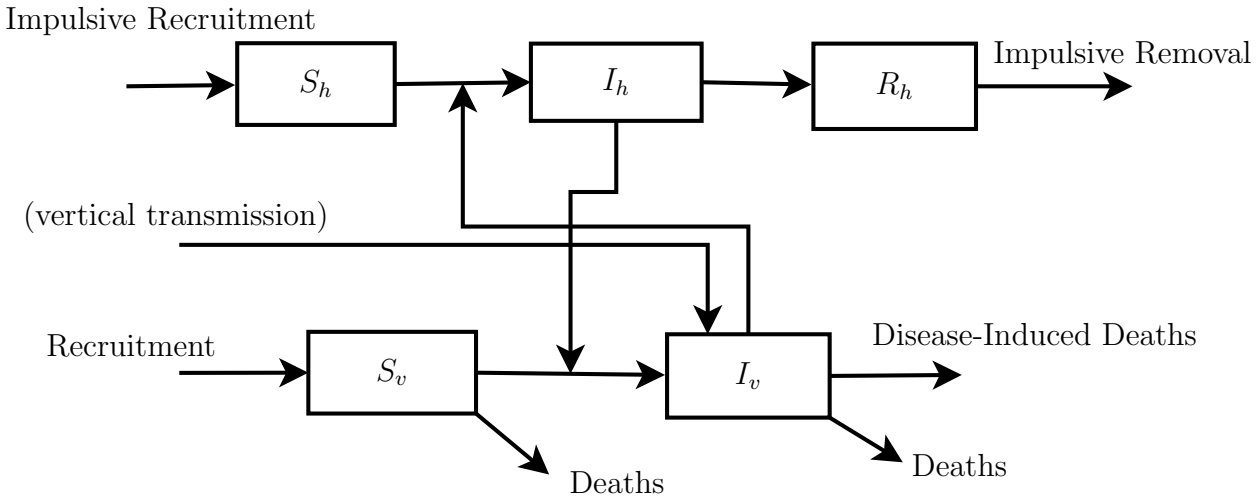


Figure 4.1: Diagram of dynamics for the ASFV model

4.2 Finite time extinction in ASFV model

Our objective is to prove that in the absence of warthogs, ASF becomes extinct within the tick population in finite time.

Theorem 4.2.1. *If $T_{k+1} - T_k$ is sufficiently large then there exists $t^* \in [T_k, T_{k+1}]$ such that $I_v(t) = 0$ for $t \geq t^*$.*

Proof. In the interval $[T_k, T_{k+1}]$ the equation for the infective class of the tick population is developed using the rest of the system and is given by,

$$\begin{aligned} \frac{\partial J_v(t,a)}{\partial t} + \frac{\partial J_v(t,a)}{\partial a} &= -\left(\mu + \delta_1 + \delta_2 I_v^{-\gamma}\right) J_v(t,a), \\ J_v(t,0) &= c\left(J_v(t,\bar{a}) + \mu I_v(t)\right). \end{aligned}$$

Then,

$$\begin{aligned} \frac{dI_v(t)}{dt} &= -\int_0^{\bar{a}} \frac{\partial J_v(t,a)}{\partial a} da - \left(\mu + \delta_1 + \delta_2 I_v^{-\gamma}\right) I_v(t) \\ &= J_v(t,0) - J_v(t,\bar{a}) - \left(\mu + \delta_1 + \delta_2 I_v^{-\gamma}\right) I_v(t) \\ &= -(1-c)J_v(t,\bar{a}) - \left((1-c)\mu + \delta_1\right) I_v(t) - \delta_2 I_v^{1-\gamma}(t) \\ &\leq -\left((1-c)\mu + \delta_1\right) I_v(t) - \delta_2 I_v^{1-\gamma}(t). \end{aligned}$$

Now,

$$\begin{aligned} \frac{dI_v(t)}{dt} &\leq -\left((1-c)\mu + \delta_1\right) I_v(t) \\ I_v(t) &\leq I_v(0) e^{-((1-c)\mu + \delta_1)} \end{aligned}$$

implies

$$\lim_{t\to\infty} I_v(t) = 0.$$

Furthermore from,

$$\frac{dI_v(t)}{dt} \leq -\delta_2 I_v(t)^{1-\gamma} = -\delta_2 I_v^{-\gamma}(t).I_v(t)$$

and Theorem 3.1.1 it follows that there exists t^* such that $I_v(t) = 0$ for $t \geq t^*$. Note that irrespective of further impulses of $T_{k+1}, T_{k+2}, \ldots$ the system remains in a disease free state. □

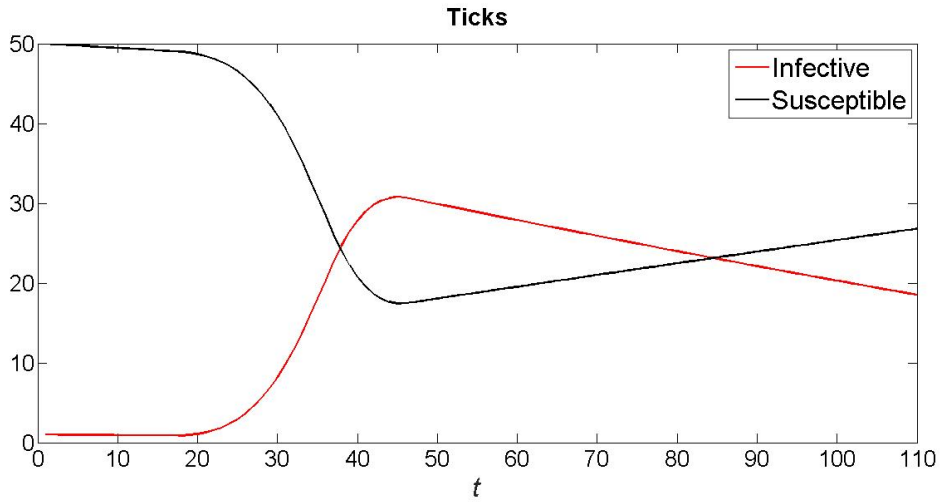
4.3 Numerical simulation and analysis

In the following section we investigate the role played by warthogs in the maintenance and spread of ASF. All simulations were executed using the following parameter values: $\beta_{vh} = 0.5$, $\beta_{hv} = 0.05$, $\mu = 0.005$, $\gamma = 0.5$, $\delta_1 = 0.0001$, $\delta_2 = 0.005$, $\alpha = 0.5$, $\bar{a} = 50$, $\Gamma = 10$ which were chosen in order to best illustrate an arbitrary scenario.

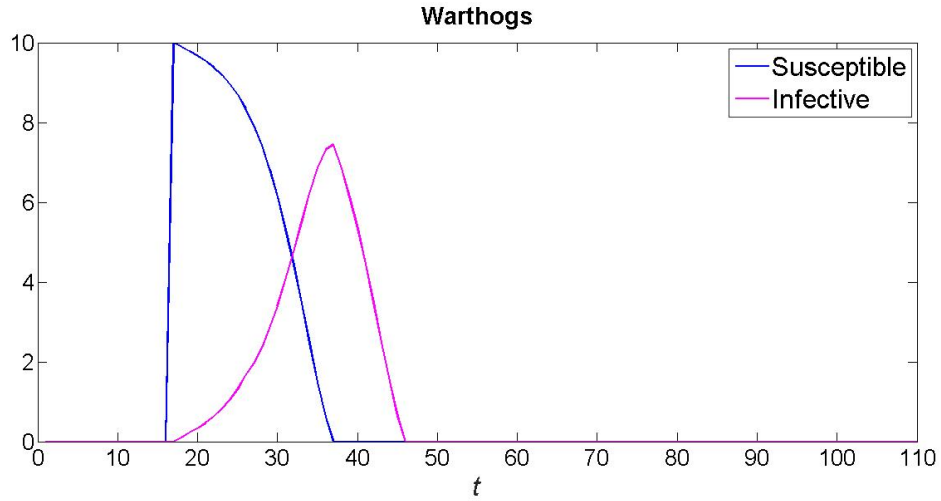
4.3.1 ASFV model without vertical transmission

In order to understand the role of vertical transmission we consider first the case when there is no such transmission, that is $c = 0$. Figure 4.2 demonstrates the effect of a solitary impulse (4.7) representing the event of a warthog family entering an infested burrow with low prevalence of ASFV in the tick population. It is clear from Figure 4.2(b) that the introduction of warthogs at $t = 16$ results in a sharp increase of infective warthogs and reaches its peak at around $t = 40$. The corresponding increase of infective ticks peaking at $t = 40$ (see Figure 4.2(a))is as a result of the availability of infective hosts. Observe that this is consistent with the biological scenario when a warthog family enters a burrow and neonatal warthogs become infected. As they develop immunity the number of infective hosts declines. At the time of exit ($t = 46$) the warthog population is fully immune ($S_h = I_h = 0$). This then causes the number of infective ticks to decrease steadily, from that time onwards.

Now we consider the effect of multiple impulses each representing a warthog family entering the burrow (Figure 4.3). Observe that at each entry into the burrow the infective ticks sharply increase to a peak and steadily decline when the warthog family exits. The repeated entry of warthogs into the burrow has resulted in a periodic 'pulse-like' oscillations of infective ticks. This implies that the time between impulses $T_{k+1} - T_k$ is not sufficiently large enough for Theorem 4.2.1 to hold and hence ASFV persists.



(a)



(b)

Figure 4.2: (a) The amplification of ASF within the tick population in the presence of warthogs. (b)The dynamics of the warthog population that inhabits an infested burrow.

Lengthening the distance between impulses or in other words the warthog families visit the burrow less frequently, we obtain Figure 4.4(a). Observe that unlike Figure 4.3(a), the infective tick population never recovers once the warthogs exit the burrow the first time (Figure 4.4(a)). In this case Theorem 4.2.1 is validated and no matter how many times the warthog family re-enters the burrow, the infective tick population will remain at 0 resulting in disease extinction in finite time.

We can conclude that the numerical simulations are consistent with the findings of Theorem 4.2.1 as the waiting time between subsequent entries into a burrow plays a key role in whether ASF will persist or become extinct within the tick population. This could possibly imply that the warthogs of Mkuze Game Reserve do not inhabit

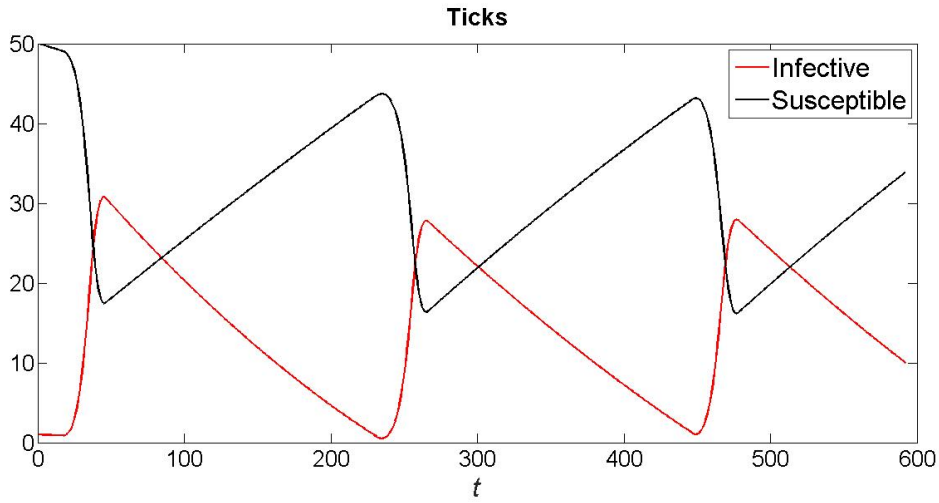
the sampled burrows frequently enough for the disease to be maintained consistently within each burrow.

4.3.2 Vertical transmission

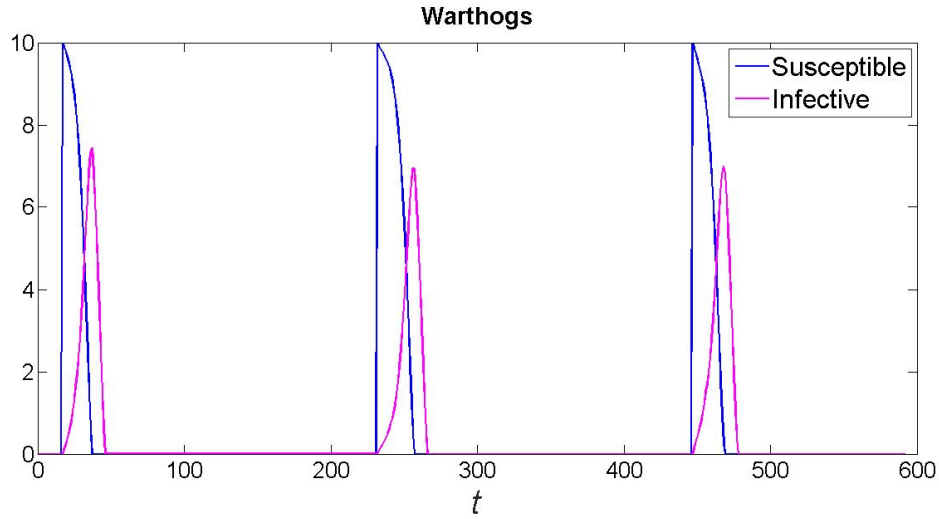
Let us now investigate the effects of vertical transmission (i.e. $c \in (0, 1)$) on disease extinction. Consider the following two scenarios: one where the warthogs are absent from the burrows for longer periods of time (Figure 4.4(b)) and another where the interval length between visits are relatively short (Figure 4.5(b)). Notice that our results once again support the findings of Theorem 4.2.1. However, comparing Figure 4.6(a) and Figure 4.4(a) it is clear that the time taken to reach extinction is considerably lengthened when vertical transmission is included into the model. This is due to the influx of infected newborns entering the infective population.

It is clear that two mechanisms play a role in ensuring the persistence of ASF in the tick population. The first is warthogs inhabiting burrows frequently at short time intervals, which results in the amplification of the number of infections within the tick population. Secondly, vertical transmission plays a crucial role in prolonging the time to disease extinction and increasing the low level prevalence of the disease. This allows the disease to be maintained within the population at a low level for extended periods of time until a warthog family inhabits the burrow again.

We then infer that it is possible that warthog families do not visit the burrows within the Mkuze Game Reserve frequently enough to allow the virus to persist. Furthermore, due to vertical transmission it is possible that the virus may still be present in isolated areas of the game reserve at levels that were too low to detect and a resurgence of the disease could occur within the game reserve should these burrows be used more often by warthogs during farrowing season. Clearly, an increase in burrow infestation rates alone is not sufficient to increase the prevalence of ASF.

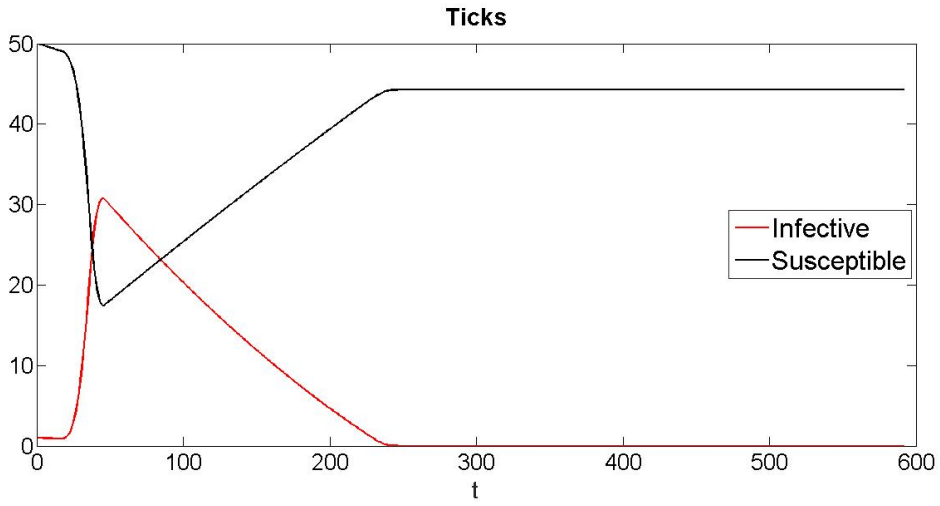


(a)

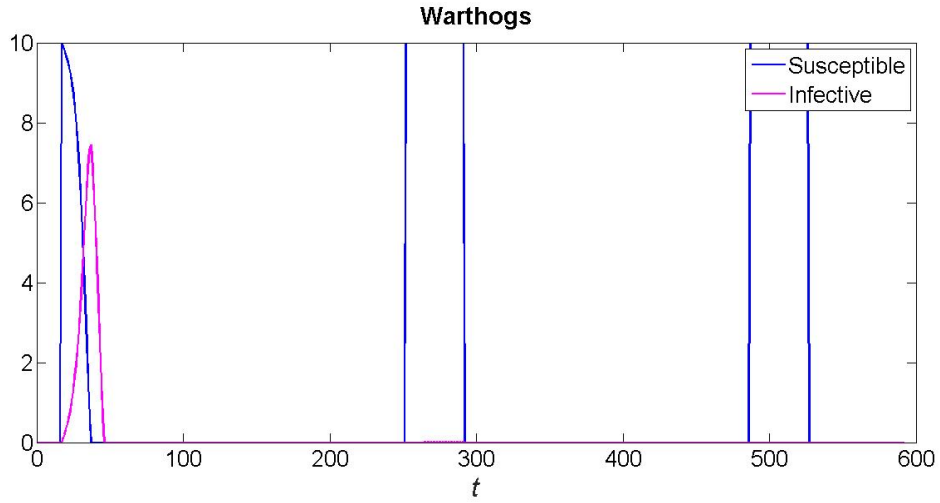


(b)

Figure 4.3: (a) The persistence of ASF within the tick population. (b) The dynamics of the warthog population as it frequently visits an infested burrow.

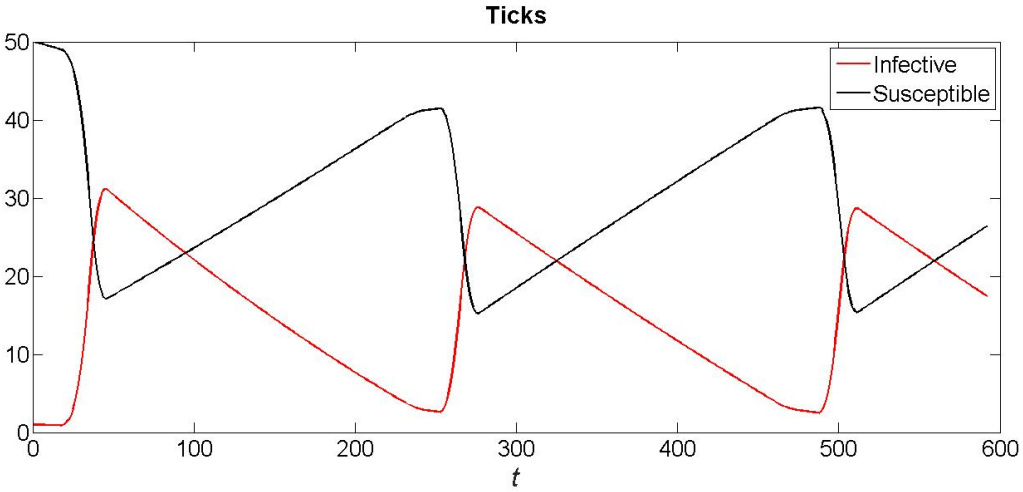


(a)

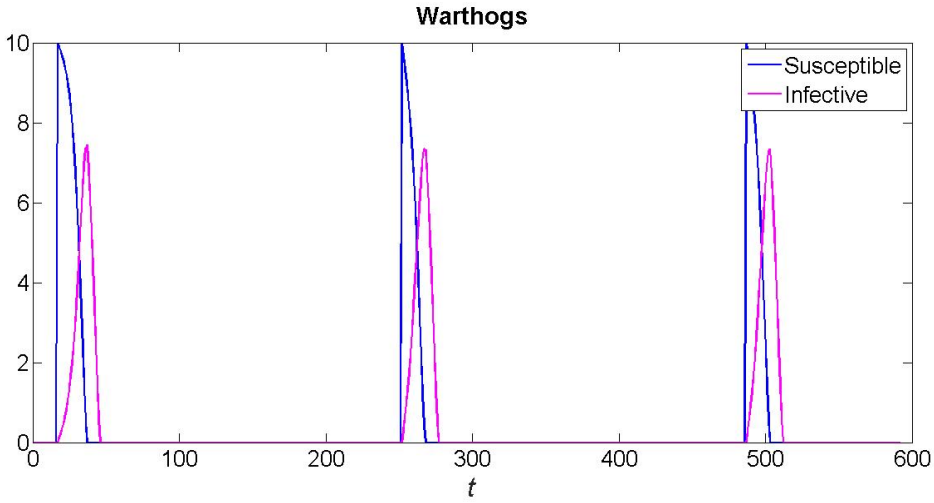


(b)

Figure 4.4: (a) Extinction of ASF within the tick population.(b) The dynamics of the warthog population as the length between visits to the burrow are increased.

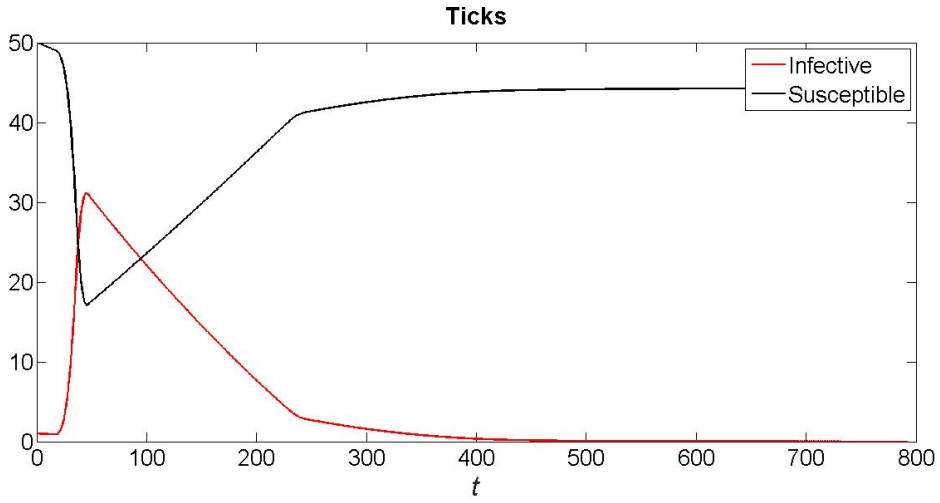


(a)

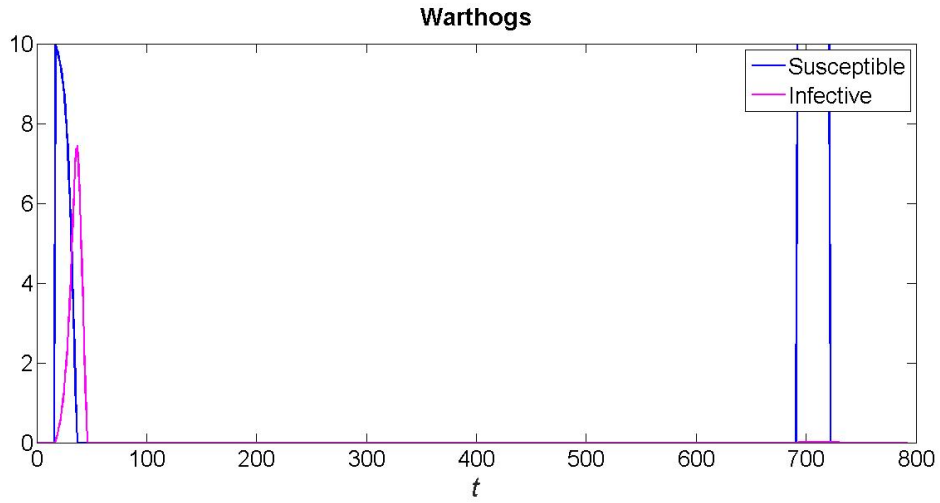


(b)

Figure 4.5: (a) Persistence of ASF within the tick population with vertical transmission.(b) The dynamics of the warthog population.



(a)



(b)

Figure 4.6: (a) Extinction of ASF within the tick population with vertical transmission.(b) The dynamics of the warthog population as the length between visits to the burrow are increased.

Chapter 5

Conclusions and future work

African Swine Fever is a viral disease that poses a significant threat to porcine production worldwide. In order to identify ideal conditions under which the virus can be eradicated from a domestic pig population, we studied a unique situation where extinction of African Swine Fever Virus occurred at the Mkuze Game Reserve.

Owing to the fact that such a situation cannot occur in a complete dynamical system, we proved existence and uniqueness for a system of ODE's in Chapter 2 (Theorem 2.2.10 and Theorem 2.2.9) using the one-sided local Lipschitz condition. This result allows us to obtain positive dynamical systems with forward uniqueness.

In order to mathematically replicate extinction within finite time, through the analysis of various ODE and PDE epidemiological models, a mechanism leading to disease eradication was identified. We observed that using a nonlinear force of infection and disease induced death rate played a crucial role in ensuring extinction within finite time. Additionally, we proved that finite time extinction for the proposed structured population models can be attained if their solutions tend to 0 with time at least exponentially. Owing to the fact that this is a stringent condition that would be challenging to implement in practice, further mathematical analysis can be undertaken in the future with the objective of relaxing this condition.

Incorporating the findings of Chapter 3, a structured PDE model for ASFV was formulated. We prove that if the time duration between a warthog family's successive inhabitation of the burrow are sufficiently long enough, then ASF becomes extinct within the tick population in finite time and will remain extinct thereafter. Moreover, our numerical simulations support this result. Lastly, it was found that vertical transmission strongly affects the length of this period.

We believe that the model for ASF can be improved by altering the model equations for the tick population to include the variable q representing how fast the tick population ages (e.g. depending on the availability of food). Then the model is given by:

$$\begin{cases} \frac{\partial S_v}{\partial t} + q\frac{\partial S_v}{\partial a} = -\beta_{hv} I_h S_v - \mu S_v \\ \frac{\partial J_v}{\partial t} + q\frac{\partial J_v}{\partial a} = \beta_{hv} I_h S_v - (\mu + \delta_1 + \delta_2 I_v^{-\gamma}) J_v. \end{cases}$$

Altering q enables us to control how rapidly the tick population ages. Since the sampled burrows at the Mkuze Game Reserve were infested with a higher proportion of adult ticks, this will allow us to investigate this unique phenomenon further.

Secondly, by developing a model whereby the gender of the ticks is taken into account in order to study the impact of unidirectional sexual transmission of ASFV from males to females.

Lastly, future work will deal with modelling the dynamics of ASFV on infected pig farms. The model would possibly have to be altered to incorporate the varying characteristics of different tick species depending on the geographical location of the farms. For example, in Europe ASFV is transmitted through the *Ornithodoros, O. erraticus* ticks [16]. This line of research will provide important insights into the mechanisms that aid disease eradication for commercial pig farming.

Bibliography

[1] Abia, L.M. , Angulo, O. and López-Marcos, J.C. (2005) 'Age-structured population models and their numerical solution', *Ecological Modelling*, 188(1), 112-136.

[2] Agarwal, R. , Hristova, S. , O'Regan, D. (2013) 'Exponential stability for differential equations with random impulses at random times.', *Advances in Differential Equations*, 2013:372.

[3] Arnot, L.F. , Du Toit, J.T. and Bastos, A.D.S. (2009) 'Molecular monitoring of African swine fever virus using surveys targeted at adult Ornithodoros ticks: a re-evaluation of Mkuze Game Reserve, South Africa', *Onderstepoort Journal of Veterinary Research*, 76, 385-392.

[4] Bainov, B. , Simeonov, P. (1993) Impulsive differential equations: periodic solutions and applications, Longman scientific and technical.

[5] Bastos, A.D.S., Arnot ,L.F. , Jacquier, M.D. and Maree, S. (2009)' A host species-informative internal control for molecular assessment of African swine fever virus infection rates in the African sylvatic cycle Ornithodoros vector', *Medical and Veterinary Entomology*, 23, 399409.

[6] Boomker, J., Horak , I.G., Booyse, D.G., Santa Meyer (1991) 'Parasites of South African wildlife, VIII. Helminth and arthropod parasites of warthogs, Phacochoerus Aethiopicus, in the eastern transvaal', *Onderstepoort J.ver.Res*, 58, 195-202.

[7] Busenberg, S., Cooke, K., and Iannelli, M.(1988). 'Endemic thresholds and stability in a class of age-structured epidemics', *SIAM Journal on Applied Mathematics*, 48(6), 1379-1395.

[8] Capasso, V., Serio, G. (1978). 'A generalization of the Kermack-McKendrick deterministic epidemic model'. *Mathematical biosciences*,42, 43-61.

[9] d'Onofrio, A. (2004). 'Vaccination policies and nonlinear force of infection: generalization of an observation by Alexander and Moghadas', *Applied Mathematics and Computation*, 168(2005), 613-622

[10] Gurtin, M. E., MacCamy, R. C. (1974). 'Non-linear age-dependent population dynamics', *Archive for Rational Mechanics and Analysis*, 54(3), 281-300.

[11] Horak , I.G., Boomker, J., De Vos, V., Potgeiter, F.T. (1988) 'Parasites of domestic and wild animals in South Africa, XXIII. Helminth and arthropod parasites of warthogs, Phacochoerus Aethiopicus, in the eastern transvaal lowveld', *Onderstepoort J.ver.Res*, 55, 145-152.

[12] Hoppensteadt, F.C. (1974). 'An age dependent epidemic model',*Journal of the Franklin Institute*, 297(5), 325-333.

[13] Hoppensteadt, F.C. (1975). Mathematical Theories of Populations: Demographics, Genetics and Epidemics. SIAM-CBMS, Philadelphia.

[14] Jori, F., Bastos, A.D. (2009) 'Role of wild suids in the epidemiology of African swine fever', *Ecohealth*, 6(2),296-310.

[15] Kleiboeker, S. B. , Scoles, G. A. (2001)' Animal Health Research Reviews', *CAB International*,2(2) :121-128.

[15] Kreyszig, E. (1989) , Introductory Functional Analysis with Applications, Wiley Classics Library.

[16] Kleiboeker, S.B. et al. (1998) 'African Swine Fever Virus Infection in the Argasid Host, Ornithodoros porcinus porcinus', *Journal of virology*, 72(3):17111724.

[17] Lakshmikantham, V., Bainov, D. D., Simeonov, P. S. (1989), Theory of Impulsive Differential Equations, World Scientific Publishing Co.

[18] Langlais, M. (1985), 'A nonlinear problem in age-dependant population diffusion', *SIAM Journal on Mathematical Analysis*, 16(3), 510-529.

[19] Penrith, M. (2009) 'African Swine Fever', *Onderstepoort Journal of Veterinary Research*, 76, 9195.

[20] Penrith, M.L., Thomson, G.R., Bastos, A.D.S (2004) Infectious Diseases of Livestock, Oxford University Press.

[21] Plowright, W., Perry, C.T., Greig, A. (1974) 'Sexual Transmission of African Swine Fever Virus in the Tick, Ornithodoros moubata porcinus, Walton', *Res.vet.Sci*, 17, 106-113.

[22] Rennie , L., Wilkinson, P.J. and Mellor, P.S. (2000) 'Effects of infection of the tick Ornithodoros moubata with African swine fever virus', *Medical and Veterinary Entomology*, 14, 355-360.

[23] Rennie , L., Wilkinson, P.J. and Mellor, P.S. (2001)'Transovarial transmission of African swine fever virus in the argasid tick Ornithodoros moubata', *Medical and Veterinary Entomology*, 15, 140-146.

[24] Stuart, A.M., Humphries, A.R (1998) Dynamical systems and numerical analysis, Cambridge university press.

[25] Thomson, G., Gainaru, M., Lewis, A. et al (1983)'The relationship between african swine fever virus, the warthog and ornithodoros species in South Africa',in *African Swine Fever*,edited by P.J. Wilkinson. Commission of the European Communities.

[26] Venturino, E.(1987). 'Nonlinearly interacting age-dependant populations', *Computers and Mathematics with Applications*, 13(9), 901-911.

[27] Webb, G. F. (1985). Theory of nonlinear age-dependent population dynamics. CRC Press.