Bovine Tuberculosis in Possums
Mathematical Modeling
Final Report
June 2021

Andres Mena
Kathleen Moriarty

Introduction:

Bovine tuberculosis is a disease that affects cattle and can be transmitted to humans in the form of a zoonosis. The disease is not only a threat to public health, it is also an economic burden because it compromises meat production. Bovine tuberculosis is difficult to eliminate since it is maintained in populations of wild mammals that act as reservoirs. Understanding the dynamics of transmission in these wild reservoirs is important to establish effective interventions to protect people from infection and to protect the meat industry from economic losses. The aim of this work is to provide a mathematical model of bovine tuberculosis in a population of brushtail possums, which are the wild reservoir of the disease in New Zealand. We first design a model with base parameters detailed in the next section of this report, and then we explore other possible models that could be used to understand the dynamics of the disease.

Model assumptions and parameters:

To build our model, we assume a population of possums living in a given area with a carrying capacity of 50 individuals. Carrying capacity refers to the maximum number of animals that the resources of an ecosystem can support. We assume the average natural mortality rate of the possums to be ⅕ per year. However, this rate changes based on the population density. The growth limiting factor can be represented by the logarithmic equation Y, which has a range from 0 to 1 and is dependent on the carrying capacity. As the population density of the homesite increases to 50, the growth limiting factor quickly increases to 0.5. As the population density grows beyond 50, the resources in the home site become scarce and the growth limiting factor increases to 1. Similarly, the birth rate in the population depends on a logarithmic function X, which ranges from 0 to 1 and decreases as the population approaches, and goes beyond, 50.

Functions for birth and death rate:

$$\chi = 1 - \frac{1}{1 + exp^{-\rho(N-\kappa)}}$$

$$Y = \frac{1}{1 + exp^{-\rho(N-\kappa)}}$$

Another important assumption about the population is that no new possums enter the homesite and no possums leave the homesite.

Other assumptions of our model are that the contact rate between juveniles and adults is the same, that there is no difference in mortality (natural or disease-related) between these two groups and that once infected, individuals maintain the disease throughout their lives. Exposed individuals are not immediately and do not become contagious for approximately 2 ½ months. It is also assumed that juvenile animals can be infected vertically by their mother. The rate of this type of infection also depends on the X function because it is determined by the birth rate of infected adult offspring. All parameters used in the model are specified in Table 1.

Paramater values

	Value	Description
L	5	Birthrate/year
v	0.1	Vertical transmission rate / year
rbj	2.1	Contact transmission rate between juveniles / year
rba	2.1	Contact transmission rate between adults / year
rbaj	2.1	Contact transmission rate between juveniles and adults / year
f	1	Rate at which Juveniles move to Adults / year
mj	0.2	Natural mortatily rate juveniles / year
s	5	Rate at which Exposed become infectious / year
da	1	bTB mortality rate for adults / year
dj	1	bTB mortality rate for juveniles / year
ma	0.2	Natural mortatily rate adults / year
k	50	Carrying capacity of home site
r	0.5	Constant for logistic growth

Table 1. Parameter Values for Base Model

Compartmental Model and Equations:

With the above assumptions and parameters, we designed a compartmental model to describe the dynamics of the disease in the possum population. To capture the heterogeneity of transmission in adults and juveniles, we divided our model into these two levels. Thus our model has 6 compartments: three for juveniles (susceptible, exposed to disease but not yet infectious, and infectious until death) and three for adults comprising the same categories. The diagram of the model is shown in Figure 1 and the set of equations that determine the dynamics of each compartment is shown in Figure 2.
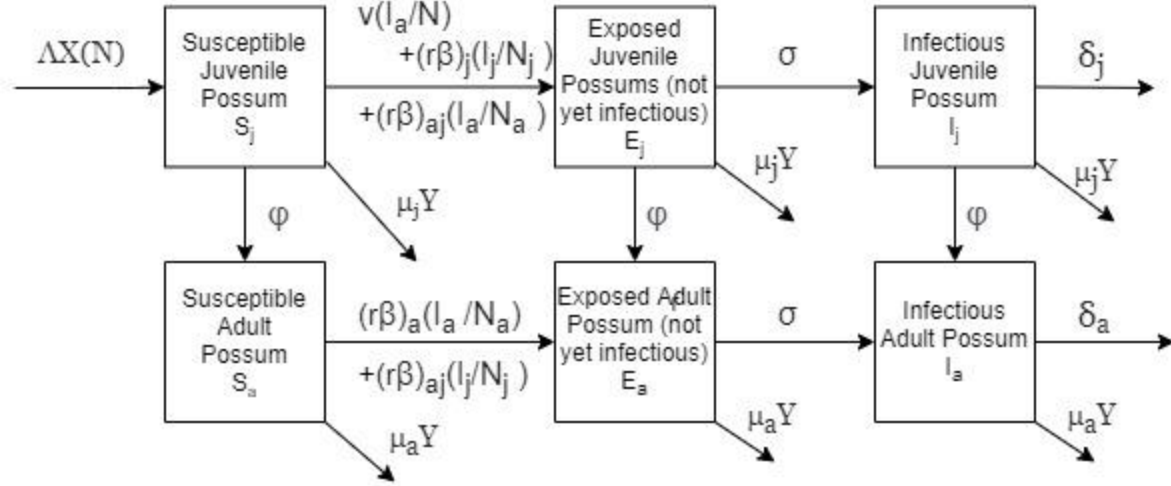
Figure 1. Diagram of Base Model

$$\frac{dS_j}{dt} = \Lambda\chi(N) - \left(v\frac{I_a}{N} + (r\beta)_j\frac{I_j}{N_j} + (r\beta)_{aj}\frac{I_a}{N_a} + \varphi + \mu_j Y\right) S_j$$

$$\frac{dE_j}{dt} = \left(v\frac{I_a}{N} + (r\beta)_j\frac{I_j}{N_j} + (r\beta)_{aj}\frac{I_a}{N_a}\right) S_j - (\sigma + \varphi + \mu_j Y) E_j$$

$$\frac{dI_j}{dt} = \sigma E_j - (\delta_j + \varphi + \mu_j Y) I_j$$

$$\frac{dS_a}{dt} = \varphi S_j - \left((r\beta)_a\frac{I_a}{N_a} + (r\beta)_{aj}\frac{I_j}{N_j} + \mu_a Y\right) S_a$$

$$\frac{dE_a}{dt} = \varphi E_j + \left((r\beta)_a\frac{I_a}{N_a} + (r\beta)_{aj}\frac{I_j}{N_j} + \right) S_a - (\sigma + \mu_a Y) E_a$$

$$\frac{dI_a}{dt} = \varphi I_j + \sigma E_a - (\delta_a + \mu_a Y) I_a$$

Figure 2. Differential Equations for Base Model

Epidemic dynamic:

We use our model to describe the dynamics of an epidemic in a possum population. The initial parameters of this epidemic were 30 susceptible adults, 20 susceptible juveniles and the entry of 1 infective adult. We used R to solve the system of equations under these conditions and generate a graph that illustrates the dynamics of the transmission (Figure 3).
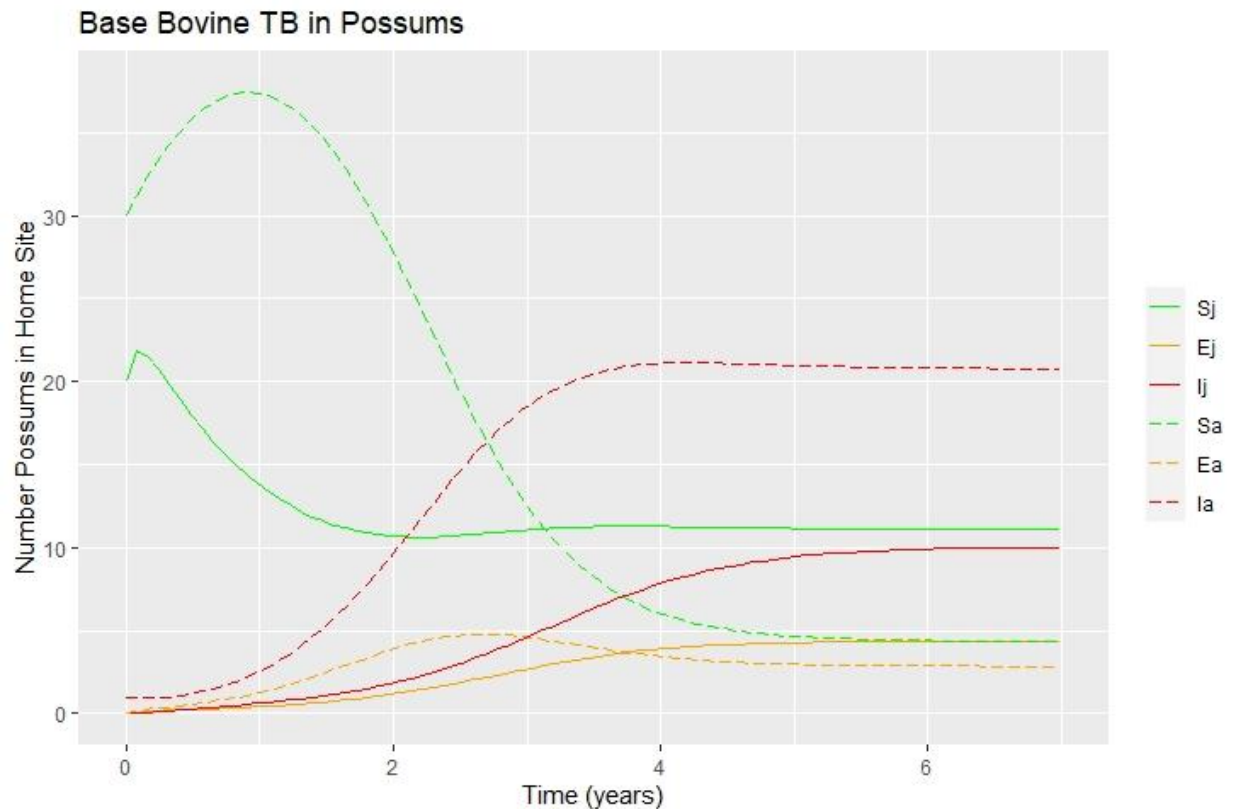
Figure 3. Graph of Numerical Solutions of Base Model

If we analyse the transmission of bovine tuberculosis under our model, we can see that in the case of adults the number of infected animals follows an exponential trajectory until the third year. The number of infected adults grows slowly until the first year, then grows rapidly until the third year when it starts to stabilize and reaches a steady state of about 21 infected animals per year from the fourth year onwards. In the case of juveniles, the number of infected follows a rather linear trajectory before reaching an equilibrium of 10 infected juveniles after the fifth year.

When looking at total population, we can see the effect of the carrying capacity. In Figure 4, the graph of total population shows a sharp increase in the first year (as can be seen in Figure 3 with the rise in susceptible juveniles) to a maximum of 56 possums, but then a gradual decline until reaching equilibrium at 53 possums.

Under our model, if an infectious individual enters a possum-susceptible population, after five years an endemic state of transmissibility is reached in which a large proportion of adults and a good proportion of juveniles are infectious, and therefore a potential danger to livestock if they live in areas close to human settlements.
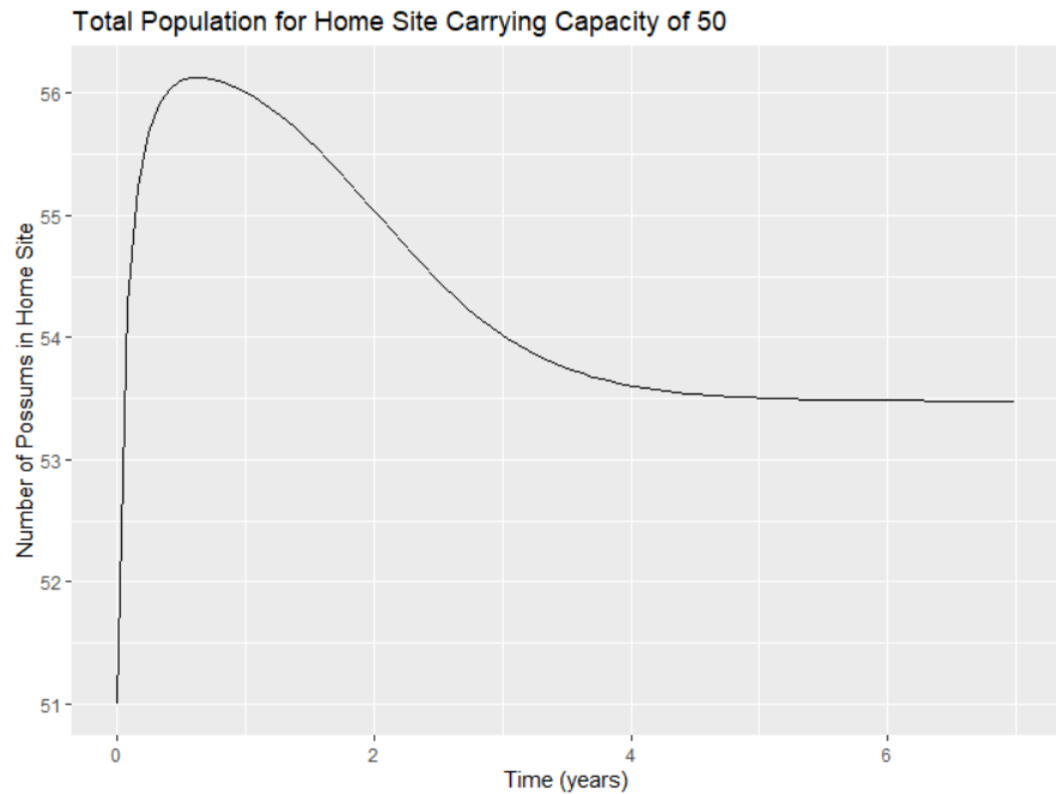
Figure 4. Total population of home site for our model with carrying capacity of 50.

Extensions

We extended the model to take advantage of the heterogenous design. We made distinct contact transmission rates and disease mortality rates for juveniles and adults. We assumed that juveniles would have less contact with other juveniles, and that when they had contact, they would have less probability of transmitting the bacteria. We also assumed that juveniles with the disease would survive longer than adults with the disease. These parameter changes can be seen in Table 2. The numeric solutions for this model can be seen in Figure 5. One difference to note between our initial model and the extended model is the dynamics of infected adults. At the disease introduction, the rate at which adults are infected is slower in this model. Additionally, at the endemic state, there are fewer infected adults. These differences are due to the increase in the contact transmission rates and disease mortality rate of adults.

Paramater values

	Value	Description
L	5	Birthrate/year
v	0.1	Vertical transmission rate / year
rbj	1.1	Contact transmission rate between juveniles / year
rba	3.1	Contact transmission rate between adults / year
rbaj	2.1	Contact transmission rate between juveniles and adults / year
f	1	Rate at which Juveniles move to Adults / year
mj	0.2	Natural mortatily rate juveniles / year
s	5	Rate at which Exposed become infectious / year
da	2	bTB mortality rate for adults / year
dj	0.5	bTB mortality rate for juveniles / year
ma	0.2	Natural mortatily rate adults / year
k	50	Carrying capacity of home site
r	0.5	Constant for logistic growth

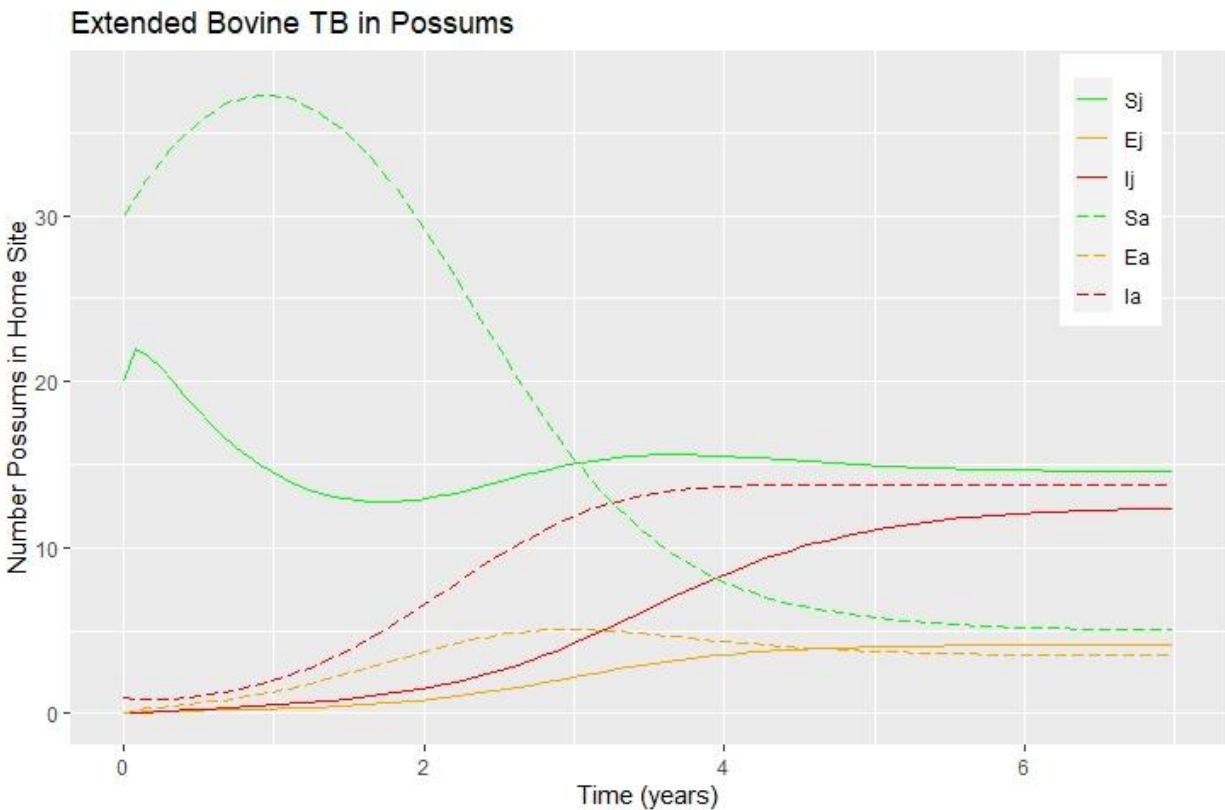*Table 2. Parameter Values for Extended Model*

Figure 5. Graph of Numerical Solutions of Extended Model

In our previous two models, there are several parameters for which it would be difficult to obtain realistic values, specifically distinct contact transmission rates for juveniles and adults. We also think there is an advantage of having a simpler model for analysis. Therefore, for the next steps, we would explore a model such as the one in Figure 6.
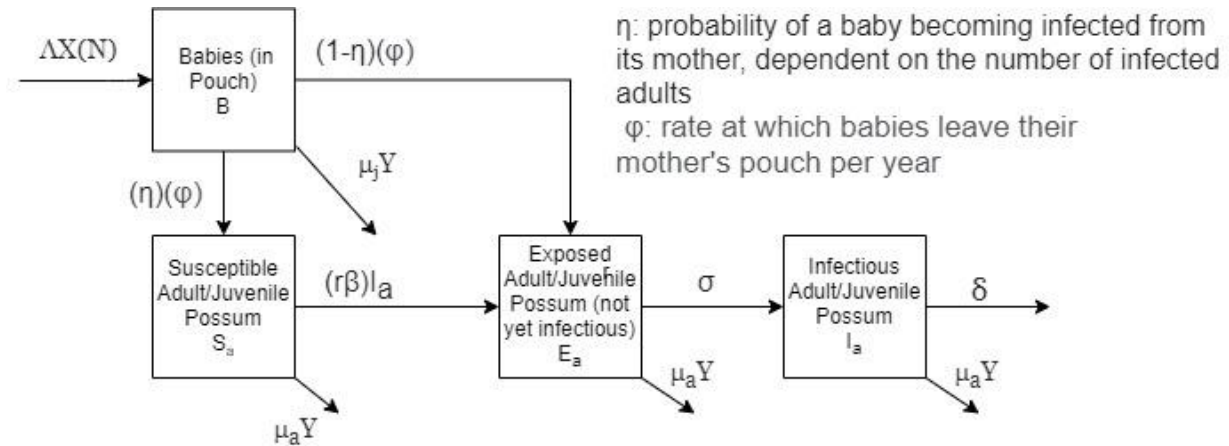

Figure 6. Graph of Simpler Model