

# Summary of BTB-brucellosis coinfection model and assumptions

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## Overview

Bovine tuberculosis (bTB) and brucellosis are positively associated at the population level. Age prevalence curves show a shift in the peak age of brucellosis infection in co-infected animals (Figure 1). We want to know why, so we investigate the costs of co-infection on three parameters relevant for disease dynamics.

1. *Host mortality rates*: bTB was associated with a 2.81 (95%CI 1.47 – 6.82) fold increase in mortality hazard and infection with brucellosis was associated with an 3.00 (95%CI 1.50 – 6.01) fold increase in mortality hazard compared to uninfected buffalo. We did not find support for an interaction between bTB and brucellosis on mortality, indicating that the mortality effects of both infections are additive in co-infected buffalo.

2. *Incidence rates*: bTB was associated with a 1.37 fold increase in the rate at which animals acquire brucellosis. This pattern occurred in one site but not the second. I think this is because the higher baseline mortality in the second site means we do not catch and diagnose infected individuals before they die and hope to test this with the model.

3. *Pregnancy rates*: We see declines in pregnancy rates with infection. However, buffalo population dynamics are more rainfall driven than disease driven (Cross et al. 2009), so we consider density dependence in births following Gao and Hethcote 1992.

23      The model then asks, (1) are changes in these rates sufficient to generate the positive  
24 co-infection patterns observed and (2) what is the consequence of brucellosis infection for  
25 the invasion of bTB? and (3) what is the consequence of bTB invasion for the dynamics of  
26 brucellosis (endemic equilibrium values).

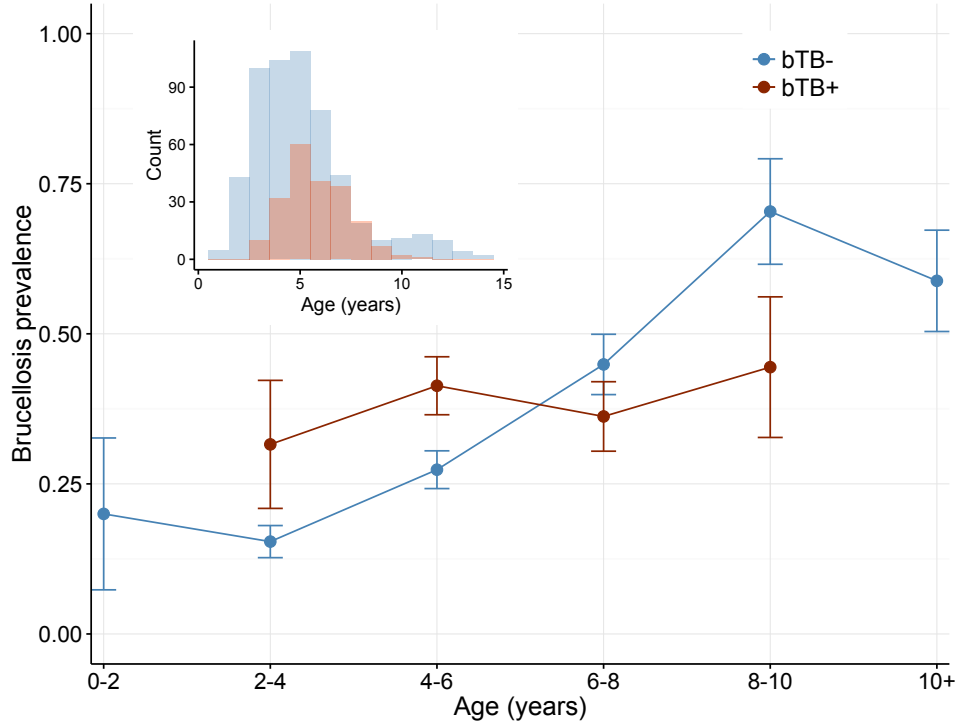


Figure 1: Age, brucellosis-prevalence curves in buffalo simultaneously uninfected (blue) or infected (red) with bTB. The inset figure shows the distribution of ages in our sample, which best cover buffalo between two and eight years old and include 796 samples from 151 repeatedly captured individuals. Ages are binned for visualization and animals that test positive are assumed to remain positive for the duration of the study. Sample sizes for TB- are: 10, 182, 209, 103, 27, 35 buffalo. Sample sizes for TB+ animals are: 0, 21, 108, 75, 21, 1 for ages 0-2, 2-4, 4-6, 6-8, 8-10, and 10+ respectively.

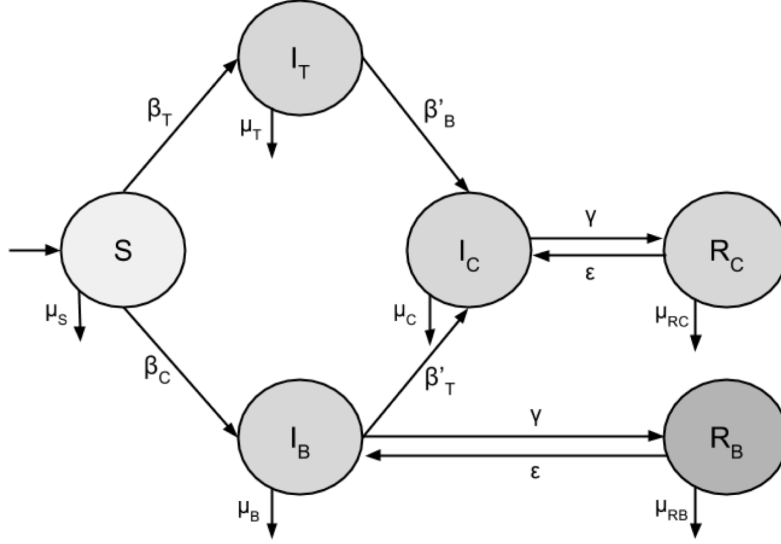


Figure 2: Diagram of model structure and assumptions. We model bTB infection as a directly transmitted, lifelong infection (Bengis 1999). We model brucellosis infection as a persistent infection, by allowing animals to recrudesce and transmit the infection. Buffalo populations experience logistic growth with density dependence in births rates that are independent of disease and for a fixed carrying capacity,  $K$  (Gao and Hethcote 1992). Transmission of both infections are assumed to be density dependent.

## 27 Model Structure and Assumptions

We developed a continuous time differential equation model to evaluate the disease dynamic consequence of bTB invasion on brucellosis dynamics and vice versa. Our model structure reflects the costs of co-infection identified for each parameter: host mortality rate, host birth rate, and disease transmission rates (Figure 2). Animals are represented with six groups: susceptible to both infections ( $S$ ), acutely infected with brucellosis ( $I_B$ ), chronically infected with or recovered from acute brucellosis ( $R_B$ ), infected with bTB ( $I_T$ ), co-infected with both pathogens ( $I_C$ ), or in the chronic stages of brucellosis and infected with bTB ( $R_C$ ). These assumptions give the following set of 6 differential equations:

$$N = S + I_T + I_B + R_B + I_C + R_C$$

$$T = I_T + I_C + R_C$$

$$B = I_B + I_C$$

$$N_b = S + b_1 I_T + b_2 I_B + b_3 R_B + b_4 I_C + b_5 R_C$$

$$\frac{dS}{dt} = bN_b \left(1 - \frac{r}{b} \frac{N}{K}\right) - \beta_T T S - \beta_B B S - \mu_S S$$

$$\frac{dI_T}{dt} = \beta_T T S - \beta'_B B I_T - \mu_T I_T$$

$$\frac{dI_B}{dt} = \beta_B B S - \beta'_T T I_B - \gamma I_B + \epsilon R_B - \mu_B I_B$$

$$\frac{dI_C}{dt} = \beta'_T T I_B + \beta'_B B I_T - \gamma I_C + \epsilon R_C - \mu_C I_C$$

$$\frac{dR_B}{dt} = \gamma I_B - \epsilon R_B - \mu_{RB} R_B$$

$$\frac{dR_C}{dt} = \beta'_T T R_B + \gamma I_C - \epsilon R_C - \mu_{RC} R_C$$

where  $N$  is the total host population and  $T$ ,  $B$ , and  $N_b$  are the numbers of buffalo contributing to tuberculosis transmission, brucellosis transmission, and births respectively.

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To evaluate the consequences of co-infection for disease invasion, we evaluate how co-infection alters the basic reproduction number ( $R_o^T$ ) of bTB.

Lets first consider the bTB only model:

$$\begin{aligned} \frac{dS}{dt} &= b(S + b_1 I_T) \left(1 - \frac{r}{b} \frac{S + I_T}{K}\right) - \beta_T S I_T - \mu S \\ \frac{dI_T}{dt} &= \beta_T S I_T - \mu_T I_T \end{aligned}$$

$R_o^T$  for bTB in the case when brucellosis is absent is,  $R_o^T = \frac{\beta_T K}{\mu_T}$ . The disease free equilibrium is  $E_o = (K, 0)$ , where the variables are denoted  $x_o = (S, I_T)$ . The endemic

equilibrium for bTB when brucellosis is absent is,  $E^* = (S_T^*, I_T^*)$ , where  $S_T^* = K \frac{1}{R_o^T}$  and

$$I_T^* = \frac{K}{2} \frac{1}{b_1} \left[ \left( \frac{bb_1 - \mu - \alpha_T}{r} - \frac{1 + b_1}{\mathcal{R}_0^T} \right) + \sqrt{\left( \frac{bb_1 - \mu - \alpha_T}{r} - \frac{1 + b_1}{\mathcal{R}_0^T} \right)^2 + 4 \frac{b_1}{\mathcal{R}_0^T} \left( 1 - \frac{1}{\mathcal{R}_0^T} \right)} \right].$$

Now consider the brucellosis only model:

$$\begin{aligned} \frac{dS}{dt} &= b(S + b_2 I_B + b_3 R_B) \left( 1 - \frac{r(S + I_B + R_B)}{K} \right) - \beta_B I_B S - \mu_S S \\ \frac{dI_B}{dt} &= \beta_B I_B S - \gamma I_B + \epsilon R_B - \mu_B I_B \\ \frac{dR_B}{dt} &= \gamma I_B - \epsilon R_B - \mu_{RB} R_B \end{aligned}$$

31  $R_o^B$  for brucellosis in the case that bTB is absent is,  $R_o^B = \frac{\beta_B K}{\mu_S + \gamma + \delta}$  CHECK ME????

32 The endemic equilibrium for brucellosis when bTB is absent is  $E^* = (S_t^*, I_{Bt}^*, R_{Bt}^*)$ , where

33  $S_t^* = 2,$

34  $I_{Bt}^* = 2,$

35  $R_{Bt}^* = 2.$

36  $R_o$  for bTB when brucellosis is present is,  $R_o^T = 2.$

37

### Notes on deriving $R_o^T$ :

1. Note there are  $n = 6$  components of this model,  $m = 3$  of which are infected with bTB. Define the vector,  $x_o = [I_T, I_C, R_C, S, I_B, R_B]^T$ , such that  $x_i$  contains the huber of individuals in each component.

2. The rate of change of  $x_i$  (e.g. the differential equations) can be represented as,  $\mathcal{F}_i(x) - \mathcal{V}_i(x)$ . Here  $\mathcal{F}_i(x)$  is the rate of appearance of new infections in compartment i and  $\mathcal{V}_i(x)$  is the rate of transfer by all other means. Noting the negative sign with  $\mathcal{V}_i(x)$  and that  $\mathcal{F}_i(x)$  only includes infections that are newly arising and does not include terms which describe the transfer of infectious individuals from one infected compartment to another.

Here,  $\mathcal{F}_i(x) = \left[ \frac{\beta_T S(I_T + I_C + R_C)}{S + I_T + I_B + I_C + R_B + R_C}, \frac{\beta_T I_B(I_T + I_C + R_C)}{S + I_T + I_B + I_C + R_B + R_C}, \frac{\beta_T R_B(I_T + I_C + R_C)}{S + I_T + I_B + I_C + R_B + R_C}, 0, 0, 0 \right]^T$ .  
 $\mathcal{V}_i(x) = [2]^T$

3. Check  $\mathcal{F}_i$  and  $\mathcal{V}_i$  meet the conditions outlined by van den Driessche and Watmough (2002) so you can use the next generation matrix,  $FV^{-1}$ , from m by m matrices of partial derivatives of  $F_i$  and  $V_i$ . (CHECK ME)  $F_i = \left[ \frac{\partial \mathcal{F}_i(x_o)}{\partial x_i} \right]$ .  $V_i = \left[ \frac{\partial \mathcal{V}_i(x_o)}{\partial x_i} \right]$ .  $x_o$  are the disease free equilibrium values of x.

4. Define bTB free equilibrium values  $x_o = [I_T = 0, I_C = 0, R_C = 0, S = S^*, I_B = I_B^*, R_B = R_B^*]^T$ . Where  $S^*$ ,  $I_B^*$ , and  $R_B^*$  are the equilibrium values of brucellosis in the absence of bTB.

5. Evaluate the F and V matrices at  $x_o$ .

Here,  $F_i = \begin{bmatrix} \frac{\beta_T S^*}{(S^* + I_B^* + R_B^*)} & \frac{\beta_T S^*}{(S^* + I_B^* + R_B^*)} & \frac{\beta_T S^*}{(S^* + I_B^* + R_B^*)} \\ \frac{\beta'_T I_B^*}{(S^* + I_B^* + R_B^*)} & \frac{\beta'_T I_B^*}{(S^* + I_B^* + R_B^*)} & \frac{\beta'_T I_B^*}{(S^* + I_B^* + R_B^*)} \\ \frac{\beta'_T R_B^*}{(S^* + I_B^* + R_B^*)} & \frac{\beta'_T R_B^*}{(S^* + I_B^* + R_B^*)} & \frac{\beta'_T R_B^*}{(S^* + I_B^* + R_B^*)} \end{bmatrix}$

Here,  $V_i = \begin{bmatrix} a & b & c \\ d & e & f \\ g & h & i \end{bmatrix}$

6. Calculate  $FV^{-1}$

7. The dominant eigenvalue of  $FV^{-1}$  is xxx.

## Approach

Mortality and Fecundity parameters:

- Data analyses informs mortality rates for each disease category in *young females aged 2-8*).
- Data analysis informs fecundity rates for each disease category in *young females aged 2-8*).
- How to extrapolate to males and other age groups (Figure 3)?

Parameters relevant to the time course of brucellosis are limited to cattle and U.S. bison:

- Pull  $\gamma$  and  $\epsilon$  from the literature.
  - Few animals were followed less than 2 years so assume our estimates are relevant for  $I_B$ .
- Still thinking about this.

Transmission:

- Data analyses inform the proportional increase in transmission with co-infection (e.g. that  $\beta'_B = 2.8 * \beta_B$ ). I hope to estimate  $\beta_B$  and  $\beta_T$  from the time sequence data.



**Parameter table**

	Value	Meaning
$b$	0.54	maximum natural birth rate for uninfected adults
$b_1$	0.20	proportional reduction in births for adults with bTB
$b_2$	0.22	proportional reduction in births for adults with brucellosis.
$b_3$	assume= $b_2$	proportional reduction in births with chronic brucellosis.
$b_4$	0.35	proportional reduction in births for co-infected adults.
$b_5$	assume= $b_4$	proportional reduction in births for co-infecteds with chronic brucellosis.
$\mu_{S_i}$	0.12, 0.04	annual mortality rate for uninfected juveniles and adults
$\mu_{T_i}$	$2.82\mu_{S_i}$	annual mortality rate for animals with bTB
$\mu_{B_i}$	$3.02\mu_{S_i}$	annual mortality rate for animals with brucellosis
$\mu_{R_{B_i}}$	$\mu_{B_i}$	annual mortality rate for animals with chronic brucellosis
$\mu_{C_i}$	$5.84\mu_{S_i}$	annual mortality rate for animals with bTB-brucellosis co-infection
$\mu_{R_{C_i}}$	$\mu_{C_i}$	annual mortality rate for co-infecteds with chronic brucellosis
$\beta_T$	fit to data	transmission rate for bTB in susceptible animals
$\beta_B$	fit to data	transmission rate for brucellosis in susceptible animals
$\beta'_T$	$\beta_T$	transmission rate for the bTB in animals infected with brucellosis
$\beta'_B$	$2.1\beta_B$	transmission rate for brucellosis in animals infected with bTB
$\gamma$	1/2	1/duration of infectious period for brucellosis
$\epsilon$	0.01	recrudescence rate
$\rho$	0.05	proportion of births from animals with brucellosis that result in infection

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Let's consider first the TB-only model:

$$\frac{dS}{dt} = bN_b \left( 1 - \frac{r}{b} \frac{N}{K} \right) - \beta_T S I_T - \mu S \quad (1)$$

$$\frac{dI_T}{dt} = \beta_T S I_T - \alpha_T I_T - \mu I_T \quad (2)$$

Then the disease free equilibrium is  $E^0 = (K, 0)$  where the population is  $x = (S, I_T)$ . The basic reproduction number is  $\mathcal{R}_0 = \frac{\beta_T K}{\alpha_T + \mu}$ . The endemic equilibrium is  $E^* = (S^*, I_T^*)$  where  $S^* = K \frac{1}{\mathcal{R}_0}$  and

$$I^* = K \left( \frac{r - \alpha_T}{2r} - \frac{1}{\mathcal{R}_0} + \frac{1}{2r} \sqrt{(r - \alpha_T)^2 + \frac{4r\alpha_T}{\mathcal{R}_0}} \right).$$

76 When  $\alpha_T = 0$ , then  $I^* = K(1 - 1/\mathcal{R}_0)$ . We fix other parameters and vary  $\beta_T$  to get endemic  
77 levels such that  $I^*/N = 10\%$ , etc.

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