Minimum cost to control bovine tuberculosis in cow-calf herds

Rebecca L. Smith[*], **Loren W. Tauer**[**], **Michael W. Sanderson**[·], and **Yrjo T. Grohn**[*]

[*]Section of Epidemiology, Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, NY 14853

[**]Dyson School of Applied Economics and Management, Cornell University, Ithaca, NY 14853

[·]Department of Clinical Sciences, Kansas State University, Manhattan, KS 66502

Abstract

Bovine tuberculosis (bTB) outbreaks in US cattle herds, while rare, are expensive to control. A stochastic model for bTB control in US cattle herds was adapted to more accurately represent cow-calf herd dynamics and was validated by comparison to 2 reported outbreaks. Control cost calculations were added to the model, which was then optimized to minimize costs for either the farm or the government. The results of the optimization showed that test-and-removal costs were minimized for both farms and the government if only 2 negative whole-herd tests were required to declare a herd free of infection, with a 2–3 month testing interval. However, the optimal testing interval for governments was increased to 2–4 months if the model was constrained to reject control programs leading to an infected herd being declared free of infection. Although farms always preferred test-and-removal to depopulation from a cost standpoint, government costs were lower with depopulation more than half the time in 2 of 8 regions. Global sensitivity analysis showed that indemnity costs were significantly associated with a rise in the cost to the government, and that low replacement rates were responsible for the long time to detection predicted by the model, but that improving the sensitivity of slaughterhouse screening and the probability that a slaughtered animal's herd of origin can be identified would result in faster detection times.

Introduction

Bovine tuberculosis (bTB), which is caused by chronic infection with *Mycobacterium bovis*, is a sporadically epidemic disease in the US cattle industry, but with endemic infection currently only in the state of Michigan (USDA:APHIS:VS, 2009). Although some states have experienced spillback from endemically infected wildlife populations, most of the

Publisher's Disclaimer: This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final citable form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

country has eradicated the disease; infections, therefore, are usually believed to be due to animal movement from endemically infected areas, primarily Mexico (USAHA, 2011). In 2011, APHIS provided funds to depopulate 7 herds and implemented a test-and-remove plan for 1 herd that was later depopulated with state funds from Michigan. One large dairy herd in CA remained under test-and-remove (USAHA, 2011). The US is now averaging 10 or fewer newly detected herds per year, but with increasing herd size (USAHA, 2011).

Despite the rarity of herd-level outbreaks (USDA:APHIS:VS, 2009), large sums of money are spent by state and federal authorities to control bTB and these expenditure may increase in the future. The financial toll on Nebraska of 2 outbreaks in 2009 was substantial; the governor appropriated $750,000 to the Department of Agriculture to cover employee overtime, outside help, and purchase of animal restraint equipment necessary for the traceback effort (USAHA, 2010). The federal costs associated with an outbreak in Indiana were $136,709 for personnel, $24,388 for travel, $111,908 for indemnity, and $8,129 for other costs (USAHA, 2011). Reducing the cost of the bTB control program, particularly personnel and travel costs, could benefit agency budgets and allow for more time and money to be spent on control of other diseases. However, a full analysis of the control system should be performed to ensure that a less stringent response is as effective as the historical control program, as improperly controlled outbreaks could lead to state or regional quarantines, which would devastate the cattle trade and potentially affect wildlife. The system can be split into two categories: testing (within a farm) and tracing (between farms); analysis of these categories will require different methods and models.

Previous work developed a model for the testing category of control of bTB in individual US cattle herds (Smith et al., 2013a) and economically analyzed that model in individual dairy herds (Smith et al., 2013b). The structure of beef cow-calf herds, however, has the potential to change both the spread of bTB within herds and to dramatically change the costs and benefits of different testing strategies. The purpose of this study, therefore, is to analyze the control of bovine tuberculosis in individual cow-calf herds and to minimize testing-related control costs while ensuring the efficacy of the control.

Materials and Methods

Model description

A schematic of the epidemiologic portion of the model is shown in Figure 1; all parameter values used in the total model are provided in Tables 1 and 2. This model considers only spread of bTB within a single herd, and does not include tracing equations or costs. Management parameters and herd-level values and costs were calculated on a national basis and by the regions defined by the USDA's Economic Research Service (USDA:ERS, 2012), using the mean, minimum, and maximum of annual values from 2008 to 2011. The states included in regional divisions are shown in Table 1. The system was modeled using a stochastic (tau-leap) methodology (Keeling and Rohani, 2008). In this method, actions occur each month in a fixed order: disease updating, then demographic updating, then testing.

Disease updating consists of first calculating the number of infections from the last month at rate lambda, which is calculated as $\frac{\beta * S(t) * I(t)}{N(t)}$ with S(t), I(t), and N(t) being the number of

susceptible, infectious, and total animals in the group at time t, respectively, with β representing the transmission coefficient. The newly infected animals are moved from the susceptible category to the latent category then allowing all infected animals to progress through disease levels (from latent to reactor and from reactor to infectious) as appropriate. Infection is calculated separately for the adult, calf, and youngstock categories of the herds, but the adult and calf herds experience the same infectious pressure, lambda.

Demographic updating first identifies the number of adults culled from each category and removes them from the herd, then identifies the number of calf births, adds these new calves to the herd, and identifies the number of calf deaths and removes them from the herd. Calf births are assumed to occur uniformly over a 3 month calving period, which is modeled as 3 monthly cohorts of calves. If the last cohort of calves has reached weaning age (7–8 months) (Short, 2001), a sufficient number of replacements to return the adult herd to its original size is randomly chosen from the calf categories (S_C, E_C, T_C, and I_C) according to their relative size; this ensures that the annual replacement rate is equal to the annual culling rate and that the herd size is maintained at a stable level. The remaining calves are moved to a youngstock cohort. Youngstock cohorts are managed separately with respect to transmission until slaughter at the age of 30 months, at which point they may be traced back to the source herd with probability P_{trace}. These youngstock cohorts are assumed to be moved to different premises, such as a stocker operation and feedlot, but each cohort is assumed to be maintained as a single group.

In a herd with initial undetected bTB infection, detection was assumed to occur by way of slaughterhouse detection of infected animals with lesions; other means of detection (trace outs, movement testing, and herd accreditation testing) were not considered. All infectious and reactor animals were considered to be at risk of slaughterhouse detection, which has a pre-determined sensitivity (Table 2), at the time of death. The probability of detection was calculated for culled adult animals at the time of culling and for slaughtered youngstock at the time of slaughter, and that probability was used in a binomial distribution to determine whether the infection is detected. If a youngstock animal was detected, the probability by which it could be traced back to the herd of origin (Table 2) was used in a further binomial distribution to determine whether the herd was detected.

In a herd in which bTB infection has been detected and which is under quarantine, testing consists of whole-herd testing (WHT) by the caudal fold test (CFT) at testing intervals of T_{ti}; all testing regulations are as described in the 2005 Uniform Methods and Rules (USDA:APHIS:VS, 2005) and, where changes have been made explicit, the 2009 Memorandum 552.47 (Clifford, 2009). In herds under the removal phase (herds with fewer than 2 WHT with no bTB-positive lesions), all animals over 2 months of age are tested by CFT and CFT-positive animals are slaughtered and subjected to post-mortem examination and PCR confirmation of all lesions. The number of infectious and reactor animals found to be positive, with probability Se_{CFT}, and the number of susceptible and latent animals found to be positive, with probability $1-Sp_{CFT}$, was determined by use of the binomial distribution. In herds under the validation phase (herds with at least 2 WHT with no bTB-positive lesions) (USDA:APHIS:VS, 2005), all animals over 6 months of age are tested by CFT and all CFT-positive animals are then tested with the comparative cervical test (CCT) or

interferon-γ (IFN-γ) test, with the binomial distribution again providing the number of animals in each category found to be positive. All positive animals are slaughtered and subjected to post-mortem examination and PCR confirmation of all lesions. It is assumed that a portion of infectious and reactor animals sent to post-mortem examination ($N_{pmexam;I,R}$) will be confirmed with probability Se_{PCR} (imperfect sensitivity) and that all susceptible and latent animals sent to post-mortem examination ($N_{pmexam;S,E}$) will be found negative (perfect specificity). If a herd under quarantine has reached a specified number of negative WHT (N_{WHT}), it is declared to be bTB-free and the quarantine is lifted. Herds under quarantine were until recently required to pass 8 negative WHT before clearance (official declaration of disease freedom): 4 tests with a 2-month T_{ti}, 1 test with a 3-month T_{ti}, and 3 tests with a 1 year T_{ti} (USDA:APHIS:VS, 2005). If a herd in the validation phase has a positive WHT, it is returned to the removal phase. In feedlots, animals known to be exposed to bTB are quarantined, then shipped to slaughter (USDA:APHIS:VS, 2005). Feeder calves under 12 months of age from a cow-calf herd that have passed a CFT test may be moved to a feedlot (USDA:APHIS:VS, 2005).

Validation

In order to validate this model, 2 observed outbreaks in cow-calf herds were reproduced with the simulated results compared to observed results.

A beef ranch in Texas beginning with 26 Red Devon cattle and one exposed animal was reported to operate on a closed basis, testing positive at slaughterhouse surveillance after 15 years, at which time it contained 331 animals. A total of 193 randomly selected animals were tested by CFT, with 52 positive and 32 of those with visible lesions.(Perumaalla et al., 1999). This herd was recreated with the model. For purposes of model fitting, it was assumed that a growing closed herd would have a low culling rate (0.1 adults/year) and a low calf mortality rate (0.1 calves/year). As the herd size grew rapidly in 15 years, it was also assumed that 60% of heifer calves (30% of all calves) would be retained until reaching the final observed herd size. It was also assumed that traceback of youngstock sent to slaughter was not possible, limiting herd detection to slaughterhouse surveillance of adult culls, as the long time to herd detection indicated a delay in the normal surveillance system. The model was run until detection for each of 100,000 iterations, discarding and replacing runs in which fadeout occurred before detection, with outputs of the final proportion of CCT-positive animals in a sample of 193 randomly selected animals and the proportion of CCT-positive animals with lesions.

An infected beef herd in Nebraska was identified by slaughter trace of a cull cow in May of 2009. Of the approximately 800 cows in the herd, over 100 responders were culled and only 1 additional cow was positive over 4 WHT with 60 day testing intervals (USAHA, 2010). A whole herd assurance test was completed 1 year later, with all animals negative (USAHA, 2011). This herd was recreated with the model, assuming 800 adult animals, a calf death loss rate of 10% and an adult culling rate of 10% (anonymous reviewer, personal communication); all other parameters were modeled as for the Northern Great Plains region (Table 1). The model was run for 100,000 iterations, with a T_{ti} of 2 months and N_{WHT} of 4

after detection, and with outputs of the number of responders culled and the number of active lesions.

Economics Results

Farm-level—At the farm level, the cost of an outbreak with only removal of test confirmed animals consisted of the unrecovered expenditures due to removal of calves testing positive at weaning, the cost of replacing test-positive adult animals, and the cost of quarantine. As we assume no cost due to quarantine, these combine to create a single cost function,

$$cost_f(t) = (repl - indem) * N_{cull}(t) + (MV - indem_{calf}) * N_{calfcull}(t) \quad [1]$$

here *repl* is the market cost of a replacement animal, *indem* is the indemnity amount paid for the average animal culled for tuberculosis, N_{cull} is the number of animals culled for positive test results, *MV* is the market value of a calf, $indem_{calf}$ is the indemnity amount paid for the average calf culled for tuberculosis, and $N_{calfcull}$ is the number of calves culled for positive test results. Under current U.S. replacement policy replacement animals represented by *indem* will often be genetically and health-wise equivalent to the culled animals with no production delays. The farmer is compensated based upon the market value of the culled animal but there is no requirement that the culled animal be replaced with an identical animal. Thus (*repl – indem*) will be net zero in most circumstances, with any deviation explored in the sensitivity analysis (below). It is assumed that *MV = indem_calf*, as the true market value of calves is easier to determine. Transportation costs are not considered.

Depopulation cost, however, would consist of the cost of replacing all adult animals, the loss of any calves present on the farm, and the loss of the next calf crop. This combines to create a cost function,

$$cost_{f,depop} = disinfect + (repl - indem) * N + \sum_m I_m * N * (1 - \mu_c) * MV \quad [2]$$

where *disinfect* is the cost of disinfecting the farm. In order to account for the loss of the following calf crop if depopulated animals were pregnant, *m* is the month in the herd's breeding cycle, and I_m is an indicator variable which is 1 if the breeding season has passed and 0 otherwise; it is assumed that replacement animals will not be pregnant. As *N* is the number of breeding adults in the herd, and μ_c is the annual death rate of calves assuming a conception rate of 100%, $N*(1-\mu_c)$ is the number of weaned calves expected in the next year.

Government-level—At the government level, the cost of an outbreak consisted solely of testing and indemnity expenses; the externality cost of a state-wide movement ban was not considered. Thus, the total government cost was:

$$costs_{gov} = \sum_t *c_{CFT}(t) + c_{CCT}(t) + N_{pmexam}(t) * (indem + disposal) - N_{pmexam;S,E}(t) * salvage + N_{pmexam;T,I}(t)* \quad [3]$$

here *t* is the testing period, c_{CFT} and c_{CCT} are the costs associated with CFT and CCT ([4] and [5]), respectively, N_{pmexam} is the total numbers of animals tested by post-mortem

examination and *indem* is the cost of their indemnity, $N_{pmexam;S,E}$ is the number of animals without lesions sent to post-mortem examination and *salvage* is the value of their carcasses, and $N_{pmexam;T,I}(t)$ is the number of animals with lesions sent to post-mortem examination and PCR and p_{PCR} is the cost of testing animals by PCR (Table 2). The variable $N_{calfcull}$ is the number of calves culled for positive test results and MV is the market value of the calves. The cost of each CFT is represented by c_{CFT},

$$c_{CFT}=A*N+2M*MR \quad [4]$$

with all variables as described previously (Dressler et al., 2010) and in Table 2. Briefly, *A* is the cost of administering the test per animal, including labor and supplies, *N* is the number of animals tested (all adult animals in the herd and all calves over 2 months of age during the removal phase or all calves over 6 months of age during the validation phase), *M* is the miles traveled by the veterinarian performing the test (conservatively assumed to be 50 miles, as the distance will vary by state due to the varying density of USDA veterinarians and staff), and *MR* is the cost of traveling per mile, specified at 55 cents. The cost of CCT, c_{CCT}, is the cost of testing all CFT-positive animals at time t, $N_{CCT}(t)$, by CCT,

$$c_{CCT}=A*N_{CCT}+2M*MR \quad [5]$$

and all CCT+ animals, N_{pmexam}, were culled and tested by enhanced inspection. Animals in the infectious and reactor categories were assumed to have lesions that would be tested by histopathologic examination and PCR.

The government-level cost of depopulation consists of indemnity and testing costs, less salvage value, gives the government cost function,

$$costs_{gov,depop}=N*(indem+disposal)+N_{T,I}*p_{PCR}-N_{S,E}*salvage+N_c*MV \quad [7]$$

where $N_{T,I}$ is the number of infectious and reactor animals in the herd, which are assumed to have lesions that will be tested by PCR at cost p_{PCR} (Table 2), $N_{S,E}$ is the number of susceptible and latent animals in the herd, which are assumed to have no lesions, and N_c is the number of calves present in the herd with market value *MV*.

At present, the value of indemnity is officially 100% of the fair market value, up to $3,000 (USDA:APHIS:VS, 2010). This value will change for each animal, but given our equations are for the herd, an average for the herd can be considered; in a New Mexico dairy herd of 1500 cows, indemnity for depopulation was calculated to cost $3,750,000, or $2,500/animal (USAHA, 2008; Wolf et al., 2000), which was approximately equal to replacement costs plus the value foregone due to early culling of a dairy cow. Therefore, this model will assume indemnity cost to be equal to the replacement cost.

Optimization

Equations [2] and [7] were separately optimized for the farm and government respectively over testing interval (range of $T_{ti} = 2$ to 12) and number of WHT needed for clearance

(range of N_{WHT} = 2 to 8) using a global search method for discrete stochastic optimization (Andradottir, 1996) over 100,000 iterations. The optimal solutions were defined as minimum cost. Constrained optimization was also implemented, in which an iteration of a solution was rejected if that iteration resulted in a herd being cleared from quarantine while retaining infected animals (false clearance).

For the purpose of economic analysis, this optimization was performed for each of the 8 regions defined by the USDA's Economic Research Service and for the national average, with parameters that vary by region presented in Table 1. All parameters without regional variation are presented in Table 2.

The model and all analyses were programmed in R 2.12.2[1], which was accessed through the Revolution R Analytics 4.3.0 interface[2].

Results

Validation

Figure 2 shows a histogram of results from 100,000 iterations for the Texas outbreak; herd size and prevalence of infection were correlated with the detection time, with all herds reaching the observed herd size within 7 years. The median detection time was 9.92 years (range 1 month to 41 years); 15% were detected at least 14 years after introduction of bTB. Of the herds detected after 14 years, the median proportion of CFT+ animals in a randomly selected sample of 193 animals was 0.26 (observed was 0.27) and the median proportion of CFT+ animals with visual lesions was 0.56 (observed was 0.62); the median size of herds detected at least 14 years after introduction of bTB was 314 animals (observed was 331).

The results of the simulation of the Nebraska outbreak closely matched the observed outbreak (figure not shown). Of the 75,685 iterations in which the model predicted that bTB would be detected in the herd, 4,991 (7%) predicted exactly the observed 1 additional infected animal and 0 and 2 additional infected animals were predicted 5,818 (8%) and 7,339 (10%) times, respectively; 37,056 iterations (49%) predicted more than 5 additional infected animals. Most iterations predicted over 100 responders culled (as observed), with the majority of iterations (61,584 or 82% of herds detected) predicting between 100 and 250 responders culled. The model predicted that the median time to detection in this herd was 61 months after introduction of a single latently infected animal, with a minimum of 1 month and a maximum of 375 months.

Optimization

Figure 3 shows the results of the optimizer for the government using national average parameters. There was a clear preference for 2 negative WHT for clearance, and a slight preference for a 2 month testing interval. If we restrict the optimizer so that it does not allow false clearance, the preferred testing interval is longer (Figure 4). The results of optimizing

---

[1]R (2011); 2.12.2
[2]Revolution R Enterprise (2011); 4.3.0

on farm costs were similar with and without constraints, with a weak preference for 2 negative WHT for clearance and a 2 month testing interval in all regions.

Model results

Assuming a testing interval of 3 months and 2 negative WHT needed to clear quarantine with national average parameters, the model predicted that herds would remain in quarantine for up to 6 months after fadeout (removal of all infected animals) had occurred (median, 3 months), with a total of 3 to 255 months in quarantine (median, 6 months). Few detected simulations (7/661) cleared quarantine before fadeout had occurred, 6 of which involved one infected adult, the remaining herd involving one infected calf. All herds experienced eventual fadeout, even those falsely clearing quarantine, which experienced fadeout between 1 and 33 months after clearing quarantine. As can be seen in Figure 5, increasing either the testing interval or the number of negative herd tests required to clear quarantine, or a combination of both, resulted in no herds clearing quarantine before eliminating infection. However, that also increased the mean government-level cost of the control program (Figure 6).

Economic Results

Figure 7 shows the distribution of government (a) and farm (b) costs for controlling a bTB outbreak in a cow-calf herd using national average parameters with a testing interval of 2 months and 3 negative WHT needed for clearance. In the detected herds, the cost to the government was substantial (see Table 3). For the government, the cost of depopulation was higher than the cost of test and remove in some, but not all, circumstances. The economic preference for test and remove decreased with an increase in the apparent prevalence in the herd at the time of detection (data not shown). The median government cost of the historical bTB control program was substantially more than the median cost of the optimal program in all regions, but the range of costs overlapped between the programs (Table 3).

In many regions, the optimal government cost distributions for depopulation either mostly or completely overlap that for test-and-remove. The difference between the cost of test-and-remove programs and the cost of depopulation, which can be considered the break-even cost to the state of the presence of an infected herd, is shown in Figure 8 for each region's government (a) and farm (b). For farms, the cost of depopulation was always higher than the cost of test and remove (Table 4), with a bimodal distribution related to the presence of calves in the herd at the time of depopulation.

Sensitivity Analysis

Figure 9 shows the results of a global sensitivity analysis on the costs to governments (a) and the time to detection (b), with a testing interval of 3 months and 2 negative whole herd tests required for clearance. For the government, increased indemnity costs, replacement costs, CFT specificity, calf market value, weaning month, and test administration cost increased the cost. Increases in the replacement rate, the sensitivity of slaughterhouse surveillance, and the probability of successful traceback of infected animals all significantly decreased the time to detection. The only parameter significantly correlated with the cost to

farms was the indemnity payment, an increase in which decreased the cost to farms (data not shown).

Discussion

This paper presents a bioeconomic model for within-herd transmission and control of bovine tuberculosis in beef cow-calf herds. Economic optimization of the model has provided guidance for more cost-effective control programs for individual herds, and sensitivity analysis has identified potential areas for improvement in these control programs.

One of the most important findings of this model was the regional variation in both the optimal testing interval for government costs and in the government's preference for depopulation versus test-and-removal. The primary cause of this variability is animal replacement cost in the different regions; the sensitivity analysis showed that indemnity was the major cost driver to the test-and-removal program, as *indem* (defined as the extra indemnity value over the loss associated with culling) was the most important parameter and *repl* (the cost to replace the culled animal, the primary component of the indemnity calculation) was the second most important parameter. Indemnity would also be the major cost driver for depopulation, more so than test-and-removal as the number of animals culled is greater in depopulation. Previous analyses have also found that indemnity payments are the largest cost of bTB outbreak control (Wolf et al., 2008). The 3 regions most preferring test-and-removal over depopulation (Heartland, Prairie Gateway, and Basin and Range) also had the 3 highest replacement costs. As this value can also vary significantly over time, the preference for depopulation should perhaps be less regional and more temporal and tied to the replacement cost, with depopulation preferred when replacement costs (and hence indemnity) are lower than average and test-and-removal preferred if replacement costs are higher than average. This contrasts directly with previous findings regarding bTB control in dairy herds, in which test-and-removal is always preferred (Smith et al., 2013b), but replacement costs in dairy herds are much higher and detection is faster, resulting in a lower prevalence at the time of detection.

Analysis of the model showed that detection times could vary widely, due to the typically low culling rate and the low probability of traceback, although the addition of movement testing and accreditation testing would likely decrease the time to detection to some extent. In the first half of 2011, 3 infected adult beef cattle were detected by slaughterhouse surveillance, one of which (the Indiana herd) led to trace investigations of over 150 cattle in 11 states and surveillance of white-tailed deer on and adjacent to the farm without finding a source or any other infected animals outside the index herd (USAHA, 2011). According to our model results, the infection could have been present in the herd for over 16 years, which would require a more extensive trace investigation than was likely considered or, indeed, feasible. Lacking sensitive detection of culled positive animals and accurate traceback from slaughter surveillance to positive herds, bTB could smolder at low levels for a long period of time; the results of this model show that a better tracking system for slaughtered animals is important to decreasing the time to detection. While the probability of traceback did not significantly affect the cost of the outbreak in a single herd, the ability to accurately track animals would likely decrease the cost of the trace investigation and improve the likelihood

of finding the infection source. This finding agrees with an economic analysis of the nationwide control program with a constant risk of introduction (Wolf et al., 2008), which concluded that improved traceability was required to eradicate the infection under the historical control program.

A small proportion of herds was predicted by the model to clear quarantine before eliminating the infection, even using the test-and-removal plan preferred by an optimization that rejected such false clearances. This was due to the slow progression of the disease, allowing for a latent period longer than the testing period. All these herds still eliminated the infection eventually. The concern, however, is that these herds could transmit the infection to other herds, increasing the potential cost of the outbreak. The impact of such herds should be assessed further; however, such an assessment would require a network model that could represent animal movements and herd connections, which is beyond the scope of the current research. The sensitivity analysis indicated that increasing the specificity of the frontline test increased the cost of a test-and-removal program. This was most likely because fewer false positive results resulted in less fortuitous culling of latent animals, allowing latent animals to remain in the herd longer; the specificity of the CFT was the most influential parameter for the number of animals culled, with an inverse relationship (data not shown).

The difference between farm and government preferences should be noted: while it is in the best interests of the government to depopulate infected farms in most regions, depopulation is never the best option for the farm owner due to the reduction in the production of calves, and therefore income, for an extended period of time. While disease control policy is often set with the government's preferences in mind, it is important that policy makers be aware of the potential conflict. The economic and psychological (Nusbaum, 2007) impact of depopulation requires careful implementation of such plans, as cooperation with farm owners is necessary for successful eradication efforts (Okafor et al., 2011). It should be noted that this model did not consider several producer-level costs that are not universal, but that could change the results; these include transportation costs for replacement animals and costs related to the reluctance of stockers and feedlots to buy calves from quarantined farms, which has been reported anecdotally (H. Morgan Scott, personal communication). As these costs could change producer preferences, they should be considered in responding to a specific outbreak.

Based on the results of the model presented here, we cannot make sweeping recommendations for bTB control in cow-calf herds. Rather, the decision of the control method (depopulation or test-and-removal) and implementation must be decided based on the circumstances at the time of detection. The USDA has implemented an evaluation policy for addressing newly detected herd infections which, although not publically available, is reported to take into account the apparent prevalence in the herd at the time of detection, the risk of further disease transmission, the effectiveness of management at mitigating disease spread, and the cost-effectiveness of depopulation. The model presented above agrees with this approach, showing that the cost-effectiveness of depopulation will vary by a number of factors, including the apparent prevalence in the herd at the time of detection. However, the findings of the model do indicate that the US would benefit from an improved method for tracking infected animals from slaughter back to their source herd. Further analysis of the

tracing aspect of the bTB control program would be beneficial, but was beyond the scope of this model.

Acknowledgments

References

Andradottir S. A Global Search Method for Discrete Stochastic Optimization. SIAM J Optim. 1996; 6:513.

Asseged B, Woldesenbet Z, Yimer E, Lemma E. Evaluation of abattoir inspection for the diagnosis of Mycobacterium bovis infection in cattle at Addis Ababa abattoir. Trop Anim Health Prod. 2004; 36:537–546. [PubMed: 15560514]

Barlow ND, Kean JM, Hickling G, Livingstone PG, Robson AB. A simulation model for the spread of bovine tuberculosis within New Zealand cattle herds. Prev Vet Med. 1997; 32:57–75. [PubMed: 9361321]

Buhr, B.; McKeever, K.; Adachi, K. Michigan Bovine Tuberculosis Bibliography and Database. St. Paul, MN: 2009. Economic Impact of Bovine Tuberculosis on Minnesota's Cattle and Beef Sector; p. 20

Clifford JR. Procedures for Managing Bovine Tuberculosis-Affected Cattle Herds. 2009

De la Rua-Domenech R, Goodchild AT, Vordermeier HM, Hewinson RG, Christiansen KH, Clifton-Hadley RS. Ante mortem diagnosis of tuberculosis in cattle: a review of the tuberculin tests, g-interferon assay and other ancillary diagnostic techniques. Res Vet Sci. 2006; 81:190–210. [PubMed: 16513150]

Dressler JB, Smith RL, Tauer LW, Schukken YH, Grohn YT. Economic analysis of the cross-reactivity of Johne's disease vaccination with tuberculosis in dairy cattle. Am J Ag Econ. 2010; 92:1446–1455.

Internal Revenue Service. 2009 Standard Mileage Rates. Washington, D.C: 2008. IR–2008–131

Kao RR, Roberts MG, Ryan TJ. A Model of Bovine Tuberculosis Control in Domesticated Cattle Herds. Proc Biol Sci. 1997; 264:1069–1076. [PubMed: 9263472]

Keeling, MJ.; Rohani, P. Modeling Infectious Diseases in Humans and Animals. Princeton University Press; Princeton, NJ: 2008.

National Agricultural Statistics Service, Agricultural Statistics Board. Agricultural Prices; Washington, D.C: 2012.

Nusbaum K. Psychologic first aid and veterinarians in rural communities undergoing livestock depopulation. J Am Vet Med Assoc. 2007; 231:692–694. [PubMed: 17764423]

Okafor CC, Grooms DL, Bruning-Fann CS, Averill JJ, Kaneene JB. Descriptive epidemiology of bovine tuberculosis in michigan (1975–2010): lessons learned. Vet Med Int. 2011; 2011:874924. [PubMed: 21776355]

Perumaalla VS, Adams LG, Payeur J, Baca D, Ficht TA. Molecular fingerprinting confirms extensive cow-to-cow intra-herd transmission of a single Mycobacterium bovis strain. Vet Micro. 1999; 70:269–276.

Short, SD. Characteristics and Production Costs of U S Cow-Calf Operations (No SBN 974-3). USDA Economic Research Service; 2001.

Smith RL, Schukken YH, Lu Z, Mitchell RM, Grohn YT. Modeling infection dynamics of Mycobacterium bovis in US cattle herds and implications for control. J Am Vet Med Assoc. 2013a; 243:411–423. [PubMed: 23865885]

Smith RL, Tauer LW, Schukken YH, Lu Z, Grohn YT. Minimization of bovine tuberculosis control costs in US dairy herds. Prev Vet Med. 2013b; 112:266–275. [PubMed: 23953679]

USAHA. Report of the Committee on Tuberculosis. 2004. http://portals5.gomembers.com/Portals/6/Reports/2004/report-tb-2004.pdf

USAHA. Report of the Committee on Tuberculosis. 2008. http://www.usaha.org/Portals/6/Reports/2008/report-tb-2008.pdf

USAHA. Report of the Committee on Tuberculosis, Tuberculosis. Minneapolis, MN: 2010. p. 1-27.

USAHA. 20112011 TB report final.

USDA, APHIS:VS. Bovine Tuberculosis Eradication: Uniform Methods and Rules. 2005. http://www.aphis.usda.gov/animal_health/animal_diseases/tuberculosis/downloads/tb-umr.pdf

USDA:APHIS:VS. A New Approach for Managing Bovine Tuberculosis_: Veterinary Services ' Proposed Action Plan. 2009. http://www.aphis.usda.gov/newsroom/content/2009/10/printable/tb_concept_paper.pdf

USDA:APHIS:VS. Proposed Bovine Tuberculosis and Brucellosis Draft Regulatory Framework. 2010. http://www.aphis.usda.gov/animal_health/tb_bruc/downloads/tb_bruc_framework.pdf

USDA:ERS. Commodity Costs and Returns: Cow-calf: 2010–11. 2012.

USDA:NASS. Quickstats. 2007. http://quickstats.nass.usda.gov

Wolf, C.; Hadrich, J.; Horan, R.; Paarlberg, P.; Kaneene, J. Economic Analysis of US TB Eradication Program. USDA Animal and Plant Health Inspection Service; 2008.

Wolf, C.; Harsh, S.; Lloyd, J. Agricultural Economics. Department of Agricultural Economics, Michigan State University; East Lansing, MI: 2000. Valuing Losses from Depopulating Michigan Dairy Herds (No. 2000–10); p. 1-18.
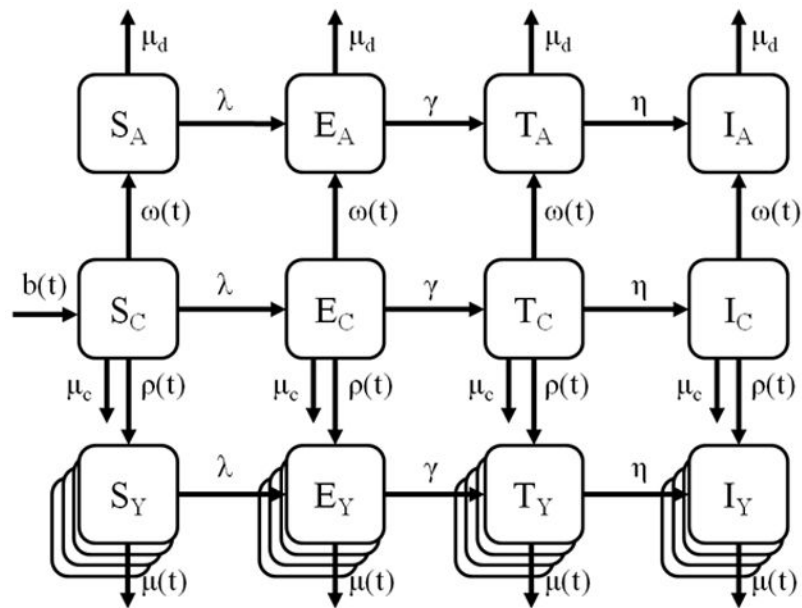
Figure 1.
Schematic of a compartment model for bovine tuberculosis in a cow-calf herd. Animals in compartments labeled with subscript A, C, and Y are adult breeding animals, calves, and youngstock, respectively. Animals enter the herd as calves during the calving season at rate b(t), such that all adults calve over a 3 month period, and all calves are subject to an annual death rate (μ_c). Susceptible animals are in S compartments, latent (exposed) animals are in E compartments, non-infectious animals that may be detected by testing are in T compartments, and infectious animals are in I compartments. Calves may enter the breeding herd at rate ($\omega(t)$); otherwise, all calves are moved to a youngstock cohort at rate ($\rho(t)$). Youngstock are slaughtered as a cohort at 30 months of age.
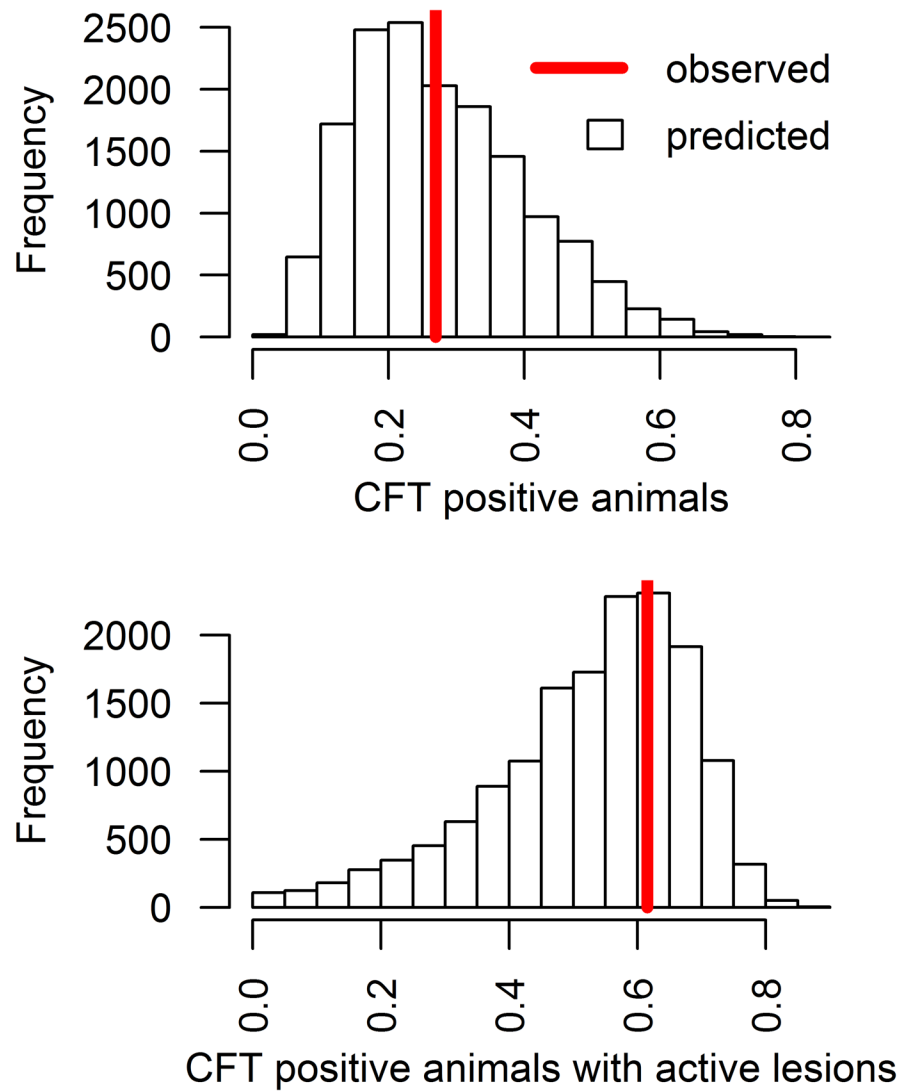
Figure 2.
Distribution of test results at the time of detection from a simulation to reproduce an outbreak in a Red Devon herd in Texas, including only herds that were detected at least 14 years after the introduction of bovine tuberculosis. Red lines are observed values; open bars indicate the predicted distribution.
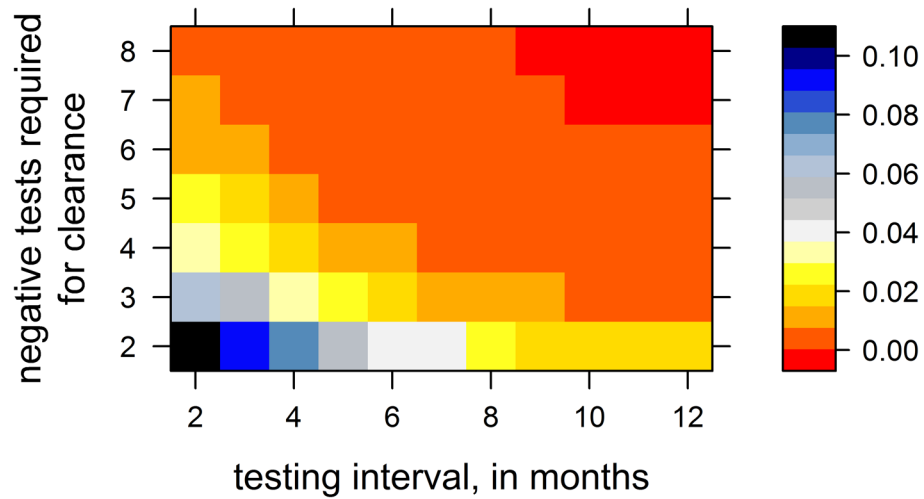
Figure 3.
Results of 100,000 iterations of a stochastic economic optimization algorithm applied to government costs associated with bovine tuberculosis detection in cow-calf herds. Costs were calculated using the national average for values that vary by region. Level (color) indicates frequency of visit by the optimization algorithm, with the optimal solution being that with a level closest to 1.
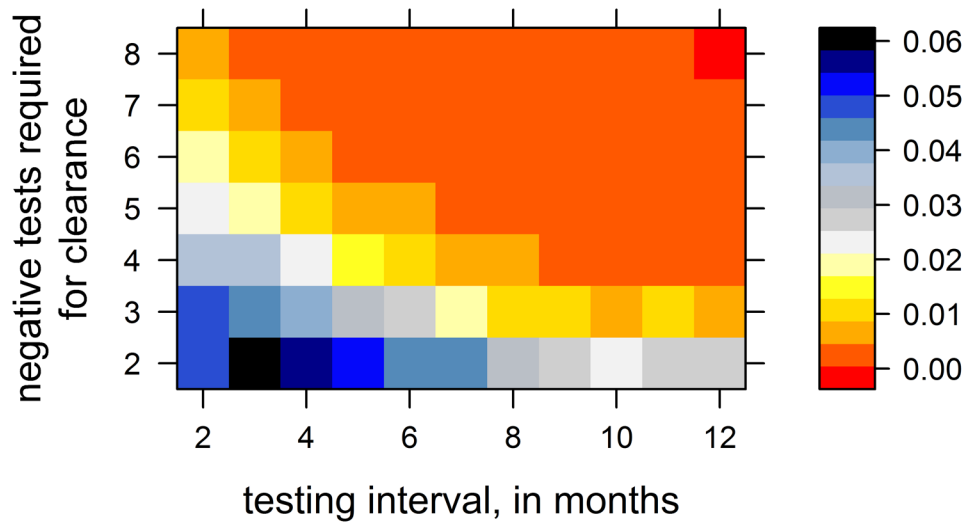
Figure 4.
Results of 1,000 iterations of a constrained stochastic economic optimization algorithm applied to government costs associated with bovine tuberculosis detection in cow-calf herds. The constrained optimizer was not allowed to prefer control strategies that led to herds falsely clearing quarantine. Costs were calculated using the national average for values that vary by region. Level (color) indicates frequency of visit by the optimization algorithm, with the optimal solution being that with a level closest to 1.
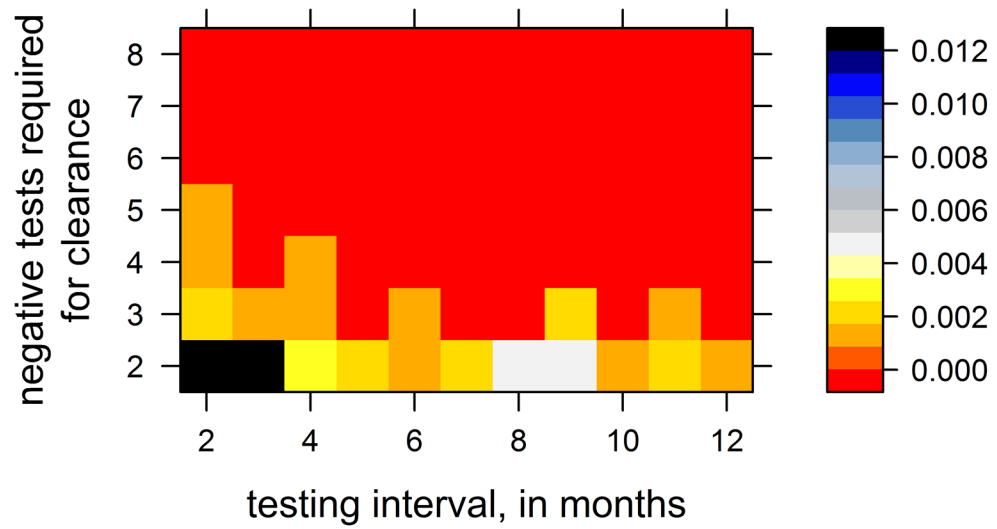
Figure 5.
Scenario analysis of the proportion of herds (out of 1000 iterations) considered to have cleared quarantine for bovine tuberculosis before the infection was truly eliminated. National-level parameters were used. Level (color) indicates frequency of occurrence.
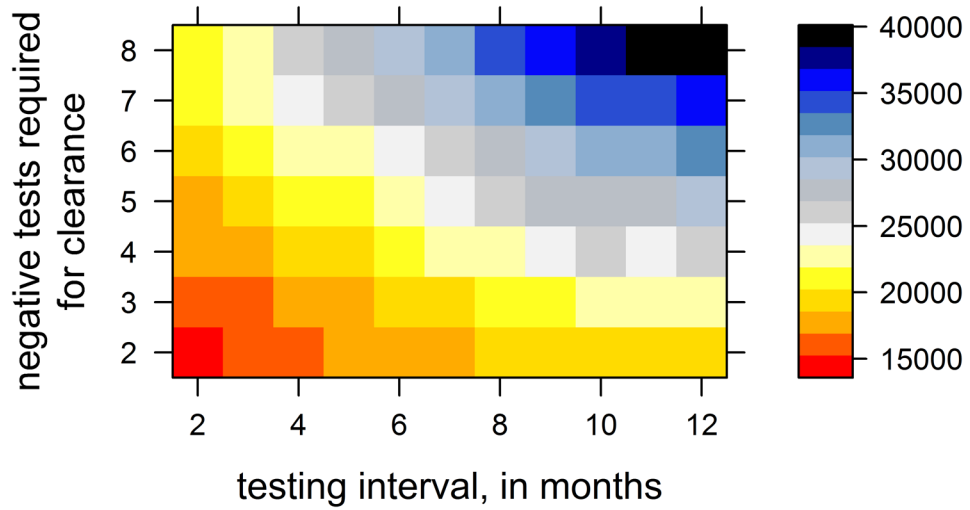
Figure 6.
Scenario analysis of the mean cost to the government (out of 1000 iterations) of a bovine tuberculosis outbreak in an average cow-calf herd with National-level parameters. Level (color) indicates mean cost to the government.
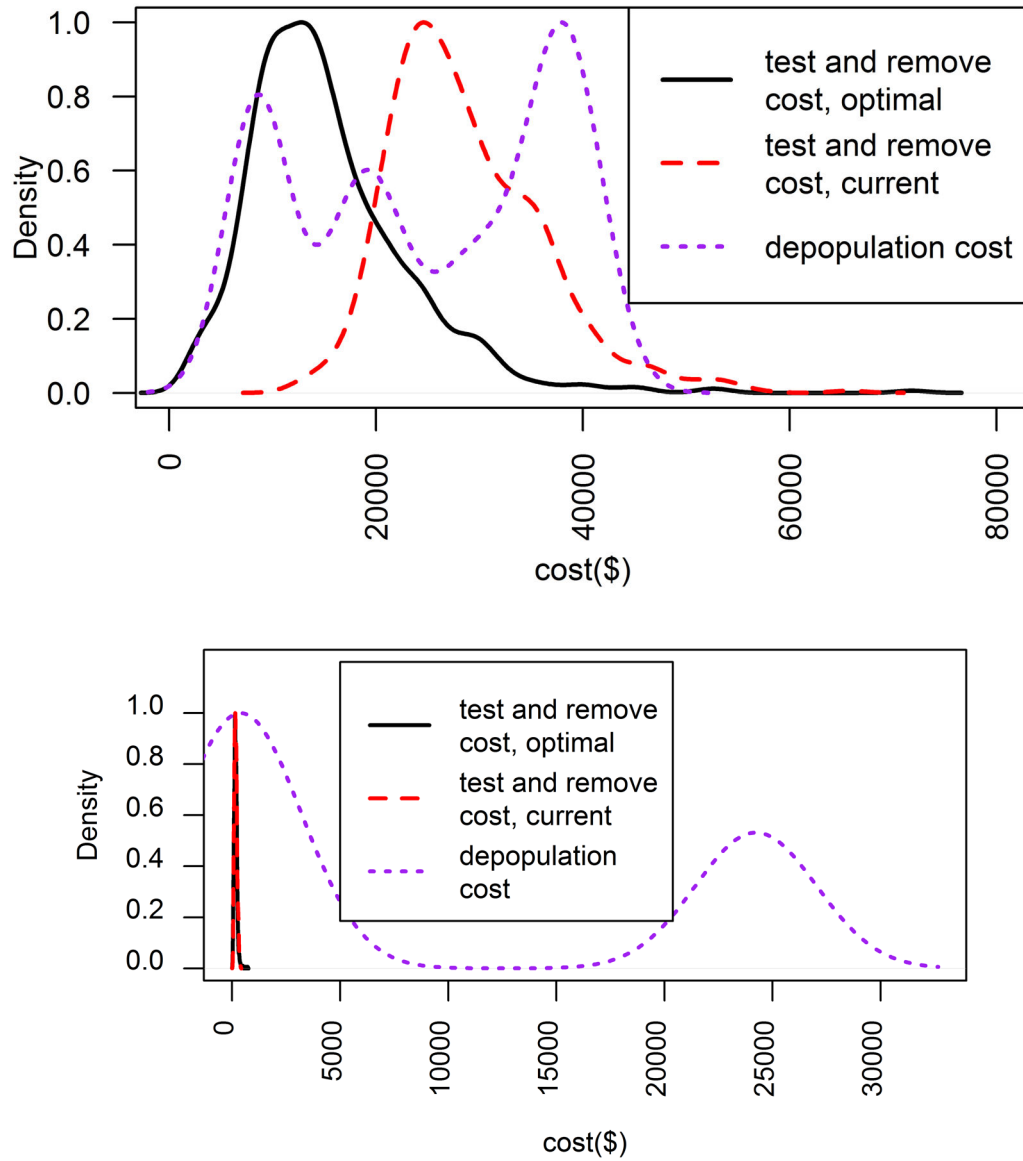
Figure 7.
Predicted cost distribution (over 1000 iterations) for government (a) and farms (b), using National-level parameters, for a bovine tuberculosis outbreak in an average cow-calf herd under either depopulation (purple short-dashed line), the historical test-and-removal program (USDA:APHIS:VS, 2005) (red long-dashed line), or optimal test-and-removal (black solid line) with a 3 month testing interval and 2 negative whole-herd tests needed to clear quarantine.
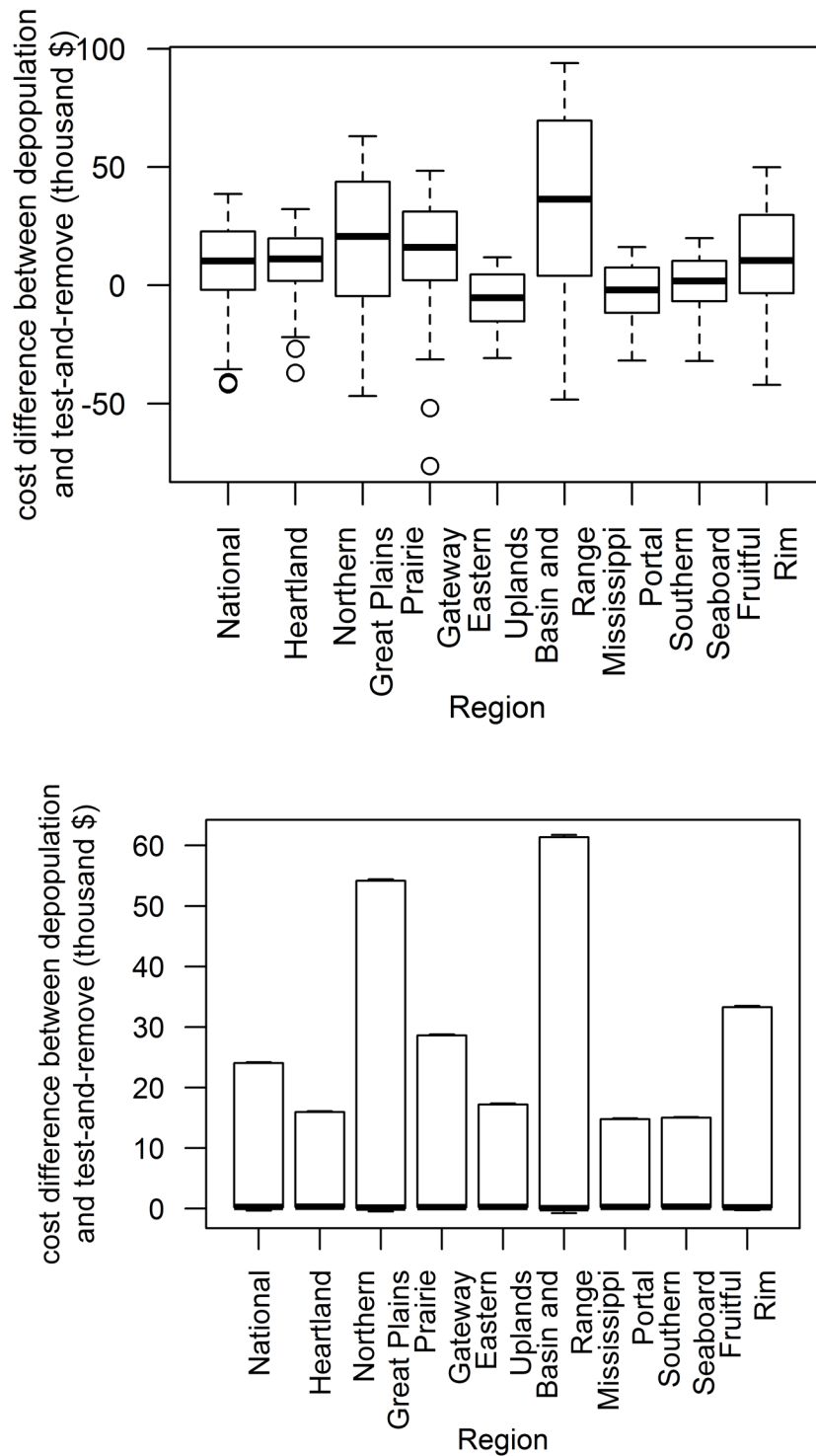
Figure 8.

Distribution of the cost difference between depopulation and the optimal test-and-removal program by region for government (a) and farms (b). Results are shown using the constrained optimal test-and-removal program (Table 4). Black lines indicate the median,

boxes indicate the upper and lower quartile, whiskers indicate the largest and smallest values within 1.5 times the interquartile range, and open circles indicate outliers.

Cost to Government

partial rank correlation coefficient
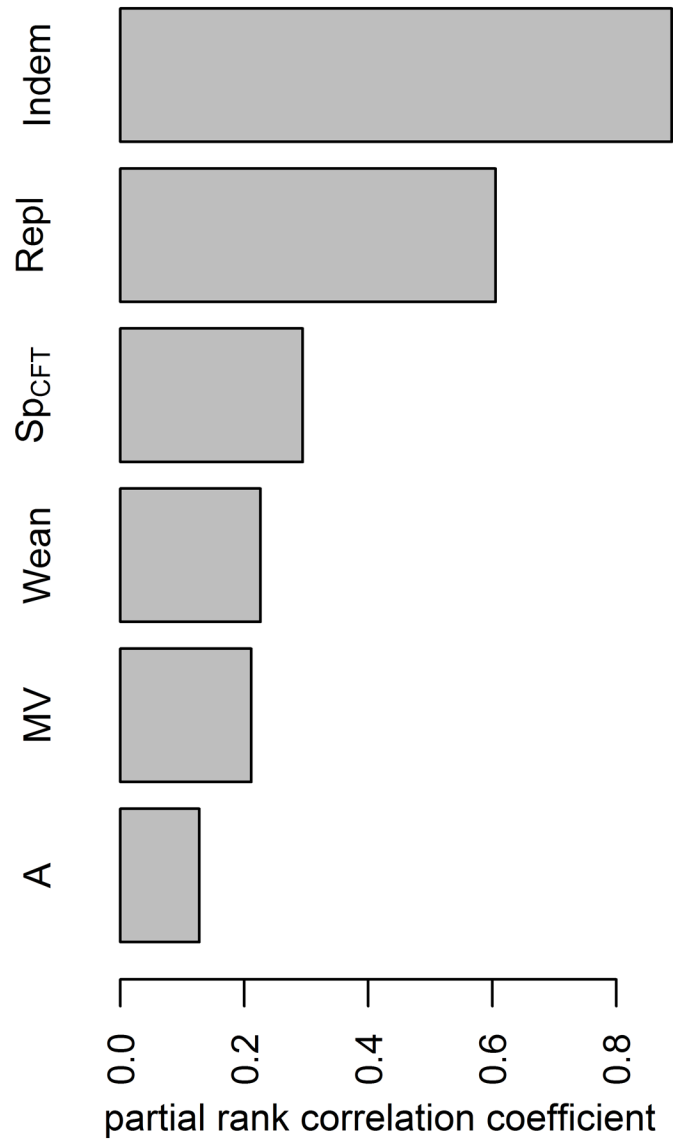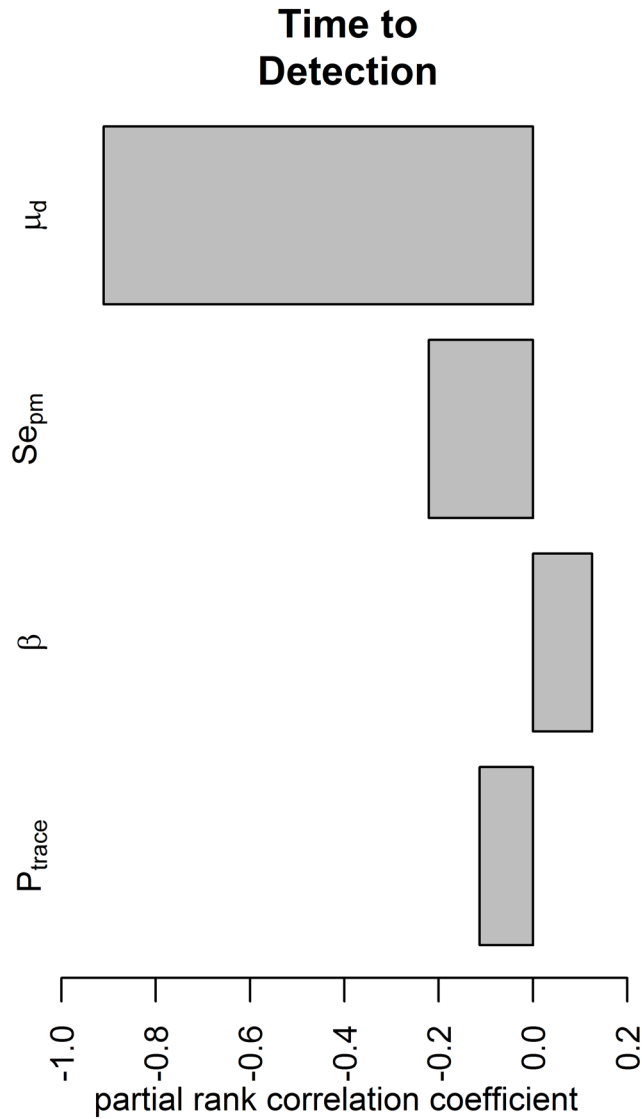
Figure 9.
Tornado plot showing the results of a global sensitivity analysis for a stochastic model predicting the cost to the government of a bovine tuberculosis outbreak in a cow-calf herd; variables shown are significantly related to the outcome with α=0.1 (using Bonferroni correction). *Indem* is the indemnity paid over the value of the animal, *Repl* is the cost of buying a replacement animal, Sp_{CFT} is the specificity of the CFT, MV is the market value of a calf, Wean is the weaning month, A is the test administration cost per animal, μ_d is the annual replacement rate, Se_{pm} is the sensitivity of the post-mortem (slaughterhouse) surveillance system, P_{trace} is the probability that an infected animal detected at slaughter will be traced back to its herd of origin, and β is the transmission coefficient.

Table 1

Costs, returns, and herd demographics for US cow-calf herds by region(USDA:ERS, 2012).

	Heartland	Northern Great Plains	Prairie Gateway	Eastern Uplands	Fruitful Rim	Basin and Range	Mississippi Portal	Southern Seaboard	National (average)
states included	IA, MO, IL, IN, OH, KY, NE, SD, MN	ND, SD, NE, MN, WY, MT, CO	TX, OK, KS, NE, CO, NM	KY, WV, VA, OH, PA, TN, NC, AL, GA	CA, AZ, OR, WA, ID, TX, FL, GA, SC	NV, CA, OR, WA, ID, MT, WY, CO, AZ, UT, NM	LA, MS, AR, TN	TX, LA, AR, MS, AL, GA, SC, NC, VA, DE, MD	
Average herd size (cow number)	63	182	108	78	133	258	74	68	100
calf death loss (%)[a]	16.9	11.2	16.5	19.0	14.8	18.4	23.4	20	17.2
Market Value ($/calf)[b]	351 (279, 426)	368 (309, 426)	367 (312, 426)	323 (256, 399)	334 (268, 408)	348 (277, 414)	328 (272, 387)	330 (266, 408)	338 (234, 489)
replacement cost ($/ cow)(USDA:NAS S, 2005)	979.51	734.29	868.57	518.93	775.83	793.30	592.86	721.74	789.91

[a] Calculated as 1-(calves weaned)/(number of cows)

[b] Average (range), 2005 to 201 0, assuming calves to weigh 300 pounds

Table 2

Parameter symbols, values, and sources used in the economic model for the cost of bovine tuberculosis control in a US cow-calf herd.

Parameter	Description	Value	Source
A	Skin test administration cost	$7.13/cow (5.77,11.33)	(Buhr et al., 2009)
M	Miles traveled by veterinarian	50 miles (40,60)	Assumed
MR	Mileage rate	$0.55/mile (0.445,0.585)	IRS (Internal Revenue Service, 2008)
P_{trace}	Probability of successfully tracing an animal detected at slaughter back to its source herd	0.33 (0.33,0.85)	(Wolf et al., 2008)
p_{PCR}	Price of PCR test	$271.25/animal (217,325.50)	(USAHA, 2004)
Salv	Salvage value of an adult cull animal	$80.00/cwt	USDA (National Agricultural Statistics Service and Agricultural Statistics Board, 2012)
Wt	Average salvage weight of an adult cull animal	1287 lbs (1250,1324)	USDA (USDA:NASS, 2007)
Sp_{CFT}	Specificity of caudal fold test	0.968 (0.755–0.99)	(de la Rua-Domenech et al., 2006)
Sp_{CCT}	Specificity of comparative cervical test	0.995 (0.788–1)	(de la Rua-Domenech et al., 2006)
Se_{CFT}	Sensitivity of caudal fold test to infectious or reactor cattle	0.839 (0.632–1)	(de la Rua-Domenech et al., 2006)
Se_{CCT}	Sensitivity of comparative cervical test	0.935 (0.75–0.955)	(de la Rua-Domenech et al., 2006)
Se_{pm}	Sensitivity of typical post-mortem inspection to infectious or reactor cattle	0.55 (0.285–0.95)	(Asseged et al., 2004)
Se_{PCR}	Sensitivity of enhanced post-mortem inspection to infectious or reactor cattle	1 (0.8–1)	assumed
β	Transmission rate	0.01/year (0.004–0.028)	(Barlow et al., 1997)
γ	Progression rate, latent to reactor	8.32 /year (8.32–26.07)	(Kao et al., 1997)
η	Progression rate, reactor to infectious	0.347 /year (0.347–4.06)	(Kao et al., 1997)
μ_d	annual replacement rate	0.17 (0.136–0.2)	assumed
disposal	Cost to dispose of infected carcasses	$75 (60–90)	
disinfect	Cost to disinfect a farm premises after depopulation	$400 (320–480)	(Wolf et al., 2008)
shipping	Cost to ship replacement cattle	$0.08/cow/mile (0.06–0.10)	(Beutler, n.d.)
distance	Distance replacement cattle are shipped	75 miles (60–90)	assumed

Table 3

Model results of government costs by region. T_{ti} is the testing interval, in months; N_{WHT} is the number of whole-herd tests required for the herd to clear quarantine. The historical government test-and-removal plan is as described in (USDA:APHIS:VS, 2005). All costs are thousands of US dollars per herd detected. A depopulation preference is noted when the cost of depopulation is predicted to be smaller than the cost of test-and-removal for that iteration; the depopulation preference is reported from the constrained optimal control strategy.

Region	Unconstrained Government Optimal T_{ti}, Nwht	Constrained[1] Government Optimal T_{ti}, Nwht	Unconstrained Optimal Government Cost (range)	Constrained[1] Optimal Government Cost (range)	Historical Government Cost (range)	Government Depopulation Cost (range)	Herds with Depopulation Preference /herd detected (proportion)
National	2,2	3,2	14.01 (2.13;68.9)	13.77 (2.07;71.82)	27.26 (12.5;65.7)	25.87 (6.99;43.73)	190/662 (0.29)
Heartland	2,2	2,2	14.13 (2.77;57.14)	14.48 (2.75;48.11)	23.41 (9.27;64.24)	27.39 (10.6;40.49)	133/630 (0.21)
Northern Great Plains	3,2	4,2	19.39 (2.86;66.65)	19.57 (2.81;75.91)	44.75 (21.57;80.13)	46.45 (5.17;72.8)	173/636 (0.27)
Prairie Gateway	2,2	3,2	17.77 (3.62;73.37)	17.85 (3.79;107.28)	33.14 (15.09;73.35)	38.72 (13.95;58.6)	133/652 (0.2)
Eastern Uplands	3,2	3,2	6.17 (−2.16;46.56)	6.24 (−1.32;32.28)	16.74 (4.96;39.63)	3.31 (−14.25;18.55)	378/651 (0.58)
Basin and Range	2,2	4,2	29.03 (4.77;131.8)	29.1 (5.18;91.96)	63.36 (31.82;121.85)	74.69 (19.36;110.7)	135/663 (0.2)
Mississippi Portal	3,2	4,2	7.71 (−0.59;38.03)	7.64 (−0.74;38.52)	17.87 (6.38;45.72)	7.1 (−7.71;20.01)	354/627 (0.56)
Southern Seaboard	3,2	3,2	10.54 (1.72;51.95)	10.5 (1.77;44.22)	19.66 (7.96;48.58)	14.34 (1.25;26.67)	290/628 (0.46)
Fruitful Rim	3,2	3,2	16.9 (3.12;76.42)	16.95 (3.11;93.7)	34.28 (15.5;82.71)	26.7 (8.02;60.17)	195/647 (0.3)

[1] Constrained optimal solutions rejected control plans resulting in false clearance of an infected herd in a given iteration.

Table 4

Constrained optimization model results of farm costs by region. T_{ti} is the testing interval, in months; N_{WHT} is the number of whole-herd tests required for the herd to clear quarantine. The historical government test-and-removal plan is as described in (USDA:APHIS:VS, 2005). All costs are thousands of US dollars per herd detected. A depopulation preference is noted when the cost of depopulation is predicted to be smaller than the cost of test-and-removal for that iteration.

Region	Farm Optimal Tti, Nwht	Optimal Farm Cost (range)	Historical Farm Cost (range)	Farm Depopulation Cost (range)	Herds with Depopulation Preference /herd detected (proportion)
National	2,2	0.16 (0.04;0.71)	0.16 (0.04;0.38)	0.40 (0.40;24.25)	4/642 (0.01)
Heartland	2,3	0.11 (0.02;0.42)	0.11 (0.02;0.31)	0.40 (0.40;16.12)	1/633 (0)
Northern Great Plains	2,3	0.27 (0.10;0.86)	0.28 (0.1;0.62)	0.41 (0.40;54.53)	32/626 (0.05)
Prairie Gateway	2,2	0.17 (0.04;0.5)	0.17 (0.04;0.44)	0.41 (0.40;28.84)	5/653 (0.01)
Eastern Uplands	2,3	0.13 (0.01;0.67)	0.13 (0.03;0.37)	0.40 (0.40;17.4)	4/649 (0.01)
Basin and Range	2,3	0.37 (0.13;1.15)	0.38 (0.11;0.89)	0.41 (0.4;61.89)	200/664 (0.3)
Mississippi Portal	2,2	0.12 (0.02;0.45)	0.12 (0.03;0.34)	0.40 (0.40;14.95)	1/610 (0)
Southern Seaboard	2,3	0.11 (0.01;0.27)	0.11 (0.02;0.32)	0.40 (0.40;15.16)	0/614 (0)
Fruitful Rim	2,2	0.2 (0.05;0.67)	0.21 (0.05;0.52)	0.41 (0.4;33.57)	5/619 (0.01)